

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:12:47 ; Search time 6749.08 Seconds
(without alignments)
11409.857 Million cell updates/sec

Title: US-10-056-454A-14_COPY_145_2790
Perfect score: 2646
Sequence: 1 ATGGTGATACACTCTCTGG.....AGCTAGTAGTAGAAGAGAA 2646

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sy:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	2646	100.0	2992	8	STU011890	AJ011890 Solanum t
2	2646	100.0	3033	6	A58164	A58164 Sequence 14
3	2581	97.5	3074	6	AR123355	AR123355 Sequence
4	2563.6	96.9	2982	8	STU011888	STU011888 Solanum t
5	2558.2	96.7	3231	6	A58168	A58168 Sequence 18
6	2551	96.4	3003	6	A58162	A58162 Sequence 12
7	2538	95.9	2955	8	STU011885	AJ011885 Solanum t
8	2514	95.0	2975	6	A58163	A58163 Sequence 13
9	2486.8	94.0	2563	6	AX256072	AX256072 Sequence
10	2471.6	93.4	2529	6	A58167	A58167 Sequence 17
11	2470.6	93.4	2523	8	STU011889	AJ011889 Solanum t
12	2465.8	93.2	2578	6	A58169	A58169 Sequence 19
13	2455	92.8	2576	6	A58166	A58166 Sequence 16
14	2435.6	92.0	2493	8	STSBEII	AJ000004 Solanum t
15	1708.6	64.6	3123	8	AB071286	AB071286 Ipomoea b
16	1509	57.0	2517	8	AB042937	AB042937 Ipomoea b
17	1429.4	54.0	3090	6	A92164	A92164 Sequence 30
18	1414.6	53.5	3360	8	AB029548	AB029548 Phaseolus
19	1370.4	51.8	3549	8	PSSBEIEN	X80009 P.sativum m
20	1369.8	51.8	1393	6	AR123356	AR123356 Sequence
21	1362	51.5	2913	6	A92162	A92162 Sequence 28
22	1317.4	49.8	2542	8	ATU22428	U22428 Arabidopsis
23	1290	48.8	2577	6	AX412751	AX412751 Sequence
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25	1285.2	48.6	2668	8	ATU18817	U18817 Arabidopsis
26	1270.8	48.0	1481	8	STU011891	AJ011891 Solanum t
27	1264.8	47.8	3015	6	E14723	E14723 Rice mRNA f
28	1264.8	47.8	3015	8	AB023498	AB023498 Oryza sat
29	1263.6	47.8	2364	6	E14724	E14724 Rice mRNA f
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33	1245	47.1	2795	8	ZMU65948	ZMU65948 Zea mays st
34	1243.6	47.0	2726	8	AF338432	AF338432 Triticum
35	1243.6	47.0	2970	8	AF286319	AF286319 Triticum
36	1242	46.9	2970	8	TASBA2	Y11282 T.aestivum
37	1240.4	46.9	2853	8	TAU66376	U66376 Triticum ae
38	1180.4	44.6	2725	6	AR106495	AR106495 Sequence
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41	644.6	24.4	2732	8	AB029549	AB029549 Phaseolus
42	641.4	24.2	2843	8	MESBERNA	X77012 M.esculenta
43	637.8	24.1	2493	8	STY08786	Y08786 S.tuberosum
44	636.2	24.0	3114	8	STSBE	X69805 S.tuberosum
45	632.4	23.9	2745	8	AF286317	AF286317 Triticum

ALIGNMENTS

RESULT 1
STU011890
LOCUS Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
DEFINITION A-6.
ACCESSION AJ011890
VERSION AJ011890.1 GI:4584512
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 2992)
AUTHORS Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,

Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2992)
Jobling, S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
Location/Qualifiers
1. .2992
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/cultivar="Desiree"
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/codon_start=1
/evidence=experimental
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/product="starch branching enzyme II"
/EC_number="2.4.1.18"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 140 ATGGTGTATACACTCTGGAGTTCGTTTTCTTCTACTGTTCCATCAGTGTACAAATCTAAT 199
QY 61 GGATTTCAGCAGTAATGGTGCAGGAGTAATGCTAATGTTCTGTTATCTTCTGAAAGAC 120
DB 200 GGATTTCAGCAGTAATGGTGCAGGAGTAATGCTAATGTTCTGTTATCTTCTGAAAGAC 259
QY 121 TCTCTTTTCACGAAGATCTTGGCTGAAAGTCTTCTTACAAATTCGAATTCGACCTTCT 180
DB 260 TCTCTTTTCACGAAGATCTTGGCTGAAAGTCTTCTTACAAATTCGAATTCGACCTTCT 319
QY 181 ACAGTTGCAGATCGGGAACTCTTGTGCTTGAACCCAGACGATGATGCTTCCATCC 240
DB 320 ACAGTTGCAGATCGGGAACTCTTGTGCTTGAACCCAGACGATGATGCTTCCATCC 379
QY 241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAAAATTCGCCAGCATCAACTGAT 300

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440 GTAGATAGTTCACAACAAATGGACACGCTAGCCAGATTAACACTGAGACGATGAGCTTGAG 499 Db
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500 CCGTCAAGTGAATCTTACAGGAAGTGTGAAGAGCTGGATTTTGGTTTCTTCACTCACTCAACTA 559 Db
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620 GATGAATCTGATAGGATCAGAGAGGGGATCCCTCCACCTTGCATGACCTTGGTCAGAAGATT 679 Db
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QY 181 ACAGTTGACATCGGGGAAAGTCCCTGTCGCTGGAAACCCAGAGTGATAGCTCCTCATCC 240
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2401 AAGCCTGGAAAATACAAAGGTTGCCCTGGACTCAGATGATCCACTTTTGGTGGCTTCGGG 2460
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2725 GAAGAAG 2784
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2641 GAAGAA 2646
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2785 GAAGAA 2790
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RESULT 3

AR123355
LOCUS AR123355 3074 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169226.
ACCESSION AR123355
VERSION AR123355.1 GI:14108321
KEYWORDS
SOURCE unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3074)
AUTHORS Ek, B., Khosnoodi, J., Larsson, C.-T., Larsson, H. and Rask, L.
TITLE Starch branching enzyme II of potato
JOURNAL Patent: US 6169226-A 1 02-JAN-2001;
FEATURES location/Qualifiers
source 1..3074
BASE COUNT 902 a 558 c 712 g 896 t 6 others
ORIGIN

Query Match 97.5%; Score 2581; DB 6; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 ATGTGTATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGATCAAAATCTAAT 60
DB 189 ATGTGTATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGATCAAAATCTAAT 248
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REFERENCE 1 (bases 1 to 2982)
AUTHORS Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M., Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
TITLE A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SBE II
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2982)
AUTHORS Jobling,S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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AUTHORS		Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,	
TITLE		Sidebottom, Christopher,M., and Westcott,R.J.	
JOURNAL		IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION	
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RESULT 6
LOCUS A58162 3003 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 12 from Patent WO9634968.
ACCESSION A58162
VERSION A58162.1 GI:3713887
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 3003)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
SIDEOTOM, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 12 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
COMMENT Other publication AU 550996 961121.
FEATURES
source
location/Qualifiers
BASE COUNT 895 a 535 c 706 g 867 t
ORIGIN
Query Match 96.4%; Score 2551; DB 6; Length 3003;
Best Local Similarity 98.3%; Pred. No. 0;
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RESULT 7
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LOCUS Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
DEFINITION A-1.
ACCESSION AJ011885
VERSION AJ011885.1 GI:4584502
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2955)
Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2955)
Jobling,S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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RESULT 8
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DEFINITION A58163
ACCESSION A58163
VERSION A58163.1 GI:3713888
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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unclassified.
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Sidebottom, Christopher,M. and Westcott,R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
Patent: WO 9634968-A 13 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
Other publication AU 5509996 961121.
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KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2529)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 17 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
COMMENT Other publication AU 5509996 961121.
FEATURES
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BASE COUNT 735 a 458 c 599 g 722 t 15 others
ORIGIN
Query Match 93.4%; Score 2471.6; DB 6; Length 2529;
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A58169 LOCUS A58169 2578 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 19 from Patent WO9634968.
ACCESSION A58169
VERSION A58169.1 GI:3713894
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 2578)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 19 07-NOV-1996;
NAT STARCH CHEM INVEST (US)
COMMENT Other publication AU 550996 961121.
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A	H	Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,		
A	H	Sidebottom, Christopher,M. and Westcott,R.J.		
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RESULT 14
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DEFINITION AJ000004
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VERSION AJ000004.1 GI:2764395
KEYWORDS Sbe-II gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2493)
Larsson,C.T.A.
Direct Submission
Submitted (30-JUN-1997) Larsson C.T.A., Department of Cell
Research, Genetic Center, Swedish University of Agricultural
Sciences, Box 7035, S-750 07 Uppsala, SWEDEN
2 (bases 1 to 2493)
Larsson,C.T., Khosnoodi,J., Ek,B., Rask,L. and Larsson,H.
Molecular cloning and characterization of starch-branching enzyme
II from potato
Plant Mol. Biol. 37 (3), 505-511 (1998)
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QY	1138	GGGTACAAATGCGCTGCAAAATTTAGCTATTTCAAGAGCAATTCATATTACGTAGTTTGGT	1197

Db	2329	CAAGAAATTTGACCAAGCTATGCAATCACTCTGAGAAAAAATACGGCTTCATGACGGCNAAA	2338
Qy	2278	CACCAGTTCATATCACGAAAGAGTAGAGAGATGATGTTGATTGAAAAAGGAAAC	2337
Db	2389	CACCAGTACATATCACCCAGGAGAGAGATAGGCTGATCATTTTGAAGGGGTGAC	2448
Qy	2338	CTAGTTTTTGTCTTAAATTTCACTGACGAAAAAGCTATTTCAGACTATCCGATAGCCTGC	2397
Db	2449	CTGCTGTTTGTCTTCAATTTCCACTGCACAAATAGTTATTTCAGATTACCGTGTAGGCTGC	2508
Qy	2398	CTGAAGCCTGGAATAATCAAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGCTTC	2457
Db	2509	TTAAAGCAGGAAAATATAAGGTAGCCTCGACTCCGACACTCGCTGTTTGGAGGGCTTT	2568
Qy	2458	GGGAGAATTGATCATATATGCGGAATTTTCACCTTTCAAGGATGGTATGATGATCGTCTC	2517
Db	2569	GGCAGAGTTTCAACCCGATGCNAAATTTTTCATTTCAAGGGGTATCAGGATGATCGTCTC	2628
Qy	2518	CGTTCAATATATGGTGTATGCACCTTGTAAACAGCAGTGGTCTATGACACTAGTAGACAAA	2577
Db	2629	CGTTCCCTTCATGGTGTACGCCACCCAGTAGAACTCGACTGGTGTACGCTCTACGCAAGGAG	2688
Qy	2578	GAAGAAGAAGAAGAGAAGAAGAAGAG	2608
Db	2689	CAGGACCAAGCAAAAACCAAGTTGAGCAATG	2719

Search completed: July 5, 2003, 17:58:41
Job time : 6772.08 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 12:28:17 ; Search time 551.364 Seconds
(without alignments)
10807.357 Million cell updates/sec

Title: US-10-056-454A-14_COPY_145_2790

Perfect score: 2646

Sequence: 1 ATGGTGTATACACTCTCTGG.....AAGTAGTAGTAGAAGAGAA 2646

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2646	100.0	3033	17	AA42630
2	2584.2	97.7	3074	18	AA42630
3	2558.2	96.7	3251	17	AA42632
4	2551	96.4	3003	17	AA42634
5	2512.4	95.0	2975	17	AA42635
6	2486.8	94.0	2563	23	ARK50301
7	2471.2	93.4	2531	17	AA42637
8	2468.4	93.3	2529	17	AA42637
9	2465.8	93.2	2578	17	AA42631

10	2451.8	92.7	2576	17	AA42636
11	1429.4	54.0	3090	19	AAV38720
12	1362	51.5	2913	19	AAV38719
13	1290	48.8	2715	21	AA45939
14	1264.8	47.8	3015	19	AAV05639
15	1251.2	47.3	2919	15	AAQ73750
16	1243.6	47.0	2726	22	AAH78337
17	1183.6	44.7	2640	19	AAV70961
18	1180.4	44.6	2665	18	AAV69729
19	1180.4	44.6	2725	19	AAV29757
20	1167.2	44.1	3039	24	ABK15494
21	1164	44.0	2968	22	AAH78342
22	1044.6	39.5	2307	21	AAZ99938
23	1033	39.0	2087	18	AAV69737
24	1031.4	39.0	2165	18	AAV69736
25	956.6	36.2	1919	19	AAV38722
26	728.8	27.5	1452	21	AAAC36957
27	632.4	23.9	4563	22	AAAF30910
28	631.4	23.9	3128	16	AAAT00774
29	628.4	23.7	2487	18	AAV69747
30	628.4	23.7	2565	18	AAV69752
31	628.4	23.7	2763	19	AAV29758
32	628.4	23.7	2771	13	AAQ24257
33	628.4	23.7	2772	18	AAV69740
34	617.2	23.3	2909	13	AAQ27778
35	610	23.1	2687	20	AAAX34646
36	603	22.8	2733	15	AAQ54674
37	603	22.8	2733	15	AAQ62135
38	589	22.3	2713	19	AAV70962
39	578.2	21.9	3075	24	AAAS94880
40	576.6	21.8	2899	22	AAH02926
41	576.6	21.8	2955	24	ABN95650
42	542	20.5	1809	18	AAV69753
43	542	20.5	1865	18	AAV69748
44	535.8	20.2	770	23	ABK50302
45	501.6	19.0	728	23	ABK50303

ALIGNMENTS

RESULT 1
AA42630
ID AA42630 standard; DNA; 3033 BP.
XX
AC AA42630;
XX
DT 25-FEB-1997 (first entry)
XX
DE Class A starch branching enzyme (19con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT CDS 145..2793
FT sig_peptide /*tag= a
FT FT 145..288
FT mat_peptide /*tag= b
FT FT 289..2790
FT FT /*tag= c
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XX WO9634968-A2.
XX
XX 07-NOV-1996.
XX
XX 03-MAY-1996; 96WO-GB01075.
XX
XX 10-APR-1996; 96GB-0007409.
XX
XX 05-MAY-1995; 95GB-0009229.
XX

Class A starch bra
Full length cassav
Full length cassav
Arabidopsis thalia
Rice type IV starc
Rice starch branch
Nucleotide sequenc
DNA encoding maize
Plasmid pBE240 ins
Zea mays starch br
Wheat starch branch
Nucleotide sequenc
DNA encoding part
Corn starch branch
Corn starch branch
cDNA encoding star
Arabidopsis thalia
Wheat starch branch
Potato starch bran
Corn starch branch
Corn starch branch
Zea mays starch br
Branching enzyme D
Plasmid pBE5 inse
Potato amylose-amy
wSBE I-D4 cDNA seq
Rice starch branch
Rice starch branch
DNA encoding maize
Human DNA sequence
Human shear stress
Gene #2148 used to
Corn starch branch
Corn starch branch
Potato starch bran
Potato starch bran

(NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
PA Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
DR P-PSDB; AAW06399.
XX New potato plant starch having high amylose content - also class A
PT starch branching enzymes and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX Claim 28-30; Page 42-46; 142pp; English.
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX Sequence 3033 BP; 900 A; 553 C; 712 G; 868 T; 0 other;
SQ
Query Match 100.0%; Score 2646; DB 17; Length 3033;
Best Local Similarity 100.0%; Pred. No 0;
Matches 2646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 145 ATGGTGATACACTCTCTGGAGTTCGTTTTCTCTACTCTTCCATCCAGTGTACAAATCTAAT 204
QY 61 GGATTCAGCAGTAATGTGATCGAGGAATGCTAATGTTCTGATTTCTTGAAGAAGCAC 120
DB 205 GGATTCAGCAGTAATGTGATCGAGGAATGCTAATGTTCTGATTTCTTGAAGAAGCAC 264
QY 121 TCTCTTTACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCGGAATCCGACCTTCT 180
DB 265 TCCTTTACGGAAGATCTTGGCTGAAAAGTCTTCTTACAATTCGGAATCCGACCTTCT 324
QY 181 ACAGTTCAGCAATCGGGAAGTCTTGTGCTGGAAGCCAGAGTGTATCTCTCATCC 240
DB 325 ACAGTTCAGCAATCGGGAAGTCTTGTGCTGGAAGCCAGAGTGTATCTCTCATCC 384
QY 241 TCAACAGACCAATTTGATTCACCTGAGACATCTCCAGAAATCCCGACATCAACTGAT 300
DB 385 TCAACAGACCAATTTGATTCACCTGAGACATCTCCAGAAATCCCGACATCAACTGAT 444
QY 301 GTAGATAGTTCACAAATGGAACAGCTAGCCAGATTAATACTGAGAAGTGTGAG 360
DB 445 GTAGATAGTTCACAAATGGAACAGCTAGCCAGATTAATACTGAGAAGTGTGAG 504
QY 361 CCGTCAAGTATCTTACAGGAAGTGTGAGAGAGCTGGATTTGCTTCACTACAACATA 420
DB 505 CCGTCAAGTATCTTACAGGAAGTGTGAGAGAGCTGGATTTGCTTCACTACAACATA 564
QY 421 CAAGAAGTGTAAACTGGAGAGTGTAAACATTAATACTCTGGAAGACAAATTAAT 480
DB 565 CAAGAAGTGTAAACTGGAGAGTGTAAACATTAATACTCTGGAAGACAAATTAAT 624
QY 481 GATGAATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGAGTGTGTCAGAAAGAT 540
DB 625 GATGAATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGAGTGTGTCAGAAAGAT 684
QY 541 TATGAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGATTCAGAGTATTCACAG 600
DB 685 TATGAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGATTCAGAGTATTCACAG 744
QY 601 TACAAGAACTGAGGAGGCAATGACAAGTATGAGGTGTTTGGAAAGCCCTTTTCTCGT 660
DB 745 TACAAGAACTGAGGAGGCAATGACAAGTATGAGGTGTTTGGAAAGCCCTTTTCTCGT 804
QY 661 GGTATGAAAAAATGGGTTTCACTCGTGTGTCAGGTATCATCTTACCGTGTGAGTGGCT 720
DB 805 GGTATGAAAAAATGGGTTTCACTCGTGTGTCAGGTATCATCTTACCGTGTGAGTGGCT 864
QY 721 CTTGGTGCACAGTCAGCTGCCCTCATTTGAGATTTCAACAATTTGGAGCCAAATGCTGCAC 780

DB 865 CTTGGTGCACAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGAGCCGAAATGCTGCAC 924
QY 781 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGCAAAATTAATGTGATGGT 840
DB 925 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGCAAAATTAATGTGATGGT 984
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DB 985 TCTCTGCAATTCCTCATGGTCCAGAGTGAAGATAGATATGAGACATCTCCATCATCGAGTGT 1044
QY 901 AAGGATTCATTCCTGCTGGATCAACTACTCTTTTACAGCTTCCTGATGAATTTCCATAT 960
DB 1045 AAGGATTCATTCCTGCTGGATCAACTACTCTTTTACAGCTTCCTGATGAATTTCCATAT 1104
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QY 1021 AAGAAACCAAGTCGCTGAGAAATATGAATCTCATATTTGAAATGAGTAGTCCGAGGCT 1080
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QY 1081 AAAATTTACTCATACGTGAATTTTAGAGATCAAGTCTTCTCCGATAAAAAGCTTGG 1140
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QY 1141 TACAATGGCTGCAAAATTTAGCTATTTCAAGAGCATTTCTTATAGCTTAGTTTGGTTAT 1200
DB 1285 TACAATGGCTGCAAAATTTAGCTATTTCAAGAGCATTTCTTATAGCTTAGTTTGGTTAT 1344
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DB 1345 CATGTCAAAATTTTGGACCAAGAGCCGTTTGGAAAGCCGCGAGACCTTAAGTCT 1404
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DB 1405 TTGATTTGAAGTCAATGAGTATGGAATTTGTTCTCATGGAATTTGTTCAAGCCAT 1464
QY 1321 GCATCAAAATTAATTTAGATGGACTGAACATTTTGTACTGCACCGATAGTGTACTTT 1380
DB 1465 GCATCAAAATTAATTTAGATGGACTGAACATTTTGTACTGCACCGATAGTGTACTTT 1524
QY 1381 CACTCTGGAGCTGCGGTTATCATTTGGATGAGGATTTCCCGCTCTTTAACTATGGAAC 1440
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DB 1705 GGATTCATGGGAATCAGGGAATACCTTTGGACTGCGCAACTGATGATGCTGTTG 1764
QY 1621 TATCTGATGCTGCTCAAGCATCTTATTCATGGGCTTTTCCAGATGCAATTAACATTTGGT 1680
DB 1765 TATCTGATGCTGCTCAAGCATCTTATTCATGGGCTTTTCCAGATGCAATTAACATTTGGT 1824
QY 1681 GAAGATTTAGGGGAATGCGGACATTTTGTATTCCTGCTCCAGAGGGGGTGTGCTGCTT 1740
DB 1825 GAAGATTTAGGGGAATGCGGACATTTTGTATTCCTGCTCCAGAGGGGGTGTGCTGCTT 1884
QY 1741 GACTATCGCTGCTATATGCAATTTCTGATAAGGATTTGAGTTCTCAAGAAACGGGAT 1800
DB 1885 GACTATCGCTGCTATATGCAATTTCTGATAAGGATTTGAGTTCTCAAGAAACGGGAT 1944
QY 1801 GAGGATTTGAGAGTGGGTGATATTTCTATACACTGACAAATAGAGATGGTCGGAAGAG 1860

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Db 1945 GAGGATTGGAGATGGGTGATATTTTCATACACTGACAAATAGAGATGGTCGAAAG 2004
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QY 2041 GAAGGGTACCTAAATTTTCATGGGAAATGAATTCGGCCACCGCTGAGTGATTTCCCT 2100
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QY 2521 TCAATTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 2665 TCAATTTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2724
QY 2581 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGAGAA 2640
Db 2725 GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAAGAAGTAGTAGAGAA 2784
QY 2641 GAAGAA 2646
Db 2785 GAAGAA 2790
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RESULT 2

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AAAT69587
ID AAAT69587 standard; cDNA; 3074 BP.
XX
AC AAAT69587;
XX
DT 26-AUG-1997 (first entry)
XX
DE Potato starch branching enzyme II gene (beII).
XX
KW Starch branching enzyme II; beII gene; potato; transgenic plant;
KW amylopectin; amylose; starch; ss.
XX
OS Solanum tuberosum.
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XX Key Location/Qualifiers
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FT sig_peptide 189..332
FT /*tag= b
FT mat_peptide 333..2822
FT /*tag= c
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PN WO9720040-A1.
XX
XX 05-JUN-1997.
XX
XX 28-NOV-1996; 96WO-SE01558.
XX
XX 19-APR-1996; 96SE-0001506.
XX 29-NOV-1995; 95SE-0004272.
XX
XX (EXBB/) EK B.
XX (KIOS/) KHOSNOODI J.
XX (LARS/) LARSSON C.
XX (LARS/) LARSSON H.
XX (RASK/) RASK L.
XX (AMYL-) AMYLOGENE HB.
XX
XX Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;
XX
XX WPI; 1997-310596/28.
XX P-PSDB; AAW19113.
XX
XX Isolated potato starch branching enzyme II - useful for altering
XX degree of amylopectin branching and amylopectin/amylose ratio in
XX potato starch
XX
XX Claim 4: Page 12-15; 24pp; English.
XX
XX A cDNA clone (AAAT69587) codes for potato starch branching enzyme II
XX (BEII) (AAW19113). It was isolated from potato tuber cDNA by PCR
XX amplification using primers (AAAT69588-89) based on tryptic peptides
XX of isolated BEII; the 5' and 3' ends of the sequence were detd. by
XX RACE. A vector comprising the whole or a functional active part of
XX the isolated sequence (sense or antisense), plus regulatory
XX sequences active in potato, can be used to produce transgenic
XX potatoes. The starch obtd. from such plants will show a changed
XX pattern of amylopectin branching and an altered amylopectin/amylose
XX ratio.
XX
XX Sequence 3074 BP; 902 A; 560 C; 710 G; 896 T; 6 other;
XX
XX Query Match 97.7%; Score 2584.2; DB 18; Length 3074;
XX Best Local Similarity 98.7%; Pred. No. 0;
XX Matches 2601; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 1 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGATCAATCTAAT 60
Db 189 ATGGTGTATACACTCTCTGGAGTTCGTTTTCCTACTGTTCCATCAGTGATCAATCTAAT 248
QY 61 GGATTCAGCAGTAATGGTGTATCGGAGGATGCTAATGTTCTTCTGTTTGAAGAACGAC 120
Db 249 GGATTCAGCAGTAATGGTGTATCGGAGGATGCTAATGTTCTTCTGTTTGAAGAACGAC 308
QY 121 TCTCTTTCAGGGAAGATCTTGGCTGAAAGTCTTCTTACAAATTCGGAATTCGACCTTCT 180
Db 309 TCTCTTTCAGGGAAGATCTTGGCTGAAAGTCTTCTTACAAATTCGGAATTCGACCTTCT 368
QY 181 ACAGTTGACGATCGGGGAAGTCTTGTGCTTGGACCCAGACAGTATAGCTCTCATCC 240
Db 369 ACAGTTGACGATCGGGGAAGTCTTGTGCTTGGACCCAGACAGTATAGCTCTCATCC 428
QY 241 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAATTCGCCAGCACTCACTGAT 300
Db 429 TCAACAGACCAATTTGAGTTCACTGAGACATCTCCAGAAATTCGCCAGCACTCACTGAT 488
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QY	301	GTAGATAGTTCACAAATGGAACACGCTAGCCAGATTAATAAAGTGAAGACGATGACGTTGAG	360		1569	CACCTCTGGAGCTCGTGGTTATCATTTGGATTTGGGATTCGCCCTCTTTAACTATGGAAC	1628
Db	489	GTAGATAGTTCACAAATGGAACACGCTAGCCAGATTAATAAAGTGAAGACGATGACGTTGAG	548		1441	TGGAGGTACTTAGGTATCTCTCTCAATTCAGAGATGGTGGTGGATGGTTCAAATTT	1500
QY	361	CGGTCAAGTGAATCTTACAGGAAGTGTGTAAGAGCTGGATTTGCTTCACTACACAACTA	420		1629	TGGAGGTACTTAGGTATCTCTCTCAATTCAGAGATGGTGGTGGATGGTTCAAATTT	1688
Db	549	CGGTCAAGTGAATCTTACAGGAAGTGTGTAAGAGCTGGATTTGCTTCACTACACAACTA	608		1501	GATGGATTTAGATTTGATGGTGCACATCAATGATGATATTCACCAACGGATTCGGTG	1560
QY	421	CAAGAGGTGGTAAACTGGAGGAGTCTAAACATTAATTAATCTCTGAAGAGCAATATTT	480		1689	GATGGATTTAGATTTGATGGTGCACATCAATGATGATATTCACCAACGGATTCGGTG	1748
Db	609	CAAGAGGTGGTAAACTGGAGGAGTCTAAACATTAATTAATCTCTGAAGAGCAATATTT	668		1561	GGATTCCTGGGAACACGAGGAGATCTTTGGACTCGCACTGATGGGATGCTGTTG	1620
QY	481	GATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACCTGGACTTGGTCAAGAAGATT	540		1749	GGATTCCTGGGAACACGAGGAGATCTTTGGACTCGCACTGATGGGATGCTGTTG	1808
Db	669	GATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACCTGGACTTGGTCAAGAAGATT	728		1621	TATCTGATGCTGGTCAACGATCTTATTCATCTGGGCTTTTCCACAGATGCAATTAACCAATTTGGT	1680
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QY	601	TACAAGAACTGAGGAGGCAATTCACAAGTATGAGGGTGGTTTGAAGGCTTTTCTCGT	660		1869	GAAGATGTTAGCGGAATGCCGACATTTTGTATTTCCCGTCCAGAGGGGGTGTGGCTTT	1928
Db	789	TACAAGAACTGAGGAGGCAATTCACAAGTATGAGGGTGGTTTGAAGGCTTTTCTCGT	848		1741	GACTATCGCTGCATATGGCAATTCGTGATTAACGGATTCGATTTGCTCAAGAAACGGGAT	1800
QY	661	GGTTATCAAAAAATGGGTTTCACTCGTGTGCTACAGGTATTCATTCACCGTGTGGGCT	720		1929	GACTATCGCTGCATATGGCAATTCGTGATTAACGGATTCGATTTGCTCAAGAAACGGGAT	1988
Db	849	GGTTATCAAAAAATGGGTTTCACTCGTGTGCTACAGGTATTCATTCACCGTGTGGGCT	908		1801	GAGGATTTGGAGAGTGGGTGATTTGTTTATCTATACACTGACAAATAGAAGATGGTTCGAAAG	1860
QY	721	CTTGGTGCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAATTCGTAC	780		1989	GAGGATTTGGAGAGTGGGTGATTTGTTTATCTATACACTGACAAATAGAAGATGGTTCGAAAG	2048
Db	909	CCTGGTGCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAATTCGTAC	968		1861	TGCTTTTCACTACCGTGAAGATTCATGCAAGCTCTAGTCGGTGATAAAGTATGACATTC	1920
QY	781	ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGCAAAATATTTGGATGGT	840		2049	TGCTTTTCACTACCGTGAAGATTCATGCAAGCTCTAGTCGGTGATAAAGTATGACATTC	2108
Db	969	ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGCAAAATATTTGGATGGT	1028		1921	TGGCTGATGGACAAGGATATGATGATTTTATGCTCTGATAGACCTCAACATCAATTA	1980
QY	841	TCCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGAGACATCOATCAGGTGTT	900		2109	TGGCTGATGGACAAGGATATGATGATTTTATGCTCTGATAGACCTCAACATCAATTA	2168
Db	1029	TCCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGAGACATCOATCAGGTGTT	1088		1981	ATAGATCGTGGGATAGCATTCACAAAGATGATTTAGGCTTGAATATGGGATTTAGGAGA	2040
QY	901	AGGATTCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCTGATGAAATTCATAT	960		2169	ATAGATCGTGGGATAGCATTCACAAAGATGATTTAGGCTTGAATATGGGATTTAGGAGA	2228
Db	1089	AGGATTCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCTGATGAAATTCATAT	1148		2041	GAAGGTACCTTAATTTTCACTGGGAAATTCGCGCCACCTGATGGATGATTTCCCT	2100
QY	961	AATGGAATACATTTATGATCCACCGAAGAGAGAGGTATATCTTCCAAACACCCAGGCCA	1020		2229	GAAGGTACCTTAATTTTCACTGGGAAATTCGCGCCACCTGATGGATGATTTCCCT	2288
Db	1149	ANTGGAATATATPATGATCCACCGAAGAGAGAGGTATATCTTCCAAACACCCAGGCCA	1208		2101	AGGCTGAACAAACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGAT	2160
QY	1021	AAGAAACCAAGTCGCTGAGAAATATATGATCTCATATTTGGAATGAGTAGTCCGAGCCT	1080		2289	AGGCTGAACAAACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGAT	2348
Db	1209	AAGAAACCAAGTCGCTGAGAAATATATGATCTCATATTTGGAATGAGTAGTCCGAGCCT	1268		2161	AAATGCAGACGAGAGATTTGACCTGGGAGATGCGAANAATTTAAGATACCGTGGTTCGAA	2220
QY	1081	AAATTAACATACAGTGAATTTTAGAGATGAAGTCTTCTCTGCAATAAAGCTTGGG	1140		2349	AAATGCAGACGAGAGATTTGACCTGGGAGATGCGAANAATTTAAGATACCGTGGTTCGAA	2408
Db	1269	AAATTAACATACAGTGAATTTTAGAGATGAAGTCTTCTCTGCAATAAAGCTTGGG	1328		2221	GAATTTGACCGGCTTATGCACTATCTTCAAGTAAATATGATTTGATCTTCAAGAAC	2280
QY	1141	TACAATGGCTGCAAAATATGGCTATTCAAGAGCATTTCTTAATACGTAGTTTGGTTAT	1200		2409	GAATTTGACCGGCTTATGCACTATCTTCAAGTAAATATGATTTGATCTTCAAGAAC	2468
Db	1329	TACAATGGCTGCAAAATATGGCTATTCAAGAGCATTTCTTAATACGTAGTTTGGTTAT	1388		2281	CAGTTTCAATCACGAAAGGATGAAGGATAGGATGATTTGATTTTGAAGAAAGAACCTA	2340
QY	1201	CATGTCACAAATTTTGGACCAAGCAGCGGTTTGGACCGCGGACGACCTTAAGTCT	1260		2469	CAGTTTCAATCACGAAAGGATGAAGGATAGGATGATTTGATTTTGAAGAAAGAACCTA	2528
Db	1389	CATGTCACAAATTTTGGACCAAGCAGCGGTTTGGACCGCGGACGACCTTAAGTCT	1448		2341	GTTTTGTCTTTAATTTTCACTGGACAAAAGCTATTCAGACTATTCGATAGCCTGCTG	2400
QY	1261	TTGATTTGATTAAGCTCAGTACCTAGGATTTGCTCTCATGGACATTTGTCACAGCCAT	1320		2529	GTTTTGTCTTTAATTTTCACTGGACAAAAGCTATTCAGACTATTCGATAGCCTGCTG	2588
Db	1449	TTGATTTGATTAAGCTCAGTACCTAGGATTTGCTCTCATGGACATTTGTCACAGCCAT	1508		2401	AAGCCTGAAAATAACAAGTTCCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGG	2460
QY	1321	GCATCAATAATACTTTAGATGGACTGAACATGTTTGAAGTGCACCGGAGTGTGTTACTTT	1380		2589	AAGCCTGAAAATAACAAGTTCCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGG	2648
Db	1509	GCATCAATAATACTTTAGATGGACTGAACATGTTTGAAGTGCACCGGAGTGTGTTACTTT	1568		2461	AGAATTGATCAATATGCGCAATTTTTCACCTTTGAAGGATGATGATGATGCTGCTCT	2520
QY	1381	CACCTCGAGCTCGTGGTTATCATTTGGAATGTTGGGATTCGCCCTCTTTAACTATGGAAC	1440				

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Db 2649 AGAATTGATCATAATGCGCAATATTTACCTTTGAAGGATGGTATGATGATGCTCTCGT 2708
QY 2521 TCAATTATGGTGTATGCACTTGTAAACACAGCAGTGGTCTATGCACTAGTAGACAAGAA 2580
Db 2709 TCNATTATGGTGTATGCACTTGTAAACACAGCAGTGGTCTATGCACTAGTAGACAAGAA 2768
QY 2581 GAAGAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2634
Db 2769 GAAGAAGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2822

RESULT 3
AAT42632
ID AAT42632 standard; DNA; 3231 bp.
XX
AC AAT42632;
XX
DT 25-FEB-1997 (first entry)
XX
DE Class A starch branching enzyme (psbe2con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT misc_RNA 45..3200
FT /*tag= a
FT /*note= "claim 34"
FT CDS 228..2855
FT /*tag= c
FT
PN WO9634968-A2.
XX
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
XX
PA (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
XX
DR WPI; 1996-506170/50.
XX
PT New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
PS Claim 31, 34; Page 53-55; 142pp; English.
XX
CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
CC The same sequence is given in Figure 8, however, nucleotides
CC 1-44 omitted.
XX
XX
SQ Sequence 3231 bp; 960 A; 577 C; 739 G; 947 T; 8 other;

Query Match 96.7%; Score 2558.2; DB 17; Length 3231;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2584; Conservative 2; Mismatches 45; Indels 0; Gaps 0;

QY 1 ATGGTGATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGTACAATCTAAT 60
Db 228 ATGGTGATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGTACAATCTAAT 287
QY 61 GGATTCAGCAGTAATGGTGATCGGAGGAATGCTAAAGTGTCTGTATTTGAAAGACAC 120
Db 1427 TACAATCGGTGCAAAATTAATGGCTATTCAGAGCATCTTATTATGCTAGTTTGGTTAT 1427
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QY 1201 CATGTCACAAATTTTTCACCAAGCAGCCGTTTGGAAACGCCGACGACCTTAAGTCT 1260
Db 1428 CATGTCACAAATTTTTCACCAAGCAGCCGTTTGGAAACGCCGACGACCTTAAGTCT 1487
QY 1261 TTGATGATAAAGCTCATGAGCTAGGAATTTGTTCTCTCATGACATGTTTTCACAGCCAT 1320
Db 1488 TTGATGATAAAGCTCATGAGCTAGGAATTTGTTCTCTCATGACATGTTTTCACAGCCAT 1547
QY 1321 GCATCAAAATTAATCTTAGATGACGACGACATGTTTGACGACCGCATAGTTGTTACTTT 1380
Db 1548 GCATCAAAATTAATCTTAGATGACGACGACATGTTTGACGACCGCATAGTTGTTACTTT 1607
QY 1381 CACTCTGGAGCTCGTGGTTATCAATTTGATGCGGATTCGCCGCTCTTTTAACTATGGAAC 1440
Db 1608 CACTCTGGAGCTCGTGGTTATCAATTTGATGCGGATTCGCCGCTCTTTTAACTATGGAAC 1667
QY 1441 TGGAGGTACTTAGGTATCTCTCTCAAAATCGGAGATGGTGGTGGATGGTTCCAATTT 1500
Db 1668 TGGAGGTACTTAGGTATCTCTCTCAAAATCGGAGATGGTGGTGGATGGTTCCAATTT 1727
QY 1501 GATGGATTTAGATTTGATGTTGACATCAATGATGATATATTCACACGCGATATCGGTG 1560
Db 1728 GRTGGATTTAGATTTGATGTTGACATCAATGATGATATATTCACACGCGATATCGGTG 1787
QY 1561 GGATTCACCTGGGAACACTACGAGGAACTTTGGACTCGCAACTGATGTGGATCGTGTG 1620
Db 1788 GGATTCACCTGGGAACACTACGAGGAACTTTGGACTCGCAACTGATGTGGATCGTGTG 1847
QY 1621 TATCTGATGCTGGTCAACGATCTTATTCATGCGGCTTTTCCGACGATGCAATACCATTGGT 1680
Db 1848 TATCTGATGCTGGCAGCATCTTATTCATGCGGCTTTTCCGACGATGCAATACCATTGGT 1907
QY 1681 GAGATCTTAGCGGAATGCGGACATTTGATTTCCGCTGCCAAGAGGGGGTGTGGCTTT 1740
Db 1908 GAGATCTTAGCGGAATGCGGACATTTGATTTCCGCTGCCAAGAGGGGGTGTGGCTTT 1967
QY 1741 GACTATCGGCTGCATATGGCAATTCGTGATAAAGCGATTCAGTTGCTCAAGAAACGGGAT 1800
Db 1968 GACTATCGGCTGCATATGGCAATTCGTGATAAAGCGATTCAGTTGCTCAAGAAACGGGAT 2027
QY 1801 GAGATTTGGAGAGTGGGTGATATTTGATCACTGACATGACAAATAGAGATGTCGGAAG 1860
Db 2028 GAGATTTGGAGAGTGGGTGATATTTGATCACTGACATGACAAATAGAGATGTCGGAAG 2087
QY 1861 TGTCTTTACATCGCTGAAAGTCATGCAAGCTCTAGTCGGGTGATAAACTATAGCATTC 1920
Db 2088 TGTCTTTACATCGCTGAAAGTCATGCAAGCTCTAGTCGGGTGATAAACTATAGCATTC 2147
QY 1921 TGGCTGATGGACAAGGATATGATGATTTTATGCTCTGGATAGACCGTCAACATCAPTA 1980
Db 2148 TGGCTGATGGACAAGGATATGATGATTTTATGCTCTGGATAGACCGTCAACATCAPTA 2207
QY 1981 ATAGATCGTGGATAGCATTCACCAAGATGATTAGGCTTGTAACTATGGGATAGGAGA 2040
Db 2208 ATAGATCGTGGATAGCATTCACCAAGATGATTAGGCTTGTAACTATGGGATAGGAGA 2267
QY 2041 GAAGGTACCTAAATTTTCATGGGAAATGAATTCGCCACCTCGATGGATTGATTCCT 2100
Db 2268 GAAGGTACCTAAATTTTCATGGGAAATGAATTCGCCACCTCGATGGATTGATTCCT 2327
QY 2101 AGGCTGAACACACCTCTCTGATGGCTCAGTAAATPCCCGGAAACCAATTCAGTTATGAT 2160
Db 2328 AGGCTGAACACACCTCTCTGATGGCTCAGTAAATPCCCGGAAACCAATTCAGTTATGAT 2387
QY 2161 AAATTCGACGAGATTTGACCTGGGAGATCGAGATATTTAAAGTACCGTGGTGGAA 2220
Db 2388 AAATTCGACGAGATTTGACCTGGGAGATCGAGATATTTAAAGTACCGTGGTGGAA 2447
QY 2221 GAATTTGACCGGCTATGACGATCTCTGAAGATAAATATGATGATTTTATGACTTCAGAAC 2280
Db 2448 GAATTTGACCGGCTATGACGATCTCTGAAGATAAATATGATGATTTTATGACTTCAGAAC 2507

QY 2281 CAGTTCATATCAGAAAGGATGAAGGAGATAGGATGATGTTTGTAAAGGAACCTA 2340
Db 2508 CAGTTCATATCAGAAAGGATGAAGGAGATAGGATGATGTTTGTAAAGGAACCTA 2567
QY 2341 GTTTTGTCTTTTAAATTTTCACTGGACAAAAGCTATTTCAGACTATCCAGATAGGCTGCTG 2400
Db 2568 GTTTTGTCTTTTAAATTTTCACTGGACAAAAGCTATTTCAGACTATCCAGATAGGCTGCTG 2627
QY 2401 AAGCTGGAAAATCAAGGTTGCCCTTGCACTCAGATGATCCACATTTTGTGGTTCGGG 2460
Db 2628 AAGCTGGAAAATCAAGGTTGCCCTTGCACTCAGATGATCCACATTTTGTGGTTCGGG 2687
QY 2461 AGAATTGATCATATGCGGAATATTTTCACTTTGAAGATGGTATGATGCTCCTCGT 2520
Db 2688 AGAATTGATCATATGCGGAATATTTTCACTTTGAAGATGGTATGATGCTCCTCGT 2747
QY 2521 TCAATTATGGTGTATGACACCTTTGAAAACACAGCTGGTCTATGCACCTAGTAGACAAGAA 2580
Db 2748 TCAATTATGGTGTATGACACCTTTGAAAACACAGCTGGTCTATGCACCTAGTAGACAAGAA 2807
QY 2581 GAAGAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAGAGAGTA 2631
Db 2808 GAAGAAGAAGAAGAAGAAGAAGTAGCAGCAGTAGAGAGAGTA 2858
RESULT 4
AAT42634
ID AAT42634 standard; DNA; 3003 BP.
XX
AC AAT42634;
XX
DT 03-MAR-1997 (first entry)
XX
DE Class A starch branching enzyme (10con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
PN W09634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
XX
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
DR WPI; 1996-506170/50.
XX
PT New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
PS Example 1; Page 38-39; 142pp; English.
XX
CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
SQ Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;
Query Match 96.4%; Score 2551; DB 17; Length 3003;
Best Local Similarity 98.3%; Pred. No. 0;
Matches 2589; Conservative 0; Mismatches 45; Indels 1; Gaps 1;
QY 1 ATGGGTATATACACTCTCTGGAGTTTCGTTTCTTCTACTGTTCATCTCCATCAGTACAGTAATCTAAT 60

PT New transformed plants with reduced endogenous starch branching enzyme
PT and heterologous glucan branching enzyme activities, useful for
PT producing starch with improved properties, which is in the food, paper
PT and chemical industries -
XX
XX
XX Example 1; Page 31-35; 61pp; English.
XX
XX The invention relates to a transformed organism, preferably a transformed
CC plant, having a reduced endogenous starch branching enzyme (SBE)
CC activity, and having a heterologous glucan branching enzyme (SBE)
CC activity. The reduced SBE activity is effected via expression of a
CC nucleotide sequence that is antisense to at least part of a SBE exon.
CC Also included are a method of producing starch with altered
CC characteristics comprising (a) providing a plant having reduced
CC endogenous SBE activity, and having heterologous SBE activity
CC (b) propagating the plant of (a) and optionally (c) obtaining starch
CC from the plant; starch obtainable from the transformed plant; and
CC a nucleic acid construct capable of directing the expression
CC of all or part of one or more antisense SBE exons and optionally one or
CC more heterologous SBE. The transformed plants are useful for producing
CC starch with modified and improved properties, which is an important raw
CC material and used in the food, paper and chemical industries. The
CC present sequence encodes Potato SBE II, used to make transgenic plants of
CC the invention.
XX
XX Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;
SQ

Query Match 94.0%; Score 2486.8; DB 23; Length 2563;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2512; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 65 TCAGCAGTATGTGATCGGAGGAACTGCTAACTGTTCTGTTATCTTGGAAAGACACTCTC 124
DB 1 TCAGCAGTATGTGATCGGAGGAACTGCTAACTGTTCTGTTATCTTGGAAAGACACTCTC 60

QY 125 TTTACGGAAGATCTTGGCTGAAAGTCTTCTTACAAATTCGGAATTCGGACCTCTACAG 184
DB 61 TTTACGGAAGATCTTGGCTGAAAGTCTTCTTACAAATTCGGAATTCGGACCTCTACAG 120

QY 185 TTGCAGCATCGGGGAAAGTCTTGTGCTGGACCCAGCTGATAGTCTCTCAPCCCTCAA 244
DB 121 TTGCAGCATCGGGGAAAGTCTTGTGCTGGACCCAGCTGATAGTCTCTCAPCCCTCAA 180

QY 245 CAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAATTCGCCAGCATCACTGATGATG 304
DB 181 CAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAATTCGCCAGCATCACTGATGATG 240

QY 305 ATAGTTCAACAATGGACACGCTAGCCAGATTTAAACTGAGACGATGACGTTGAGCCGT 364
DB 241 ATAGTTCAACAATGGACACGCTAGCCAGATTTAAACTGAGACGATGACGTTGAGCCGT 300

QY 365 CAAGTGATCTTACAGGAAGTGTGAGACGCTGGATTTTGGTTCTATCACTACAACTACAAG 424
DB 301 CAAGTGATCTTACAGGAAGTGTGAGACGCTGGATTTTGGTTCTATCACTACAACTACAAG 360

QY 425 AAGTGGTAACTGGAGAGTCTAAAACATTAATATCTCTGGAAGACAAATTTATGATG 484
DB 361 AAGTGGTAACTGGAGAGTCTAAAACATTAATATCTCTGGAAGACAAATTTATGATG 420

QY 485 AATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGACTTGGTCAGAGATTTATG 544
DB 421 AATCTGATAGATCAGAGAGGGGATCCCTCCACCTGGACTTGGTCAGAGATTTATG 480

QY 545 AAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGTATTCAGAGTATTCACAGTACA 604
DB 481 AAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGTATTCAGAGTATTCACAGTACA 540

QY 605 AGAACTGAGGAGGCAATTCAGCAAGTATGAGGTTGGTTTGGAGCCCTTTCTCGTGGTT 664
DB 541 AGAACTGAGGAGGCAATTCAGCAAGTATGAGGTTGGTTTGGAGCCCTTTCTCGTGGTT 600

QY 665 ATGAAAAATGGGTTTCTACTCTAGTCTACAGTATCACTTACCGTGAGTGGGCTCTTG 724
DB 661 ATGAAAAATGGGTTTCTACTCTAGTATTAATGATTTAGTTTCTGTCAGAAACGGGATGAG 1740

DB 601 ATGAAAAATGGGTTTCTACTCGTAGTCTACAGGATFACATTTACCGTGAAGTGGCTCTCTG 560
QY 725 GTCCCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAAATTTGGAGCGCAAAATGCTGACATTA 784
DB 661 GTCCCCAGTCAGCTGCCCTCATTTGGAGATTTCAACAAATTTGGAGCGCAAAATGCTGACATTA 720
QY 785 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATTAATGTCGATGGTTCTC 844
DB 721 TGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATTAATGTCGATGGTTCTC 780
QY 845 CTGCAATTCCTCATGGTCCAGAGTGAAGATGATGAGACTTCCATCATCAGGTGTTAAGG 904
DB 781 CTGCAATTCCTCATGGTCCAGAGTGAAGATGATGAGACTTCCATCATCAGGTGTTAAGG 840
QY 905 ATTCCATTCCTGCTTGGATCAACTACCTCTTACAGCTTCTCTGATGAAATTCCTCAATATAATG 964
DB 841 ATTCCATTCCTGCTTGGATCAACTACCTCTTACAGCTTCTCTGATGAAATTCCTCAATATAATG 900
QY 965 GAATACATATGATGATCCACCGAGAGAGAGGTATATCTTCCACACCCACGCGCAAGA 1024
DB 901 GGATATATATGATGATCCACCGAGAGAGAGGTATATCTTCCACACCCACGCGCAAGA 960
QY 1025 AACCAAGTCGTCAGAAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGGCTAAAA 1084
DB 961 AACCAAGTCGTCAGAAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGGAACTAAAA 1020
QY 1085 TTAACATCATACGCTGAATTTTAGAGATGAAGTCTTCTCTCGCATAAAAAGCTTGGGTACA 1144
DB 1021 TTAACATCATACGCTGAATTTTAGAGATGAAGTCTTCTCTCGCATAAAAAGCTTGGGTACG 1080
QY 1145 ATGGCTGCAAAATTTATGCTATTCAGAGCATCTTATTACGCTAGTCTTGGTTATCATG 1204
DB 1081 ATGGCTGCAAAATTTATGCTATTCAGAGCATCTTATTATGCTAGTCTTGGTTATCATG 1140
QY 1205 TCACAAATTTTTTGCACCAAGCAGCCGTTTGGAGCCGCGGACGCTTAAAGTCTTTGA 1264
DB 1141 TCACAAATTTTTTGCACCAAGCAGCCGTTTGGAGCTCCGAGCAGCTTAAAGTCTTTGA 1200
QY 1265 TTGATAAGCTCATGAGCTAGGAATTTGTTCTTCATCGGACATTTGTCACAGCATGATG 1324
DB 1201 TTGATAAGCTCATGAGCTAGGAATTTGTTCTTCATCGGACATTTGTCACAGCATGATG 1260
QY 1325 CAATAATACCTTATGAGTGAACATGTTTGTGCTGACCGAGTAGTGTGTTACTTCTACT 1384
DB 1261 CAATAATACCTTATGAGTGAACATGTTTGTGCTGACCGAGTAGTGTGTTACTTCTACT 1320
QY 1385 CTGAGCTCGTGGTTATCAITGGATTTGGGATTTCCGCTCTTTAACTATGAGAACTGGG 1444
DB 1321 CTGAGCTCGTGGTTATCAITGGATTTGGGATTTCCGCTCTTTAACTATGAGAACTGGG 1380
QY 1445 AGGTACTAGTATCTCTCTCAATGCGGATGTTGGTGGATGCGGTTCAAAATTTGATG 1504
DB 1381 AGGTACTAGTATCTCTCTCAATGCGGATGTTGGTGGATGCGGTTCAAAATTTGATG 1440
QY 1505 GATTAGATTTGATGGTGTGACATCAATGATGATATTCACACGAGTATTCGCTGGGAT 1564
DB 1441 GATTAGATTTGATGGTGTGACATCAATGATGATATTCACACGAGTATTCGCTGGGAT 1500
QY 1565 TCAGTGGAACTACGAGGAATTTTGGACTTCGCAACTGATGTCGATGCTGTGTGTATC 1624
DB 1501 TCAGTGGAACTACGAGGAATTTTGGACTTCGCAACTGATGTCGATGCTGTGTGTATC 1560
QY 1625 TGATGCTGGTCAACATCTTATTCATGGGCTTTTCCAGATGCAATTCACATTTGGTGAAG 1684
DB 1561 TGATGCTGGTCAACATCTTATTCATGGGCTTTTCCAGATGCAATTCACATTTGGTGAAG 1620
QY 1685 ATGTTAGCGGAATCGCGACATTTTGTATTTCCGTCGCAAGAGGGGGTGTGGCTTTGACT 1744
DB 1621 ATGTTAGCGGAATCGCGACATTTTGTATTTCCGTCGCAAGATGGGGTGTGGCTTTGACT 1680
QY 1745 ATCGGCTGCATGATGCAATTTGCTGATAAAGCAATTTGCTTCAAGAAACGGGATGAGG 1804
DB 1681 ATCGGCTGCATGATGCAATTTGCTGATAAAGCAATTTGCTTCAAGAAACGGGATGAGG 1740

QY	1805	ANTGGAGATGGGTGATATTTGTTTCATACACTGCACAAATAGAAGATGTCGCGAAAGTGTG	1864
DB	1741	ANTGGAGATGAGTGAATTTGTTTCATACACTGCACAAATAGAAGATGTCGCGAAAGTGTG	1800
QY	1865	TTTCATACGCTGAAGTCATGATCAAGCTCTAGTCGGTGATAAACTATAGCATTTCTGGC	1924
DB	1801	TTTCATACGCTGAAGTCATGATCAAGCTCTAGTCGGTGATAAACTATAGCATTTCTGGC	1860
QY	1925	TGATGGACAAGGATATGATGATTTTATGCTCTGGATAGACCGTCACATCATTAATAG	1984
DB	1861	TGATGGACAAGGATATGATGATTTTATGCTCTGGATAGACCGTCACATCATTAATAG	1920
QY	1985	ATCGTGGGATAGANTCCACAGATGATTAGGCTTTACTATGGATTAGGAGGAGAAG	2044
DB	1921	ATCGTGGGATAGANTCCACAGATGATTAGGCTTTACTATGGATTAGGAGGAGAAG	1980
QY	2045	GGTACCTTAAATTTTCATGGGAAATGAATTCGGCCACCCCTGAGTGGATTTCCCTTAGGG	2104
DB	1981	GGTACCTTAAATTTTCATGGGAAATGAATTCGGCCACCCCGAGTGGATTTCCCTTAGGG	2040
QY	2105	CTGAACAACACCTCTCTGATGGCTCAGTAAATCCCGGAACCAATTCAGTTATGATAAAT	2164
DB	2041	CTGAACAACACCTCTCTGATGGCTCAGTAAATCCCGGAACCAATTCAGTTATGATAAAT	2100
QY	2165	GCAGACGGAGATTGACCTGGGAGATGCAGAAATTTAGATACCGTGGTTCGAAGAAT	2224
DB	2101	GCAGACGGAGATTGACCTGGGAGATGCAGAAATTTAGATACCGTGGTTCGAAGAAT	2160
QY	2225	TTGACCGGCTATGTCAGTATCTTGAAGATAAATATCAGTTTATGACTTTCAGAACCACT	2284
DB	2161	TTGACCGGCTATGTCAGTATCTTGAAGATAAATATCAGTTTATGACTTTCAGAACCACT	2220
QY	2285	TCATATCAGAAAGGATGAAGGATAGGATGATTGTTTGTAAAGAAAGAAACCTAGTTT	2344
DB	2221	TCATATCAGAAAGGATGAAGGATAGGATGATTGTTTGTAAAGAAAGAAACCTAGTTT	2280
QY	2345	TTGCTCTTAAITTTTCTACTGGACAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGC	2404
DB	2281	TTGCTCTTAAITTTTCTACTGGACAAAAGCTATTCAGACTATCGCATAGCCTGCCTGAAGC	2340
QY	2405	CTGGAATAACAGGTTGGCTTTGGACTCAGATGATCCACTTTTTTGGTGGCTTCGGAGAA	2464
DB	2341	CTGGAATAACAGGTTGGCTTTGGACTCAGATGATCCACTTTTTTGGTGGCTTCGGAGAA	2400
QY	2465	TTGATCATAAATCCGGAATATTTTCACCTTTTGAAGGATGGTATGATCATCTCTCTGTTCAA	2524
DB	2401	TTGATCATAAATCCGGAATATTTTCACCTTTTGAAGGATGGTATGATCATCTCTCTGTTCAA	2460
QY	2525	TTATGTTGTATGCACCTTGTAACACAGCATGGTCTATTCACACTAGTACAGAAAGAAAG	2584
DB	2461	TTATGTTGTATGCACCTTAGGACAGCAGTGGTCTATTCACACTAGTACAGAAAGAAAG	2520
QY	2585	AGAAGAAGAAGAAGAAGAAGTAGCAGC	2618
DB	2521	AGAAGAAGTAGCAGTAGTAGAAGAAGATGAAC	2554

RESULT 7

RESULT /
DATA17267

DATE / 20 /
TD DATE

AAI
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YY

XX

AC
AAT

33

DT 03-1

XX 3

DE Class:

XX

KW Sta:

KW amy

XX

So solar

XX

PN	W09G34968-A2.
XX	
XX	07-NCV-1996.
PF	
XX	03-MAY-1996; 96WO-GH01075.
XX	
PR	10-APR-1996; 96GB-0007409.
PR	05-MAY-1995; 95GB-0009229.
XX	
PA	(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX	
PI	Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI	Sidebottom CM, Westcott RJ;
XX	
DR	WPI; 1996-506170/50.
DR	P-PSDB; AAR93804.
XX	
PT	New potato plant starch having high amylose content - also class A
PT	starch; branching enzyme and corresp. DNA to alter the viscosity of
PT	starch; for use in food, biodegradable products, adhesives, etc.
XX	
PS	Example 1; Fig 9; 142pp; English.
XX	
CC	Class A starch branching enzyme (SBE) has been obtained from
CC	potatoes. In class A SBE mols., a flexible N-terminal domain,
CC	is found, which is not found in class B mols.
CC	This sequence was obtained by direct sequencing of PCR fragments
CC	amplified from first strand cDNA. Nucleotides which could not
CC	be unambiguously assigned are indicated using standard IUPAC
CC	notation.
XX	
SQ	Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;

Query Match	93.4%	Score 2471.2;	DB 17;	Length 2531;
Best Local Similarity	98.2%;	Pred. No. 0;		
Matches 2482;	Conservative	11;	Mismatches	34;
			Indels	0;
			Caps	0;

QY	87	GAATGCTAAATGTTTCTGTATCTTGAAAAAGCACTCTCTTTTACGGGAAGATCTTGCTGA	146
Db	1	GGATGCTAAATGTTTCTGTATCTTGAAAAAGCACTCTCTTTTACGGGAAGATCTTGCTGA	60
QY	147	AAAGTCTTCTTACAAATTCGAAATTCGACCTTCTACAGTTGCGAGCAFCGGGGAAAGTCCT	206
Db	61	AAAGTCTTCTTACAAATTCGAAATTCGACCTTCTACAGTTGCGAGCAFCGGGGAAAGTCCT	120
QY	207	TGTGCTTGGAAACGACAGATGATAGTCTCATCTCTCAACAGACCAATTTTACGTTTCACTGA	266
Db	121	TGTGCTTGGAAACGACAGATGATAGTCTCATCTCTCAACAGACCAATTTTACGTTTCACTGA	180
QY	267	GACATCTCCAGAAAAATTCGCCAGCATCAACTGATGTAGATAGTTTCAACAATGGACACGC	326
Db	181	GACATCTCCAGAAAAATTCGCCAGCATCAACTGATGTAGATAGTTTCAACAATGGACACGC	240
QY	327	TAGCCAGATTAAACATGAGAACGATCAAGTTGAGCCGTCAGTGATCTTTACAGGAAGTGT	386
Db	241	TAGCCAGATTAAACATGAGAACGATCAAGTTGAGCCGTCAGTGATCTTTACAGGAAGTGT	300
QY	387	TGAAGAGCTGGATTTTGGCTTCATCACTTACAACATACAAGAAGTGTTGAATCTGAGGAGTCT	446
Db	301	TGAAGAGCTGGATTTTGGCTTCATCACTTACAACATACAAGAAGTGTTGAATCTGAGGAGTCT	360
QY	447	TAAACATTAATPACTTCTGAAGAGACAATTTATGATGAATCTGATAGGATCAGAGAGAG	506
Db	361	TAAACATTAATPACTTCTGAAGAGACAATTTATGATGAATCTGATAGGATCAGAGAGAG	420
QY	507	GGGCATCCCTCCACCTGGACCTTGGTCAGAAGATTTATGAAATAGACCCCTTTTGACAAA	566
Db	421	GGGCATCCCTCCACCTGGACCTTGGTCAGAAGATTTATGAAATAGACCCCTTTTGACAAA	480
QY	567	CTATCGTCAACACCTTTGATTACAGGTTATTCACAGTACAGAACCTGAGGGAGGCAATTGA	626
Db	481	CTATCGTCAACACCTTTGATTACAGGTTATTCACAGTACAGAACCTGAGGGAGGCAATTGA	540

Class A starch branching enzyme (direct sequencing).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum; amylose; viscosity; potato; ss.

Solanum tuberosum.

XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX Solanum tuberosum.
XX WO9634968-A2.
XX 07-NOV-1996.
XX 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
XX 05-MAY-1995; 95GB-0009229.
XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX Example 1; Page 51-53; 142pp; English.
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;
Query Match 93.3%; Score 2468.4; DB 17; Length 2529;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2481; Conservative 10; Mismatches 36; Indels 0; Gaps 0;
QY 87 GAATGCTAATGTTCTGTATCTTGAAGAAGCAGCTCTCTTACAGGAAGATCTTGCTGA 146
DB 1 GGATGCTAATGTTCTGTATCTTGAAGAAGCAGCTCTCTTACAGGAAGATCTTGCTGA 60
QY 147 AAAGTCTTCTTACAATTCGAATTCGACCTTCTACAGTTGCGAGCATCGGGGAAGTCCT 206
DB 61 AAAGTCTTCTTACAATTCGAATTCGACCTTCTACAGTTGCGAGCATCGGGGAAGTCCT 120
QY 207 TGTGCTGGAAATCCAGAGTGAAGTCCCTCATCTTCAACAGCAATTTGAGTTCACTGA 266
DB 121 TGTGCTGGAAATCCAGAGTGAAGTCCCTCATCTTCAACAGCAATTTGAGTTCACTGA 180
QY 267 GACATCTCCAGAAATTTCCCGAGCATCAACTGATGTAGATAGTTCAACAAATGGAACACGC 326
DB 181 GACATCTCCAGAAATTTCCCGAGCATCAACTGATGTAGATAGTTCAACAAATGGAACACGC 240
QY 327 TAGCCAGATTAAACTGGAAGCATGACGTTGAGCGGTCAAGTGAATCTTACAGGAAGTGT 386
DB 241 TAGCCAGATTAAACTGGAAGCATGACGTTGAGCGGTCAAGTGAATCTTACAGGAAGTGT 300
QY 387 TGAAGAGCTGGATTTTGTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 446
DB 301 TGAAGAGCTGGATTTTGTCTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 360
QY 447 TAAACATTAATACTCTTGAAGACAAATTTATGATGAATCTGATAGGATCAGAGAGAG 506
DB 361 TAAACATTAATACTCTTGAAGACAAATTTATGATGAATCTGATAGGATCAGAGAGAG 420
QY 507 GGGCATCCCTCACTGAGCTTGGTTCAGAAATTTATGAATAGACCCCTTTTGACAAA 566
DB 421 GGGCATCCCTCACTGAGCTTGGTTCAGAAATTTATGAATAGACCCCTTTTGACAAA 480
QY 567 CTATCGTCAACACCTTGATTACAGGTATTCAGATACAGAACTGAGGAGGCAATTGA 626
DB 481 CTATCGTCAACACCTTGATTACAGGTATTCAGATACAGAACTGAGGAGGCAATTGA 540

QY 627 CAAGTATCAGGGTGGTTTGAAGCCCTTTTCGCGGGTTATGAAAAAATGGGTTTCACATCG 686
DB 541 CAAGTATCAGGGTGGTTTTCAGGCTTTTTCGCGGGTTATGAAAAAATGGGTTTCACATCG 600
QY 687 TAGTGCTACAGGTATCACTTACCGTGTAGTGGGCTCTTGGTCCCGAGTCAGCTGCCCTCAT 746
DB 601 TAGTGCTACAGGTATCACTTACCGTGTAGTGGGCTCTTGGTCCCGAGTCAGCTGCCCTCAT 660
QY 747 TGGAGATTTCAACAATTTGGGACGCAAAATGCTGACATTAATGACTCGGAATGAATTTGGTGT 806
DB 661 TGGAGATTTCAACAATTTGGGACGCAAAATGCTGACATTAATGACTCGGAATGAATTTGGTGT 720
QY 807 CTGGAGATTTTCTGCCAAATAATGTGGATGGTCTCTCTCAATTCCTCATGGTCCAG 866
DB 721 CTGGAGATTTTCTGCCAAATAATGTGGATGGTCTCTCTCAATTCCTCATGGTCCAG 780
QY 867 AGTGAAGATAGGTATGGACACTCCATCAGGTGTTTAAAGATTCATTCCTGCTGGATCAA 926
DB 781 AGTGAAGATAGGTATGGACACTCCATCAGGTGTTTAAAGATTCATTCCTGCTGGATCAA 840
QY 927 CTACTCTTTACAGCTTCTCTGATGAAATTCCTATAATGGAATACATTAATGATGATCACC 986
DB 841 CTACTCTTTACAGCTTCTCTGATGAAATTCCTATAATGGAATACATTAATGATGATCACC 900
QY 987 AGAGGAGAGGTATATCTTCCAAACCCAGCCCAAGAAACCAAGTCGCTGAGAAATA 1046
DB 901 AGAGGAGAGGTATATCTTCCAAACCCAGCCCAAGAAACCAAGTCGCTGAGAAATA 960
QY 1047 TGAATCTCATATTTGGAATGAGTGTGCGGAGCTTAAATTAACATCATACGTGAATTTAG 1106
DB 961 TGAATCTCATATTTGGAATGAGTGTGCGGAGCTTAAATTAACATCATACGTGAATTTAG 1020
QY 1107 AGATGAAGTCTTCTCTCGCATATAAAAGCTTGGGTACAATGCGCTGCAAAATTAATGGCTAT 1166
DB 1021 AGATGAAGTCTTCTCTCGCATATAAAAGCTTGGGTACAATGCGCTGCAAAATTAATGGCTAT 1080
QY 1167 TCAAGAGCATCTTATACCTAGTTTGGTATCATGTCACAAATTTTTCGACCAAG 1226
DB 1081 TCAAGAGCATCTTATATATGCTAGTTTGGTATCATGTCACAAATTTTTCGACCAAG 1140
QY 1227 CAGCGGTTTGGAAAGCCCGACGACCTTAAGTCTTTGATTTGATTAAGACTCATGAGCTAGG 1286
DB 1141 CAGCGGTTTGGAAAGCCCGACGACCTTAAGTCTTTGATTTGATTAAGACTCATGAGCTAGG 1200
QY 1287 AATGTTGTTCTCATGGACATTTGTTCAAGCCATGCAATCAAAATTAATTAATTAATGAGCT 1346
DB 1201 AATGTTGTTCTCATGGACATTTGTTCAAGCCATGCAATCAAAATTAATTAATTAATGAGCT 1260
QY 1347 GAACATGTTTGAAGTCACTGACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTAATG 1406
DB 1261 GAACATGTTTGAAGTCACTGACCGATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTAATG 1320
QY 1407 GATGTTGGGATTTCCCGCTCTTTAACTATGCAAACTGGGAGTACTTAGGTATCTCTCTC 1466
DB 1321 GATGTTGGGATTTCCCGCTCTTTAACTATGCAAACTGGGAGTACTTAGGTATCTCTCTC 1380
QY 1467 AAAICGAGATGGTGGTTGGAATCGCTCAAAATTTGATGATTTAGATTTGATGGTGTGAC 1526
DB 1381 AAAICGAGATGGTGGTTGGAATCGCTCAAAATTTGATGATTTAGATTTGATGGTGTGAC 1440
QY 1527 ATCAATGATGATATTTACCAACCGATATTCGGTGGGATTCACATGGGAACCTACAGGAATA 1586
DB 1441 ATCAATGATGATATTTACCAACCGATATTCGGTGGGATTCACATGGGAACCTACAGGAATA 1500
QY 1587 CTTTGACCTCGGAACGATGTGGATGCTGTTGTTATCTCATGCTGCTCAACCATCTTAT 1646
DB 1501 CTTTGACCTCGGAACGATGTGGATGCTGTTGTTATCTCATGCTGCTCAACCATCTTAT 1560
QY 1647 TCATGGGCTTTTCCAGATGCAATTAACCATTTGTTGAAGATGTTAGCGGAATGCGGACAT 1706
DB 1561 TCATGGGCTTTTCCAGATGCAATTAACCATTTGTTGAAGATGTTAGCGGAATGCGGACAT 1620

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QY 1707 TTGATATCCGCTCAAGAGGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATTC 1766
Db 1621 TTGATATCCGCTCAAGAGGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATTC 1680
QY 1767 TGATAACGAGTATGAGTTCGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATGT 1826
Db 1681 TGATAAATGAGTATGAGTTCGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATGT 1740
QY 1827 TCATACACTGACAAATAGAGATGGTCGGAAAGTGTGTTTCATAGCTCAAGATCATGA 1886
Db 1741 TCATACACTGACAAATAGAGATGGTCGGAAAGTGTGTTTCATAGCTCAAGATCATGA 1800
QY 1887 TCAAGCTCTAGTCGGGTGATAAACTATAGCATTTCTGGCTGATGACAAAGATATGTATGA 1946
Db 1801 TCAAGCTCTAGTCGGGTGATAAACTATAGCATTTCTGGCTGATGACAAAGATATGTATGA 1860
QY 1947 TTTTATGGCTCTGGATAGACCGTCACATCATTAATAGATCGTGGGATAGCATGACAA 2006
Db 1861 TTTTATGGCTCTGGATAGACCGTCACATCATTAATAGATCGTGGGATAGCATGACAA 1920
QY 2007 GATGATAGGCTTGTAACTATGAGTATGAGGATGAGGAGAGGTGACCTAAATTTTCATGGAAA 2066
Db 1921 GATGATAGGCTTGTAACTATGAGGATGAGGAGAGAGGTGACCTAAATTTTCATGGAAA 1980
QY 2067 TGAATTCGGCCACCCTGAGTGGATGATTTCCCTAGGGCTGAACACACCTCTCTGATGG 2126
Db 1981 TGAATTCGGCCACCCTGAGTGGATGATTTCCCTAGGGCTGARCAACACCTCTCTGATGG 2040
QY 2127 CTCAGTAATCCCGGAAACCAATTCAGTTATGATAAATGACGAGGAGATTTGACCTGGG 2186
Db 2041 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAAATGACGAGGAGATTTGACCTGGG 2100
QY 2187 AGATGACAGATATTTAAGATACCGTGGTTCAGAGATTTTACCGGCTATGACGATGCT 2246
Db 2101 AGATGACAGATATTTAAGATACCGTGGTTCAGAGATTTTACCGGCTATGACGATGCT 2160
QY 2247 TGAAGATAAATATGAGTTTATGACTTCAGAACACAGTTTCATATCAGAAAGATGAAG 2306
Db 2161 TGAAGATAAATATGAGTTTATGACTTCAGAACACAGTTTCATATCAGAAAGATGAAG 2220
QY 2307 AGATGAGATGATGTTATTTGAAAGAAACCTAGTTTTCCTTTTAAATTTTCACTGGAC 2366
Db 2221 AGATGAGATGATGTTATTTGAAAGAAACCTAGTTTTCCTTTTAAATTTTCACTGGAC 2280
QY 2367 AAAAGCTATTCAGACTATCGATAGCTGCTGAAGCCTGGAATACAAAGTTGCGCTT 2426
Db 2281 AAAAGCTATTCAGACTATCGATAGCTGCTGAAGCCTGGAATACAAAGTTGCGCTT 2340
QY 2427 GGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATTCATATATGCCGAATATTT 2486
Db 2341 GGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATTCATATATGCCGAATATTT 2400
QY 2487 CACCTTTCAAGGATGGTATGATGATGCTGCTGCTCAATTTATGTTATGACCTGTAA 2546
Db 2401 CACCTTTCAAGGATGGTATGATGATGCTGCTGCTCAATTTATGTTATGACCTGTAG 2460
QY 2547 AACAGCAGTGGTCTATGACCTATGAGACAAAGAAAGAAAGAAAGAAAGAAAGAA 2606
Db 2461 AACAGCAGTGGTCTATGACCTATGAGACAAAGAAAGAAAGAAAGAAAGAAAGAA 2520
QY 2607 AGAAGTA 2613
Db 2521 NGAAGAA 2527
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RESULT 9

AAT42631

ID AAT42631 standard; DNA; 2578 BP.

XX

AC AAT42631;

XX

DT 25-FEB-1997 (first entry)

XX

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DE Class A starch branching enzyme (psbe2con.seq - clone psU90).
XX Starch branching enzyme: SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
OS Solanum tuberosum.
PH Key Location/Qualifiers
FT CDS 24..2567
FT /*tag= a
FT sig_peptide 24..56
FT /*tag= b
FT mat_peptide 57..2564
FT /*tag= c
PN WO9634968-A2.
XX 07-NOV-1996.
XX 03-MAY-1996; 96WO-GB01075.
XX 10-APR-1996; 96GB-0007409.
XX 05-MAY-1995; 95GB-0009229.
XX (NAT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
DR P-PSDB; AAW06400.
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX Claim 32; Page 55-56; 142pp; English.
PS Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX Sequence 2578 BP; 770 A; 462 C; 616 G; 730 T; 0 other;
SQ
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Query Match 93.2%; Score 2465.8; DB 17; Length 2578;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 2482; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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QY 135 GATCTTGGCTGAAAAGTCTTCTTACAAATCCGAATTCGAACTTCTACAGTTGCAGCATC 194
Db 56 GATCTTGGCTGAAAAGTCTTCTTACAAATTCGAAATTCGAACTTCTACAGTTGCAGCATC 115
QY 195 GGGGAAAGTCTTGTGCTGGAAACCCAGAGTATAGTCTCCTCATCTCAACAGACCAATT 254
Db 116 GGGGAAAGTCTTGTGCTGGAAACCCAGAGTATAGTCTCCTCATCTCAACAGACCAATT 175
QY 255 TGAGTTCACTGAGACATCTCCAGAAAATTCGCCAGATCACTCACTGATGATGATGATCAAC 314
Db 176 TGAGTTCACTGAGACATCTCCAGAAAATTCGCCAGATCACTCACTGATGATGATGATCAAC 235
QY 315 AATGGAACACGCTACCGAGATTAACAACTGAGAACCATGACGTTGAGCCGTCAAGTGATCT 374
Db 236 AATGGAACACGCTACCGAGATTAACAACTGAGAACCATGACGTTGAGCCGTCAAGTGATCT 295
QY 375 TACAGGAAGTGTGAGAGAGCTGGATTTTTCCTTCATCACTTACAACTACAAAGAGTGTAA 434
Db 296 TACAGGAAGTGTGAGAGAGCTGGATTTTTCCTTCATCACTTACAACTACAAAGAGTGTAA 355
QY 435 ACTGGAGGAGTCTAAAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 494
Db 356 ACTGGAGGAGTCTAAAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 415
QY 495 GATCAGAGAGAGGGGCGATCCCTCCACCTGGACTTGGTCTAGAGATTTATGAAATAGACCC 554
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416 GATCAGAGAGGGGCATCCCTCCACCTGGACTGGTCAGAGATTATGAATAGACC 475
QY CCTTTTGACAAACTATCGTCAACACTTGATTACAGGTATTACAGTATCAAGAAACTGAG 614
Db CCTTTTGACAAACTATCGTCAACACTTGATTACAGGTATTACAGTATCAAGAAACTGAG 535
QY GGAGCAATIGACAAGTAGAGGTGGTTTGGAGCCCTTTTCTCGTGGTTATGAATAAT 674
Db GGAGCAATIGACAAGTAGAGGTGGTTTGGAGCCCTTTTCTCGTGGTTATGAATAAT 595
QY GGGTTTCACTCGTAGTACAGGTATACATTACCGTAGTGGGCTTGGTCCAGTC 734
Db GGGTTTCACTCGTAGTACAGGTATACATTACCGTAGTGGGCTTGGTCCAGTC 655
QY AGCTGCCCTCATTTGGAGATTCAACAATTGGGAGCGCAAAATGCTGACATATGACTCGAA 794
Db AGCTGCCCTCATTTGGAGATTCAACAATTGGGAGCGCAAAATGCTGACATATGACTCGAA 715
QY TGAATTTGGTCTCGGAGATTTTCTGCCAAATAATGTGGATGTTCTCTCGCAATTC 854
Db TGAATTTGGTCTCGGAGATTTTCTGCCAAATAATGTGGATGTTCTCTCGCAATTC 775
QY TCATGGTCCAGAGTGAAGATACGTATGGACATCCATCAGGTGTTAAGGATTCATTC 914
Db TCATGGTCCAGAGTGAAGATACGTATGGACATCCATCAGGTGTTAAGGATTCATTC 835
QY TGCTTGGATCAACTACTCTTTACAGCTTCTGTGTAATCCATATCAATGAAATACATTA 974
Db TGCTTGGATCAACTACTCTTTACAGCTTCTGTGTAATCCATATCAATGAAATACATTA 895
QY TGATCCCGGAGAGAGGTATATCTTCCACACCCAGCGCAAGAAACCAAGTC 1034
Db TGATCCCGGAGAGAGGTATATCTTCCACACCCAGCGCAAGAAACCAAGTC 955
QY GCTGAGATATGAATCTCATATTGGAATGAGTAGTCCGAGCCTAAATTAACATCA 1094
Db GCTGAGATATGAATCTCATATTGGAATGAGTAGTCCGAGCCTAAATTAACATCA 1015
QY CGTGAATTTAGAGTGAAGTCTCTCTCGCAATTAAGTCTTGGTATCATGTCACAAATTT 1154
Db CGTGAATTTAGAGTGAAGTCTCTCTCGCAATTAAGTCTTGGTATCATGTCACAAATTT 1075
QY AATTATGGCTATTCAAGAGCATTTCTATTATGCTAGTTTGGTATTGATGTCACAAATTT 1214
Db AATTATGGCTATTCAAGAGCATTTCTATTATGCTAGTTTGGTATTGATGTCACAAATTT 1135
QY TTTTGACCAAGCAGCGGTTTGGAGCCCGAGACCTTAAGTCTTTGATTGATAAGC 1274
Db TTTTGACCAAGCAGCGGTTTGGAGCCCGAGACCTTAAGTCTTTGATTGATAAGC 1195
QY TCATGAGCTAGGAATTTGCTTCTCATGGACATTTTCAGAGCATTCATCAATATAC 1334
Db TCATGAGCTAGGAATTTGCTTCTCATGGACATTTTCAGAGCATTCATCAATATAC 1255
QY TTTAGATGGACTGAACATGTTTACGCGACCGGATGTTTACTTTTCACTCTGGAGTCG 1394
Db TTTAGATGGACTGAACATGTTTACGCGACCGGATGTTTACTTTTCACTCTGGAGTCG 1315
QY TGCTTATCATGATGCGGATTTCCGCGCTTTTAACTATGGAATTCAGATGAGGTACTAG 1454
Db TGCTTATCATGATGCGGATTTCCGCGCTTTTAACTATGGAATTCAGATGAGGTACTAG 1375
QY GTATCTTCTCAAAATGCGAGATGGTGGTTGGATGGTTCCTCAAAATTCAGATGAGTT 1514
Db GTATCTTCTCAAAATGCGAGATGGTGGTTGGATGGTTCCTCAAAATTCAGATGAGTT 1435
QY TGAATGTTGACATCAATGATGATATTCACCGGATTCGCTGGGATTCAGTGGAA 1574
Db TGAATGTTGACATCAATGATGATATTCACCGGATTCGCTGGGATTCAGTGGAA 1495
QY CTACGAGGATATCTTTGGACTCCCACTGATGAGTGGTGTGTGTATCTGTATGCTGGT 1634
|||||

Db 1496 CTACGAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTGTATCTGATGCTGT 1555
QY 1635 CAACGATCTATTATTCATGGGCTTTTCCAGATCAATACCATTTGGTGAAGACTTAGCGG 1694
Db 1556 CAACGATCTATTATTCATGGGCTTTTCCAGATCAATACCATTTGGTGAAGACTTAGCGG 1615
QY 1695 AATGCCGACATTTTGTATTCCTGTCACAGAGGGGGTGTGTGGCTTTGACTATCGGCTGCA 1754
Db 1616 AATGCCGACATTTTGTATTCCTGTCACAGATGGGGTGTGTGGCTTTGACTATCGGCTGCA 1675
QY 1755 TATGCCAATTCGTGATTAACGATTCAGTTTCTCAAGAACCGGATGAGGATTTGAGAT 1814
Db 1676 TATGCCAATTCGTGATTAACGATTCAGTTTCTCAAGAACCGGATGAGGATTTGAGAT 1735
QY 1815 GGGTGATATTTGTTCATACACTGACAAATAGAAAGATGGTCGGAAGAGTGTGTTTCATACGC 1874
Db 1736 GGGTGATATTTGTTCATACACTGACAAATAGAAAGATGGTCGGAAGAGTGTGTTTCATACGC 1795
QY 1875 TGAAGTCAATGATCAAGCTTAGTCGGTGTATAAACTATAGCATTTCTGGCTGAIGGACAA 1934
Db 1796 TGAAGTCAATGATCAAGCTTAGTCGGTGTATAAACTATAGCATTTCTGGCTGAIGGACAA 1855
QY 1935 GGATATGATGATTTTATGGCTCTGATAGACCGTCAACATCATTTAATAGATCTGGGAT 1994
Db 1856 GGATATGATGATTTTATGGCTCTGATAGACCGTCAACATCATTTAATAGATCTGGGAT 1915
QY 1995 AGCATTCACAAAGATGATTAGGCTTGTAACTATGGGATTTAGGAGGAGAGGTACTATAA 2054
Db 1916 AGCATTCACAAAGATGATTAGGCTTGTAACTATGGGATTTAGGAGGAGAGGTACTATAA 1975
QY 2055 TTTTATGGGAATTAATTCGGCCACCTTGGGATTTGATTTCCCTAGGGCTGAACAAACA 2114
Db 1976 TTTTATGGGAATTAATTCGGCCACCTTGGGATTTGATTTCCCTAGGGCTGAACAAACA 2035
QY 2115 CCTCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGATTAATGCAGACGAG 2174
Db 2036 CCTCTCTGATCAGTAAATTCGGGAAACCAATTCAGTTATGATTAATGCAGACGAG 2095
QY 2175 ATTTGACCTGGAGATGCAGAAATTTAAGATACCGTGGTTCGAAGAAATTTGACCGGCC 2234
Db 2096 ATTTGACCTGGAGATGCAGAAATTTAAGATACCGTGGTTCGAAGAAATTTGACCGGCC 2155
QY 2235 TATCAGTATCTTTGAAGATAATATGAGTTTATGACTTCAGAACACCATTCATATCAG 2294
Db 2156 TATCAGTATCTTTGAAGATAATATGAGTTTATGACTTCAGAACACCATTCATATCAG 2215
QY 2295 AAAGGATGAAGAGATAGGATGATTGATTTGAAAAGGAAACCTAGTTTGTCTTAA 2354
Db 2216 AAAGGATGAAGAGATAGGATGATTGATTTGAAAAGGAAACCTAGTTTGTCTTAA 2275
QY 2355 TTTTCACTGGACAAAAAGCTATTCAGACTATPCGATAGCCCTGCAAGCCTGGAATAA 2414
Db 2276 TTTTCACTGGACAAAAAGCTATTCAGACTATPCGATAGCCCTGCAAGCCTGGAATAA 2335
QY 2415 CAAGGTTGCTTGGACTCAGATGATCCACATTTTGGTGGCTTCGGGAGAAATGATATAA 2474
Db 2336 CAAGGTTGCTTGGACTCAGATGATCCACATTTTGGTGGCTTCGGGAGAAATGATATAA 2395
QY 2475 TGCCGAATATTTACCTTTTGAAGGATGATATGATGATGCTCTGCTCAATATATGGTGA 2534
Db 2396 TGCCGAATATTTACCTTTTGAAGGATGATATGATGATGCTCTGCTCAATATATGGTGA 2455
QY 2535 TGACCTTTGAAAACAGCAGTGGTCTATGCACCTAGTAGACAAAGAAAGAAAGAA 2594
Db 2456 TGACCTTTGAAAACAGCAGTGGTCTATGCACCTAGTAGACAAAGAAAGAAAGAA 2515
QY 2595 AGAAGAGAGAGAGAACTACAGCAGTAGAAGAAAGTAGTAGTAGAGAA 2643
Db 2516 AGAAGAGAGAGAGTAGTAGCAGTAGTAGAAGAAAGTAGTAGTAGAGAAAGAA 2564

AAAT2636 standard; DNA; 2576 BP.
AAAT2636;
03-MAR-1997 (first entry)
Class A starch branching enzyme (85con.seq) cloned in QE32.
Starch branching enzyme: SBE; class A; class B; Solanum tuberosum;
amylose; viscosity; potato; ss.
Solanum tuberosum.
wO9634968-A2.
07-NOV-1996.
03-MAY-1996; 96WO-GB01075.
10-APR-1996; 96GB-0007409.
05-MAY-1995; 95GB-0009229.
(NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
Sidebottom CM, Westcott RJ;
WPI; 1996-506170/50.
New potato plant starch having high amylose content - also class A
starch branching enzyme and corresp. DNA to alter the viscosity of
starch; for use in food, biodegradable products, adhesives, etc.
Example 1; Page 49-51; 142pp; English.
Class A starch branching enzyme (SBE) has been obtained from
potatoes. In class A SBE mols., a flexible N-terminal domain,
is found, which is not found in class B mols.
Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;
Query Match 92.7%; Score 2451.8; DB 17; Length 2576;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2480; Conservative 0; Mismatches 27; Indels 2; Gaps 1;
QY 135 GATCTTGGCTGAAAAGTCTTACAAATCCGAATTCGGACTTCAGTTCAGTTCAGCATC 194
DB 56 GATCTTGGCTGAAAAGTCTTACAAATTCGAATTCGGACTTCAGTTCAGCATC 115
QY 195 GGGGAAAGTCTTGTGCTGGAACCCAGAGTGATGCTCCTCAATCCCTCAACAGCAAT 254
DB 116 GGGGAAAGTCTTGTGCTGGAACCCAGAGTGATGCTCCTCAATCCCTCAACAGCAAT 175
QY 255 TGAGTTCACGTAGACATCTCCAGAAATTCAGAGATCACTGATGATGATGATGATGAT 314
DB 176 TGAGTTCACGTAGACATCTCCAGAAATTCAGAGATCACTGATGATGATGATGATGAT 235
QY 315 AATGGAACAGCTAGCCAGATTAATACTGGAACGATGAGCTTGAGCCGCTCAAGTGATCT 374
DB 236 AATGGAACAGCTAGCCAGATTAATACTGGAACGATGAGCTTGAGCCGCTCAAGTGATCT 295
QY 375 TACAGGAAGTGTGAAGAGCTGGATTTTGGCTTCATCACTCACTCACTCACTCACTCACT 434
DB 296 TACAGGAAGTGTGAAGAGCTGGATTTTGGCTTCATCACTCACTCACTCACTCACTCACT 355
QY 435 ACTGGAGAGCTTAAACATTAATACTCTGAGAGACATTAATGATGATGATGATGATGATG 494
DB 356 ACTGGAGAGCTTAAACATTAATACTCTGAGAGACATTAATGATGATGATGATGATGATG 415
QY 495 GATCAGAGAGGGGCGATCCCTCCACCTGGACTTGGTGGTGGTGGTGGTGGTGGTGGTGG 554
DB 416 GATCAGAGAGGGGCGATCCCTCCACCTGGACTTGGTGGTGGTGGTGGTGGTGGTGGTGG 475

QY 555 CTTTTGACAAACTATCGTCAACACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 614
DB 476 CTTTTGACAAACTATCGTCAACACCTTGATGATGATGATGATGATGATGATGATGATGATGATG 535
QY 615 GGAGGCAATTGACAAAGTATGAGGCTGTTGGAGGCTTTTCTGCTGGTTATGAAAAAT 674
DB 536 GGAGGCAATTGACAAAGTATGAGGCTGTTGGAGGCTTTTCTGCTGGTTATGAAAAAT 595
QY 675 GGGTTTCACTCGTAGTCTACAGGTATCACTTACCGTGAGTGGGCTTTGGTGGCCAGTC 734
DB 596 GGGTTTCACTCGTAGTCTACAGGTATCACTTACCGTGAGTGGGCTTTGGTGGCCAGTC 655
QY 735 AGCTGCCCTCATTTGGAGATTTCACAAATTTGGAGCGAAATGCTGACATTTAGCTCGGAA 794
DB 656 AGCTGCCCTCATTTGGAGATTTCACAAATTTGGAGCGAAATGCTGACATTTAGCTCGGAA 715
QY 795 TGRATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGATGGTCTCTCTGCAATTC 854
DB 716 TGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGATGGTCTCTCTGCAATTC 775
QY 855 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTCTTAAGGATTCATTC 914
DB 776 TCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTCTTAAGGATTCATTC 835
QY 915 TGCTTGGATCAACTACTCTTTTACAGTTCCTGATGAAATTCATATATGGAATTAATTA 974
DB 836 TGCTTGGATCAACTACTCT--TACAGTTCCTGATGAAATTCATATATGGAATTAATTA 893
QY 975 TGATCCACCGAGAGGAGGTATATCTTCCACACCCAGCGGCAAGAAACCAAGTC 1034
DB 894 TGATCCACCGAGAGGAGGTATATCTTCCACACCCAGCGGCAAGAAACCAAGTC 953
QY 1035 GCTGAGAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGAGCTTAAATTAATCATA 1094
DB 954 GCTGAGAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGAGCTTAAATTAATCATA 1013
QY 1095 CGTGAATTTAGAGATGAAGTCTTCTCGATGAAATGAGTTCCTGATGAAATGAGTTCG 1154
DB 1014 CGTGAATTTAGAGATGAAGTCTTCTCGATGAAATGAGTTCCTGATGAAATGAGTTCG 1073
QY 1155 AATATGCTATTCAAGAGCATTCCTTATAGCTAGTTCCTGATGAAATGAGTTCGATGAA 1214
DB 1074 AATATGCTATTCAAGAGCATTCCTTATAGCTAGTTCCTGATGAAATGAGTTCGATGAA 1133
QY 1215 TTTTGCACCAAGAGCCGCTTTTGAAGCCCGAGACCTTAAGTCTTTGATGATGATAAGC 1274
DB 1134 TTTTGCACCAAGAGCCGCTTTTGAAGCCCGAGACCTTAAGTCTTTGATGATGATAAGC 1193
QY 1275 TCATGAGCTAGGAATTTGTTCTCATGAGCATTTTTCACAGCCATGATGATGATGATGATG 1334
DB 1194 TCATGAGCTAGGAATTTGTTCTCATGAGCATTTTTCACAGCCATGATGATGATGATGATG 1253
QY 1335 TTTAGATGAGTGAACATGTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1394
DB 1254 TTTAGATGAGTGAACATGTTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1313
QY 1395 TGGTTATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1454
DB 1314 TGGTTATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1373
QY 1455 GTATCTTCTCTCAATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1514
DB 1374 GTATCTTCTCTCAATGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1433
QY 1515 TGATGGTGTGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1574
DB 1434 TGATGGTGTGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1493
QY 1575 CTACAGGAATGATTTGAGTCCGAACTGATGATGATGATGATGATGATGATGATGATGATG 1634
DB 1494 CTACAGGAATGATTTGAGTCCGAACTGATGATGATGATGATGATGATGATGATGATGATG 1553
QY 1635 CAACGATCTTATTCATGGGCTTTTCCAGATGCAATTTACCATTTGGTGAAGATGTTAGCGG 1694

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Db 1554 CAACGATCTTATTCATGGCTTTCCAGATGCAATACCATTGCTGAAGATTTAGCGG 1613
Qy 1695 AATCCGACATTTTGTATTCCTCCGCAAGAGGGGGTGTGGCTTTGACTATCGGCTGCA 1754
Db 1614 AATCCGACATTTTGTATTCCTCCGCAAGATGGGGTGTGGCTTTGACTATCGGCTGCA 1673
Qy 1755 TATGGCAATTCCTGATAAACGATTTGAGTTGCTCAAGAAACGGGATGAGGATTTGAGAGT 1814
Db 1674 TATGGCAATTCCTGATAAACGATTTGAGTTGCTCAAGAAACGGGATGAGGATTTGAGAGT 1733
Qy 1815 GGGTGATATTTCTATACACATGCAAAATAGAGATGCTCGGAAAAGTGTGTTTCATAGC 1874
Db 1734 GGGTGATATTTCTATACACATGCAAAATAGAGATGCTCGGAAAAGTGTGTTTCATAGC 1793
Qy 1875 TGAAGTCATGATCAAGCTCTAGTCGGTGATGATGATGATGATGATGATGATGATGATGAT 1934
Db 1794 TGAAGTCATGATCAAGCTCTAGTCGGTGATGATGATGATGATGATGATGATGATGATGAT 1853
Qy 1935 GGATATGATGATTTTATGGCTCTGGATAGACCTGCAACATCATTATAGATGCTGGGAT 1994
Db 1854 GGATATGATGATTTTATGGCTCTGGATAGACCTGCAACATCATTATAGATGCTGGGAT 1913
Qy 1995 AGCATTCACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2054
Db 1914 AGCATTCACAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1973
Qy 2055 TTTTCATGGGAAATCAATTCGGCCACCTGAGTTCATGATGATGATGATGATGATGATGATGAT 2114
Db 1974 TTTTCATGGGAAATCAATTCGGCCACCTGAGTTCATGATGATGATGATGATGATGATGATGAT 2033
Qy 2115 CTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2174
Db 2034 CTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2093
Qy 2175 ATTGACCTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2234
Db 2094 ATTGACCTGGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2153
Qy 2235 TATGCACTATCTTGAAGATAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2294
Db 2154 TATGCACTATCTTGAAGATAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2213
Qy 2295 AAAGGATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2354
Db 2214 AAAGGATGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2273
Qy 2355 TTTTCACTGGACAAAAGCTATTCAGACTATCCGATAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2414
Db 2274 TTTTCACTGGACAAAAGCTATTCAGACTATCCGATAGCTGCTGCTGCTGCTGCTGCTGCTGCT 2333
Qy 2415 CAAGGTTGGCTTGGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2474
Db 2334 CAAGGTTGGCTTGGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2393
Qy 2475 TGGCGAATATTCACCTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2534
Db 2394 TGGCGAATATTCACCTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2453
Qy 2535 TGCACCTTTGAAACAGCAGTGGTCTATGCACTAGTATGATGATGATGATGATGATGATGATGAT 2594
Db 2454 TGCACCTTTGAAACAGCAGTGGTCTATGCACTAGTATGATGATGATGATGATGATGATGATGAT 2513
Qy 2595 AGAAGAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2643
Db 2514 AGAAGAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2562
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RESULT 11

AAV38720

ID AAV38720 standard; DNA; 3090 BP.

XX

AC AAV38720;

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XX 21-SEP-1998 (first entry)
XX Full length cassava tuber cDNA in pSJ146.
XX Starch branching enzyme; SBE; cassava; ss.
XX Manihot esculenta.
XX Key Location/Qualifiers
XX misc_feature 35..2760
XX /tag= a
XX /note= "these nylcotides are SBE II sequence, the
XX 131..2677 reminder are derived from the plamsid"
XX /tag= b
XX /product= SBE II
XX WO9820145-A2.
XX 14-MAY-1998.
XX 04-NOV-1997; 97WO-GB03032.
XX 05-NOV-1996; 96GB-0023095.
XX (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Jobling SA, Safford R;
XX WPI: 1998-286958/25.
XX P-PSDB; AAW62600.
XX Starch branching gene from cassava - useful for producing altered
XX plants giving modified starch
XX Claim 2; Fig 13; 67pp; English.
XX The present sequence encodes starch branching enzyme (SBE) II. It
XX was isolated from cassava tubers. The products can be used for
XX producing plants having altered starch quantities and qualities.
XX They can also be used for producing altered plants such as cassava,
XX banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
XX and rice plants.
XX Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;
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Query Match

Best Local Similarity 54.08; Score 1429.4; DB 19; Length 3090;

Matches 1909; Conservative 0; Mismatches 606; Indels 96; Gaps 2;

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Qy 7 TATACACTCTCTGGAGTTCGTTTTCCTACTGTCCATCAGTACAAATCTAATGGATTC 66
Db 140 TACACTCTATCAGGCATACGTTTCTCTGTGACCTTCACCTACAAATCTCAGCTCACC 199
Qy 67 AGCAGTAAATGCTATCGGAGGAGGATGCTAATG---TTTCTCTATTTGAAAAAGCACTCT 123
Db 200 AGCTTCATCGGCTGCAAGGACCTCTCTCTGGCTTTCTCTCTCTGAGAGAGGAGCTG 259
Qy 124 CTTTCACGGAGAGATCTTGGCTGAAAGTCTCTTACAAATCCGAATCCGACCTTCTACA 183
Db 260 TTTCTCTGGAGAGATCTTGGCTGAAAGTCTCTTATGAATCTGACCTCTCAAAATTAAC 319
Qy 184 GTTTCAGCATCGGGGAAAGTCTTGTGCTTGAACCCAGAGTACAGTCTCATCTCTCA 243
Db 320 GTCTCTGCATCTGAGAGGTCCTTGTTCGATGATCAGATTGCTGCTCTTCTTCTCA 379
Qy 244 ACAGACCAATTTGAGTTCAGTACATCTCCAGAAAATTTCCCGCATCACTGATGTA 303
Db 380 ACATATCAATTAGAAACCACTGSCACAGITTTTGAGGAAATCCAGGTTCTTGTGTAGCA 439
Qy 304 GATAGTTCACAATGGAACAGCTGACCCAGATTAACACTGAGAACGATGACGTTGACCG 363
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Db 440 GAGAGCTCTTGTGATGGAAGATGATAAGAAATGTTGAGGAGATCAAGTAAAAAAGAGTCG 499
QY 364 TCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTTGGCTTCATCACTACAACATACAA 423
Db 500 ----- 499
QY 424 GAAGGTGTTAACTGGAGGAGTCTAAACATTAATFACCTCTGGAAGAGACAAATTAATGAT 483
Db 500 -----GTTCCTATGTCATGAGACAAATTAGCATI 526
QY 484 GAATCTGATAGATACAGAGAGGGGCGATCCCTCCACCTGGACTGGCTGGTCAGAGATTTAT 543
Db 527 GGAAAAGTGAATCTAAACCAAGGTCCATTCCTCCACCTGGCAGTGGGCGAGAAATATAT 586
QY 544 GAAATAGACCCCTTTTGCACAACTATCGTCAACACCTTGAATACAGGTATTCACAGTAC 603
Db 587 GACATAGATCCAAGCTTGGCAGGTTCCTCGTCAGCATCTTGACTACCGATATTCACAGTAC 646
QY 604 AAGAAACTGAGGAGGCAATTTGACAAAGTATGAGGGTGGTTTGGAAAGCCTTTTCTCGTGGT 663
Db 647 AAAAGGCTGGTGAGGAAATTGACAAAGTATGAAGGTGGTTTGGATGCATCTCTCGTGA 706
QY 664 TATGAAAAATGGTTTCACTCGTACTGCTACAGGTATCACCTTACCGTGAAGTGGCTCTT 723
Db 707 TTTGAAAAGTTTGGTTTACGAGTGAACAGGAATACCTTATAGGGAATGGGCACCT 766
QY 724 GGTGCCAGTCAGCTGCCCTCATTTGGAGATTTTCAACAATTTGGACGCAAAATGCTGACATT 783
Db 767 GGAGCTACGTGGGCTGCNCTTATGGAGATTTCAACAATTTGGAATCCTATGACAGATGC 826
QY 784 ATGACTCGGAATGAAATTTGGTGCTCGGAGATTTTCTGCGCAAAATATGTTGGATGTTCT 843
Db 827 ATGACTCGGAATGAGTTTGGTGCTCGGAGATTTTTCGCAAAATACGCGAGATGTTCA 886
QY 844 CTTGCAATCTCTCATGGTCCAGAGTGAAGATAGTATGGACATCCATCAGGTGTTAAG 903
Db 887 CCACCAATTCCTCATGGTCTCGAGTAAGATAGCAATGATCTCCATCAGGTGTTAAG 946
QY 904 GATTCCATTCCTGCTGGATCAACTACTCTTTTACAGCTTCCCTGATGAATTTCCATATAAT 963
Db 947 GATTCAATTCCTGCTGGATCAAGTTCTCAGTTTCAGGCACCTGGTGAATCCCATACAA 1006
QY 964 GGAATACATATGATCCACCGAAGGAGGAGGTATATCTTCAACACCCACGCCCAAG 1023
Db 1007 GCCATATACATATGATCCACCAAGGAGGAGAAATATGTTGTCAAACATCCTCAGGCCAAG 1066
QY 1024 AAACCAAAGTCGCTGAGAATATATGAATCTCATTTGGAATGAGTACTCCGGAGCCTAAA 1083
Db 1067 AGACCAAAATCATTAGATTTATGAATCTCATGTTGGGATGAGTATGAGGCCAATA 1126
QY 1084 ATTAACATATGCTGGAATTTTAGAGATGAAGTCTTCTCCATGATGAATTTAGGCTGAGTAC 1143
Db 1127 ATTAACATATGCTGGAATTTTAGAGATGATATGCTTCTCCATGATGAATTTAGGCTGAGTAC 1186
QY 1144 AATGCGCTGCAATTTAGCTATTCAGAGCATCTTTATACGCTAGCTTTTGGTTATCAT 1203
Db 1187 AATGCTGTTAGATCATGGGTATTCAGAGCATCTTATGCTAGTTTGGGTACCAT 1246
QY 1204 GTCAAAATTTTTCACCAAGCAGCGCTTTTGGAGCGCCGACGACCTTAACTGCTTTG 1263
Db 1247 GTCAAAATTTTTCACCAAGCAGCGCTTTTGGAGCTTGGAACTCCTGATGATTCAGCTTTA 1306
QY 1264 ATTGATAAGCTATGAGCTAGGAATTTGTTCTCATGAGCATTTGTTACAGCCCATGCA 1323
Db 1307 ATAGATAAGCTATGATGATAGGCTGCTTCTCATGGAATATTTGATCATGAGCATGCG 1366
QY 1324 TCAAAATATCTTTTAGATGGGCTGAACATGTTTCACTGCACCGATAGTTGTTACTTTTCA 1383
Db 1367 TCAAAATATAGTTTGGATGGGCTGAACATGTTTATGATGGATAGTACACTACTTCCAC 1426
QY 1384 TCTGAGCTGCTGTTATCATTTGATTTGGATTTGGGATTCGCGCCCTTTTAACTATGGAACCTG 1443
Db 1427 TCGGATACACGGGCTCATCTTGGTTGGGAGCTCTGCTTTCACATATGGAAGCTGG 1486

1444 GAGGTACTTAGGTATCTTCTCTCAAAATCCAGATGTTGGTGGATGCGTTCAAATTTGAT 1503
Db 1487 GAGGTGCTAAGATTTCTTCTTCAAAATGCAAGATGTTGGTGGAGAGTACAGGTTTAT 1546
QY 1504 GGATTTAGATTTGATGTTGACATCAATGATATATTCACACGAGTATTCGGTGGGA 1563
Db 1547 GGTTTATAGATTTTATGGGGTACTTCCATGATGTACATCCCAATGGTTGACGATGCT 1606
QY 1564 TTCACCTGGGAATACAGGAAATCTTTGGACTCGCACTGATGTTGATGTTGTTGAT 1623
Db 1607 TTTTACTGGCACTACATGATGATTTGGATATGCAACTGATGTAGATGCTGATTTAT 1666
QY 1624 CTGATGCTGCTAACAGATCTTATCATGGGCTTTTCCAGATGCAATTCATTTGTTGAA 1683
Db 1667 TTTGATGCTTGTGAATGATATGATTCAGGCTCTTTTCCCTGAGGCTGTTCACATGTTGAA 1726
QY 1684 GATGTTAGCGGAATCGGACATTTTGTATTTCCCTCCAAAGAGGGGCTTGTGGCTTTGAC 1743
Db 1727 GATGTTAGCGGAATCGGACATTTTGTATTTCCCTCCAAAGAGGGGCTTGTGGCTTTGAT 1786
QY 1744 TATCGGCTGATATGCAATTTGCTGATTAACGGATGAGTTGCTTCAAGAAACGGGATGAG 1803
Db 1787 TACGCTCTCCACATGGCCATTTGCCGATAAATGGATTCAGATTTCTTAAAGAAAGAGATGAG 1846
QY 1804 GATTTGAGAGTGGGTGATTTTTCATACACTGCAAAATACAGATGCTCGGAAACGTT 1863
Db 1847 GACTGGAAATGGGTGACATTTGTCATACACTTCCAAACAGAGGTTGGTGGAAATATG 1906
QY 1864 GTTTCATACCTGAAAGTCATGATCAAGCTCTAGTCGTTGATATAAACTATAGCATTTCTGG 1923
Db 1907 GTTGCTTATGCTGAAAGTCATGACCAAGCTCTTGTGGTGACAAACTATTTGATTTTGG 1966
QY 1924 CTGATGACAAAGGATATGATGATTTTATGGCTCTGGATAGACCGCTCAACATCATATA 1983
Db 1967 CTGATGACAAAGGATATGATGATTTTATGGCTCTGGATAGACCGCTCAACATCATATA 2026
QY 1984 GATGCTGGATAGCATTTGCACAGATGATTTAGGCTTTTAACTATGGATAGGAGGAGAA 2043
Db 2027 GATGCTGGAATAGCATTTGCACAAATGATCAGGCTTATTAACATGGGCTTAGGCGGAGAA 2086
QY 2044 GGTGACCTAAATTTTATGGGAAATGAATTCGCGCCACCTGAGTGGATTTGATTTCCCTAGG 2103
Db 2087 GGATTTTGAATTTTATGGGAAATGAATTTGACATCTGATGATTTGATTTTCCAAAGA 2146
QY 2104 GCTGAACAAACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGATAAA 2163
Db 2147 GGGATCGACATCTGCGCAATGGTAAAGTAAATTCAGGGAACAAACACAGTTATGATAAA 2206
QY 2164 TGCAGCGGAGATTTGACCTGGGAGATGCAGAAATTTTAAAGATACCGGCTTGCAGAA 2223
Db 2207 TGGCGCTGATGATTTGATCTAGGTGATGACAGATCTTAAAGATCTTCTGAGCAGGAG 2266
QY 2224 TTTTACCGGCTCTGATGATTTTGAAGATAAAATGATTTATGATCTCAGAACACACAG 2283
Db 2267 TTTGATCAGGCAATGCAACATCTTGAAGAAGCTTATGCTTTCATGACCTCTGAGCAGGAG 2326
QY 2284 TTTTACCGGCTCTGATGATTTTGAAGATAAAATGATTTATGATCTCAGAACACACAG 2343
Db 2327 TATATATCAGGAGGATGAGGAGATCGGATCATTTGTTTGGAGGGGAAACCTGTT 2386
QY 2344 TTTGCTTTTAAATTTTCACTGGCAAAAAAGCTATTTCAGACTATTCGATACCTGCTGAAG 2403
Db 2387 TTTGATTTCACTTTTATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 2446
QY 2404 CCTGGAATAACAAGTTTGGCTTTGACTCAGATGATCCACTTTTGGTGGGCTTCCGGGAGA 2463
Db 2447 TCAGGAAGTACAAGATTTTGGACTCGGATGATGGCTTGTGTTGGAGGCTTCAACAGG 2506
QY 2464 ATTGATCATATGCGGAATATTTTCACTTTGAAGGATGATGATGATGATGATGATGATGAT 2523
Db 2507 CTTAGTCTATGATGCGGAGCACTTCACTTTCAGGCTGATGATGATGATGATGATGATGATGAT 2566

Db 1607 TAGTGAAGTCCAAAGTTCGATCCGGTGAAGATGGTGGTTCGATTCATATCG 1666
QY 1749 GCTGATATGGAATTCGTGATAAAGCGATTGAGTTGCTCAAGAAACGGGATGAGATTG 1808
Db 1667 TCTCCACATGGCTGTTGCTGATAAATGGTGGATTTATTCAGAGAGAGATGAAGATTG 1726
QY 1809 GAGAGTGGTGTATTTGTCATACACTGACAAATAGAGATGGTGGAAAGTGTCTTC 1868
Db 1727 GAAATGGGTGACATTTGATATGCTGACCAACAGCGGGTGGTTGAAAAGTGTCTTC 1786
QY 1869 ATACGCTGAAGTCATGATCAAGCTCTAGTCGGTGATAAACTATAGCAATTCCTGGCTGAT 1928
Db 1787 TTATGCTGAAGTCATGACACAGCCCTTGTGGTGACAAAACCTATTGCAATTTGGCTGAT 1846
QY 1929 GGACAGGATATGATGATTTATGCTCTGATAGACCGTCAACATCATTAATAGATCG 1988
Db 1847 GGACAGGATATGATGATCTGATGCTCTGACAGACCACTACCTCTCATATAGATCG 1906
QY 1989 TGGGATAGCATTCACAAAGATGATTAGGCTTGTAACTATGGGATTAGGAGAGAAAGGTA 2048
Db 1907 TGGAGTAGCATTCGACAAATGATCAGGCTTATACCATGGGATTAGCGGAGAGAGATA 1966
QY 2049 CCTAAATTCATGGGAAATGAATTCGGCCACCTGAGTGGATGATTTCCCTAGGCGTGA 2108
Db 1967 TTTGAATTTATGGGAAATGAATTTGGACACCCCGAGTGGATGATTTTCCAAGAGGTGA 2026
QY 2109 ACACACCTCTCTGATGGCTCAGTAATCCCGGAAACCAATTCAGTTATGATTAATGTCAG 2168
Db 2027 TCTACATCTTCCAGTGGTAAATTTGTTCTCGGAAACAATACAGTTATGATTAATGTCAG 2086
QY 2169 ACGGATTTGACCTGGGAGATGACAGAAATTTAAAGTACCGTGGTGTGAAAGAAATTTGA 2228
Db 2087 GCGTAGTTTATCTAGGCAATTCAGAGCATCAGATATCATGGAATGCAAGATTGTA 2146
QY 2229 CCGGCTATGCGATGCTTGAAGATAAATGATGATTTATGACTTCAGAACACCACTGTCAT 2288
Db 2147 TCAAGCAATTCAGCATCTTGAAGAAGCCTAIGTTTTCATGACTTCTGAGCACCAATACAT 2206
QY 2289 ATCAGAAAGGATGAAGGATAGGATGATTTGATTTGAAAGGAAACCTAGTTTGT 2348
Db 2207 ATCAGGAAGGATGAAGGATCGGATCATCTGTCAGAGGGGAAACCTCGTTTGT 2266
QY 2349 CTTTAAATTTCACTGGACAAAAGCTATTCAGACTATTCGATAGCCCTGCTGAAAGCCTGG 2408
Db 2267 ATTCATTTTCACTGGACTAGCAGCTATTCGGATTTACCGAGTTGGCTGCTTAAAGCCAGG 2326
QY 2409 AAAATCAAGGTTGCTTGGACTGACATGATGATCCACTTTTGGTGGCTTCGGGAGAAATGA 2468
Db 2327 AAAGTACAAGATAGTCTTGGATTCAGATGATCCCTTTGTTGGAGGCTTTGGCAGGCTTAG 2386
QY 2469 TCATAATGCCGAATATTTCACCTTTGAAGGATGATGATGATGATGATGATGATGATGATGAT 2528
Db 2387 TCATGATGAGAGACATTCAGCTTTGAAGGGTGTAGATAAACCGGCTCGATCCTCAT 2446
QY 2529 GGTGATGACCTTTGTAAGACAGAGTGGTCTATGCACTAGTAGACAAAAGAGAAAGA 2588
Db 2447 GGTGATACACCATGTAGACAGCAGTGGTCTATGCTTTAGTGGAGGATGAAGTGGAGAA 2506
QY 2589 AGAAGAGAGAGAGAGAGAGAGAGTAGCAGCAGTACAGAGATGATGATGATGATGATGATGAT 2646
Db 2507 TGAATGGAACTCTGCGCGTGAAGATATATCTTAAACACAGAGGTTCTGAAAGCAGGAA 2564

RESULT 13

AAC45939

ID AAC45939 standard; DNA; 2715 BP.

XX AAC45939;

XX AAC45939;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.

xx Hybridisation assay; genetic mapping; gene expression control;
kw protein identification; signal transduction pathway;
kw metabolic pathway; promoter; termination sequence; ss.
xx Arabidopsis thaliana.

xx EP1033405-A2.
xx 06-SEP-2000.
xx 25-FEB-2000; 2000EP-0301439.
xx 25-FEB-1999; 99US-0121825.
xx 05-MAR-1999; 99US-0123180.
xx 09-MAR-1999; 99US-0123548.
xx 23-MAR-1999; 99US-0125788.
xx 23-MAR-1999; 99US-0126284.
xx 29-MAR-1999; 99US-0126785.
xx 01-APR-1999; 99US-0127462.
xx 06-APR-1999; 99US-0128234.
xx 08-APR-1999; 99US-0128714.
xx 16-APR-1999; 99US-0129845.
xx 19-APR-1999; 99US-0130077.
xx 21-APR-1999; 99US-0130449.
xx 23-APR-1999; 99US-0130510.
xx 23-APR-1999; 99US-0130891.
xx 28-APR-1999; 99US-0131449.
xx 30-APR-1999; 99US-0132048.
xx 30-APR-1999; 99US-0132407.
xx 04-MAY-1999; 99US-0132484.
xx 05-MAY-1999; 99US-0132485.
xx 06-MAY-1999; 99US-0132486.
xx 07-MAY-1999; 99US-0132487.
xx 11-MAY-1999; 99US-0132863.
xx 14-MAY-1999; 99US-0134218.
xx 14-MAY-1999; 99US-0134219.
xx 14-MAY-1999; 99US-0134221.
xx 14-MAY-1999; 99US-0134370.
xx 18-MAY-1999; 99US-0134768.
xx 19-MAY-1999; 99US-0134941.
xx 20-MAY-1999; 99US-0135124.
xx 21-MAY-1999; 99US-0135353.
xx 24-MAY-1999; 99US-0135629.
xx 25-MAY-1999; 99US-0136021.
xx 27-MAY-1999; 99US-0136392.
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Db 443 AGAGGAGGATTCACCTCTCTGGAGATGGGAGAGATATATGACATTCATCTTATTTGA 502

QY 563 CAAACTATCGTCAACACCTTGATTACAGGTATTACAGTACAGTACAGAACTGAGGAGGCAA 622
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Db 503 ACAGTCATCGTATATCATCTTGATTACCGGATATGGCGAGTACAGAACTCCGTGAAGAAA 562

QY 623 TTGACAAGTATGAGGTGGTTTGGAGCCCTTTTCTCGTGGTTATGAAAAATGGTTTCA 682
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QY 683 CTCGTAGTGTACAGGTATCAGTACCTTACCTGAGTGGGCTCTTGGTCCCGAGTCAGTGGCCC 742
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QY 743 TCATTGGAGATTTCACAAATTTGGGAGCAAAATGCTGACATTTATGACTCGGAATGATTTG 802
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 683 TGATCGGAGATTTTAACTACTGGAATGCCAAATCTGATGATGTTATGGCTCGGAAGACTTTG 742

QY 803 GTGCTGGGAGATTTTCTGCGCAAAATATGATGGATGGTTTCTCTCTGCAATTCCTCATGGGT 862
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 XX PF
 XX 24-JUN-1996; 96JP-0162983.
 XX PR
 XX (MTS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA (MITK) MITSUI TOATSU CHEN INC.
 XX WPI; 1998-133625/13.
 XX DR
 XX P-PSDB; RAW41763.
 XX PT
 XX Rice starch branching enzyme gene - synthesises amylopectin to yield
 PT high quality starch
 XX PS
 XX Claim 4; Pages 5-8; 13pp; Japanese.
 XX CC
 XX The present sequence encodes the rice type IV starch branching
 CC enzyme, which has the ability to synthesise amylopectin. The
 CC quality of starch is improved by the use of the protein.
 XX SQ
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 Best Local Similarity 75.0%; Pred. No. 0;
 Matches 1581; Conservative 0; Mismatches 527; Indels 0; Gaps 0;

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 DB 554 TGAACCAACTGTGGAGGATTAACCAACAGAGTATCCCAACACAGGAGATGGCGAGAAGAT 613
 QY 540 TTATGAATAGACCCCTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTACA 599
 DB 614 ATACCAAAITGACCAATGCTGGAAGGATTTCGGAACCACTTCGACTACCGATACAGTGA 673
 QY 600 GTACAAACAACTGAGGAGGCAATTGACAAGTATGAGGTTGGAGGCTTTCTCG 659
 DB 674 ATCAACAGAGATGCGTCGACGTAATTGACCAACATGAAAGGTGGCTTGGATGCAITTTCTCG 733
 QY 660 TGGTTATGAAAAAATGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTGAGTGGGC 719
 DB 734 TGGTTAGAAAAGCTTGGATTACCCCGACGCTGAAGGATTAACCTACCGAGAAATGGGC 793
 QY 720 TCCTGGCCAGTCAGTCCCTCAATGGAGATTTCACAAATGGGACGCAAAATGCTGA 779
 DB 794 ACCTGGAGCAGACTCTGCAGCAATAGTAGTGACTTCAACAAITGGAAACCAATGCGA 853
 QY 780 CATTATGACPCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGCAATTAATGGAGTGG 839
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 QY 840 TTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGTATGGACACTCCATCCAGGTGT 899
 DB 914 ATCCCTGTCTATTCCTCATGGCTCAGCTGTAAAGATTGCGATGGAATACACCACTTGGCGT 973
 QY 900 TAAGGATTCATTCCTTGGATCAACTACTCTTTACAGCTTCCCTGGAATTCATATA 959
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 QY 960 TAATGAATACATTATGATCCACCCGAGAGGAGAGGTATATCTTCCACACCCAGCGCC 1019
 DB 1034 CAACGGTATATATATGATCCACTGAAGAAGAAAATATGATTTCCAACTCCTCAACC 1093
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 QY 1080 TAAATTAAGTACATGATGAAATTTAGAGATGAAGTCTTCCPCGCATAAAAAGCTTGG 1139
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 DB 1934 GTGTGTTTACTTATGACAGAAAGTCAATGACCAAGCACTAGTTGCTGACAGACTATGCAAT 1993
 QY 1920 CTGCTGATGGACAAAGATATGATGATTTTATGGCTCTGGATAGACCGCTCAACATCAAT 1979
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 QY 1980 AATAGATCGTGGGATAGCAITTCGCAAGATGATAGGCTTGTACTATAGGATTAGAGG 2039
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 QY 2160 TAAATGACAGCGAGATTTGACCTGGGAGATGAGATATTTAAGATACCGCTGGTGGCA 2219
 DB 2234 TAAATGCCGCTGATGATTTGACCTTGGAGATGAGATTTACTTAGATATCATGATGCA 2293
 QY 2220 AGAATTTGACCGGCTCTATGAGTATCTTGAAGATAAATAGCTTTATGACTTATGAGAA 2279
 DB 2294 AGAGTTTGATCAGGCCATGCGCATCTTGGAGGAAATATGAGTTTATGACATCTGAGCA 2353


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QY 1496 AATTGATGATTAGATTTGATGGTGTGACATCAATGATGATATATTACACCGGATTAT 1555
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QY 1916 CATTCGCGCTGATGGACAGGATATGATGATTTTATGGCTCGGATAGACCGTCAACAT 1975
Db 1944 CATTCGCTGATGGACAGGATATGATGATTTTATGGCTCTGGACAGACCGGCAACAC 2003
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Db 2004 CTAGCATTCATCGTGGATAGCATTCATTAATGATTAGACTTATCAAAATGGGGTTAG 2063
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Db 2064 GAGGAGAGGGTATCTTAATTTTATGGGAATGAGTTCGGACATCCTGATGGATTGATT 2123
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Db 2184 ATGATAAATGCGTCGAGATTTGACCTGGGTGATCGGACTATCTTAGGTATCGTGGCA 2243
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Db 2504 GAGAACACCAAGAGGCAGCA 2623

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Job time : 565.364 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:31:27 ; Search time 115.381 seconds
(without alignments)
7032.959 Million cell updates/sec

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Perfect score: 2646

Sequence: 1 ATGGTGATACACTCTCTGG.....AAGTAGTAGTAGAAGAGAA 2646

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1369.8	51.8	1393	4	US-09-087-277-3
5	1180.4	44.6	2665	4	US-09-087-894-1
6	1180.4	44.6	2665	4	US-09-087-894-1
7	1033	39.0	2087	4	US-08-941-445A-14
8	1031.4	39.0	2087	4	US-09-257-894-9
9	631.4	23.2	3128	3	US-09-257-894-8
10	628.4	23.7	2487	4	US-08-716-449-1
11	628.4	23.7	2565	4	US-09-257-894-24
12	628.4	23.7	2565	4	US-08-941-445A-16
13	628.4	23.7	2772	4	US-09-257-894-12
14	617.2	23.3	2502	4	US-08-104-158-1
15	542	20.5	1809	4	US-09-257-894-25
16	542	20.5	1865	4	US-09-257-894-20
17	368.8	13.9	11478	3	US-08-981-803-29
18	368.8	13.9	11478	4	US-08-983-440-29
19	358.6	13.6	5402	4	US-08-221-017B-194
20	103.8	3.9	414	4	US-09-257-894-2
21	71	2.7	2426	4	US-08-528-026C-3
22	66.6	2.5	16442	3	US-08-781-891-208
23	63.6	2.4	5394	3	US-08-688-376-1
24	63.6	2.4	4403765	4	US-09-103-840A-2
25	63.6	2.4	4411529	4	US-09-103-840A-1
26	58.4	2.2	405	2	US-08-299-074A-1
27	58.4	2.2	405	4	US-09-399-773-1

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c 29	57.6	2.2	188	1	US-08-466-670-21	Sequence 21, Appl
c 30	57.6	2.2	188	2	US-08-291-011-1	Sequence 1, Appl
c 31	57.6	2.2	188	4	US-09-266-065-1	Sequence 1, Appl
c 32	57	2.2	43795	3	US-08-742-185-101	Sequence 101, App
c 33	56.4	2.1	252	1	US-08-623-906A-1	Sequence 1, Appl
c 34	55.6	2.1	7218	1	US-08-232-463-14	Sequence 14, Appl
c 35	55.4	2.1	2223	1	US-08-257-073-4	Sequence 4, Appl
c 36	53	2.0	571	4	US-09-257-894-16	Sequence 16, Appl
c 37	53	2.0	1276	4	US-09-177-325-2	Sequence 2, Appl
c 38	53	2.0	1276	4	US-09-411-812A-2	Sequence 2, Appl
c 39	53	2.0	1276	4	US-09-590-113-2	Sequence 2, Appl
c 40	53	2.0	3211	2	US-08-574-959A-8	Sequence 8, Appl
c 41	53	2.0	3211	4	US-09-357-014-8	Sequence 8, Appl
c 42	53	2.0	3901	2	US-08-574-959A-6	Sequence 6, Appl
c 43	53	2.0	3901	4	US-09-357-014-6	Sequence 6, Appl
c 44	52	2.0	3337	1	US-08-072-610-1	Sequence 1, Appl
c 45	52	2.0	3337	2	US-08-719-822B-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-087-277-1

; Sequence 1, Application US/09087277B

; Patent No. 6169226

; GENERAL INFORMATION:

; APPLICANT: EK, BO

; APPLICANT: KHOSNOODI, Jamshid

; APPLICANT: LARSSON, Clas-Tomas

; APPLICANT: LARSSON, Hakan

; APPLICANT: RASK, Lars

; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO

; FILE REFERENCE: 003300-486

; CURRENT FILING DATE: 1998-05-29

; EARLIER APPLICATION NUMBER: US/09/087,277B

; EARLIER FILING DATE: 1996-11-28

; EARLIER APPLICATION NUMBER: SE 9504272-7

; EARLIER FILING DATE: 1995-11-29

; EARLIER APPLICATION NUMBER: SE 9601506-0

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 3074

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: Description of Unknown Organism: bell gene

; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum

; OTHER INFORMATION: (potato)

; NAME/KEY: CDS

; LOCATION: (189)..(2825)

; FEATURE:

; NAME/KEY: sig_peptide

; LOCATION: (189)..(332)

; FEATURE:

; NAME/KEY: mat_peptide

; LOCATION: (333)..(2825)

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (92)..(2156)

; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are

; OTHER INFORMATION: n wherein n = A, C, G or T.

; NAME/KEY: misc_feature

; LOCATION: (285)..(287)

; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val

; OTHER INFORMATION: or Phe.

; FEATURE:

✓ 102e
date
to
late

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; NAME/KEY: misc.feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc.feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-087-277-1

Query Match          97.5%; Score 2581; DB 4; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGTGATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGTACAAATCTAAT 60
DB 189 ATGGTGATACACTCTCTGGAGTTCGTTTCCCTACTGTTCCATCAGTGTACAAATCTAAT 248
QY 61 GGATTGAGCAGTAAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTTGAAAAAGCAC 120
DB 249 GGATTGAGCAGTAAATGGTGATCGGAGGAATGCTAATGTTTCTGTATTCTTTGAAAAAGCAC 308
QY 121 TCTCTTTACGGAGATCTTGGCTGAAAGCTCTTCTTACAAATTCGGAATTCGACCTTCT 180
DB 309 TCTCTTTACGGAGATCTTGGCTGAAAGCTCTTCTTACAAATTCGGAATTCGACCTTCT 368
QY 181 ACAGTTGCACATCGGGAAAGTCCTTGCTGGACCCAGAGTATGCTCCTCATCC 240
DB 369 ACAGTTGCACATCGGGAAAGTCCTTGCTGGACCCAGAGTATGCTCCTCATCC 428
QY 241 TCAACAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAAATTCGCCAGCATCAACTGAT 300
DB 429 TCAACAGACCAATTTGAGTTTCACTGAGACATCTCCAGAAAATTCGCCAGCATCAACTGAT 488
QY 301 GTAGATAGTTCAACAATGGAAACGCTAGCCAGATTAACACTGAGAACGATGAGTTGAG 360
DB 489 GTAGATAGTTCAACAATGGAAACGCTAGCCAGATTAACACTGAGAACGATGAGTTGAG 548
QY 361 CCGTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTGCTTCATCACTACAACCTA 420
DB 549 CCGTCAAGTGATCTTACAGGAAGTGTGAAGAGCTGGATTTGCTTCATCACTACAACCTA 608
QY 421 CAAGAAGTGGTAAACTGGAGAGTCTTAAACATTAATACTTCTGAAGAGACAATTAAT 480
DB 609 CAAGAAGTGGTAAACTGGAGAGTCTTAAACATTAATACTTCTGAAGAGACAATTAAT 668
QY 481 GATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACTGGACTTGGTTCAGAAAT 540
DB 669 GATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACTGGACTTGGTTCAGAAAT 728
QY 541 TATCAAAATAGACCCCTTTTGCACAAACTATGCTCAACACCTTGATTAACAGTATTCACAG 600
DB 729 TATCAAAATAGACCCCTTTTGCACAAACTATGCTCAACACCTTGATTAACAGTATTCACAG 788
QY 601 TACAAGAACTGAGGGAGCAATGACAAGTATGAGGGTGGTGGAGGCTTTTCTCGT 660
DB 789 TACAAGAACTGAGGGAGCAATGACAAGTATGAGGGTGGTGGAGGCTTTTCTCGT 848
QY 661 GGTATCAAAAAATGGTTTTCACCTGCTAGTGTACAGTATCACTTACCGTACGTTGGCT 720
DB 849 GGTATCAAAAAATGGTTTTCACCTGCTAGTGTACAGTATCACTTACCGTACGTTGGCT 908
QY 721 CTTGGTCCCGAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTGAC 780
DB 909 CTTGGTCCCGAGTCAGCTGCCCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTGAC 968
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QY 781 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGAAATAATGTGGATGGT 840
DB 969 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCGAAATAATGTGGATGGT 1028
QY 841 TCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATAGTATGGACACATCCATCAGGTGTT 900
DB 1029 TCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATAGTATGGACATCCATCAGGTGTT 1088
QY 901 AAGGATTCCTATTCCTGCTTGGATCAACTACTCTTTTACAGCTTCTGATGAAATTCATAT 960
DB 1089 AAGGATTCCTATTCCTGCTTGGATCAACTACTCTTTTACAGCTTCTGATGAAATTCATAT 1148
QY 961 AATGGAATCATATGATTCACCCGGAAGAGAGAGTATATCTTCCAAACCCACGGCCA 1020
DB 1149 AATGGAATCATATGATTCACCCGGAAGAGAGAGTATATCTTCCAAACCCACGGCCA 1208
QY 1021 AAGAAACCAAGTCGCTGAGNATATATGAATCTCATATTTGAATGAGTAGTCCCGAGCCT 1080
DB 1209 AAGAAACCAAGTCGCTGAGNATATATGAATCTCATATTTGAATGAGTAGTCCCGAGCCT 1268
QY 1081 AAAATTAACCTACATACGTGAATTTTGGAGATGAAGTCTTCTCCTGCATAAAAAAGCTTGGG 1140
DB 1269 AAAATTAACCTACATACGTGAATTTTGGAGATGAAGTCTTCTCCTGCATAAAAAAGCTTGGG 1328
QY 1141 TACAATCGCTGCAAAATTTATGGCTATTCAAGAGCATTTTATTACGCTAGTTTGGTTAT 1200
DB 1329 TACAATCGCTGCAAAATTTATGGCTATTCAAGAGCATTTTATTATGCTAGTTTGGTTAT 1388
QY 1201 CATGTCACAAATTTTTTGGACCAAGCAGCCGTTTGGACGCCGCGACGACCTTAAGTCT 1260
DB 1389 CATGTCACAAATTTTTTGGACCAAGCAGCCGTTTGGACGCCGCGACGACCTTAAGTCT 1448
QY 1261 TTGATTGATAAAGCTCATGAGTAGGAATTTGTTCTCATGAGCATTTGTTTACAGCCAT 1320
DB 1449 TTGATTGATAAAGCTCATGAGTAGGAATTTGTTCTCATGAGCATTTGTTTACAGCCAT 1508
QY 1321 GCATCAAAATATATCTTTAGTAGGACTGNACATGTTTGNACTGCACCGATAGTTTACTT 1380
DB 1509 GCATCAAAATATATCTTTAGTAGGACTGNACATGTTTGNACTGCACCGATAGTTTACTT 1568
QY 1381 CACTCTGGAGTCTGCTGGTTATCATTTGGATGGGATTCGCCCTCTTTAACTATGGAAC 1440
DB 1569 CACTCTGGAGTCTGCTGGTTATCATTTGGATGGGATTCGCCCTCTTTAACTATGGAAC 1628
QY 1441 TGGAGGTACTTACGATTCCTCTCAAAATCGGAGATGGTGGTGGATGCGTTCAAATTT 1500
DB 1629 TGGAGGTACTTACGATTCCTCTCAAAATCGGAGATGGTGGTGGATGCGTTCAAATTT 1688
QY 1501 GATGGATTTAGATTTGATGGTGTGACATCAATGATGATATTTCAACCGGATTAFCGGTG 1560
DB 1689 GATGGATTTAGATTTGATGGTGTGACATCAATGATGATATTTCAACCGGATTAFCGGTG 1748
QY 1561 GGATTCCTGCGAACTACGAGGAATACFTTTGGACTCGCAACTGATGTGGAATGCTGTTG 1620
DB 1749 GGATTCCTGCGAACTACGAGGAATACFTTTGGACTCGCAACTGATGTGGAATGCTGTTG 1808
QY 1621 TATCTGATGCTGGTCAACGATCTTATTCATGGGTTTTTCCAGATGCAATTAACATTTGGT 1680
DB 1809 TATCTGATGCTGGTCAACGATCTTATTCATGGGTTTTTCCAGATGCAATTAACATTTGGT 1868
QY 1681 GAAATGTTACGGAAATGCCACATTTTGTATTTCCCGTCCAGAGGGGGTGTGGCTTT 1740
DB 1869 GAAATGTTACGGAAATGCCACATTTTGTATTTCCCGTCCAGAGGGGGTGTGGCTTT 1928
QY 1741 GACTATCGCTGTCATATGGCAATTCGTGATAAAGGATTTGAGTTGCTCAAGAAACGGGAT 1800
DB 1929 GACTATCGCTGTCATATGGCAATTCGTGATAAAGGATTTGAGTTGCTCAAGAAACGGGAT 1988
QY 1801 GAGGATTTGAGAGTGGGTGATTTGTTTTCATGACATGACAAATAGAGATGTTGTCGGAAG 1860
DB 1989 GAGGATTTGAGAGTGGGTGATTTGTTTTCATGACATGACAAATAGAGATGTTGTCGGAAG 2048
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QY 1861 TGTGTTTCATAGCTGAAAGTCAATGATCAAGCTCTAGTCGGTGTAAACACTATAGCATTC 1920
Db 2049 TGTGTTTCATAGCTGAAAGTCAATGATCAAGCTCTAGTCGGTGTAAACACTATAGCATTC 2108
QY 1921 TGGCTGTAGGCAAGGATATGATGATTTATGGCTCTGGATAGACCGTCAACATCATTA 1980
Db 2109 TGGCTGTAGGCAAGGATATGATGATTTATGGCTCTGGATAGACCGTCAACATCATTA 2168
QY 1981 ATAGATCTGGGATAGAGTTCACAAAGATGATTAGGCTTGTAACATGGATTAGAGGA 2040
Db 2169 ATAGATCTGGGATAGAGTTCACAAAGATGATTAGGCTTGTAACATGGATTAGAGGA 2228
QY 2041 GAAGGATACCTAAATTTTCATGGGAATGAATTCGGCCACCTCTAGTGGATGATTCCT 2100
Db 2229 GAAGGATACCTAAATTTTCATGGGAATGAATTCGGCCACCTCTAGTGGATGATTCCT 2288
QY 2101 AGGCTGAACACACCTCTCTGATGGCTCAGTAATCCCGGAACCAATTCAGTTATGAT 2160
Db 2289 AGGCTGAACACACCTCTCTGATGGCTCAGTAATCCCGGAACCAATTCAGTTATGAT 2348
QY 2161 AAATGCAGACGGAGATTGACCTGGGAGATGCAGAAATTTAAAGATACCGTGGTTCGAA 2220
Db 2349 AAATGCAGACGGAGATTGACCTGGGAGATGCAGAAATTTAAAGATACCGTGGTTCGAA 2408
QY 2221 GAATTTGACCGGCTATGCAGTATCTTGAAGATAAATATGATGATTCAGTTCAGAAC 2280
Db 2409 GAATTTGACCGGCTATGCAGTATCTTGAAGATAAATATGATGATTCAGTTCAGAAC 2468
QY 2281 CAGTTTCATATCAGCAAGGATGAGGATAGGATGATGATTTGATTTGAAAAGGAAACCTA 2340
Db 2469 CAGTTTCATATCAGCAAGGATGAGGATAGGATGATGATTTGATTTGAAAAGGAAACCTA 2528
QY 2341 GTTTTGTCTTTAATTTTCTACTGGACAAAAGCTATTTCAGACTATCGCATAGCTGCTG 2400
Db 2529 GTTTTGTCTTTAATTTTCTACTGGACAAAAGCTATTTCAGACTATCGCATAGCTGCTG 2588
QY 2401 AAGCTGGAATAACAGGTTGCTTGGACTCAGATGATCCACTTTTGTGGCTTCGGG 2460
Db 2589 AAGCTGGAATAACAGGTTGCTTGGACTCAGATGATCCACTTTTGTGGCTTCGGG 2648
QY 2461 AGAATTCATCATATGCGGATATTTTCACTTTGAAGATGATGATGATGATGATGATGAT 2520
Db 2649 AGAATTCATCATATGCGGATATTTTCACTTTGAAGATGATGATGATGATGATGATGAT 2708
QY 2521 TCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2580
Db 2709 TCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2768
QY 2581 GAAGAAGAAGAAG 2634
Db 2769 GAAGAAGAAGAAG 2822

RESULT 2
US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakau
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29

; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

Query Match 97.5%; Score 2581; DB 4; Length 3074;
Best Local Similarity 98.7%; Pred. No. 0;
Matches 2599; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 1 ATGCTGTATACACTCTCTGGAGTTCGTTTCTTCTACTGTTCCATCAGTGTACAAATCTAAT 60
Db 189 ATGCTGTATACACTCTCTGGAGTTCGTTTCTTCTACTGTTCCATCAGTGTACAAATCTAAT 248
QY 61 GGATTCAGCAGTAATGTTGATCGGAGGAATGCTAATGTTCTGTATTCTTGAAAAAGCAC 120
Db 249 GGATTCAGCAGTAATGTTGATCGGAGGAATGCTAATGTTCTGTATTCTTGAAAAAGCAC 308
QY 121 TCTCTTTACAGGAAGATCTTGGCTGAAAAGTCTTCTTACAAATCCGAATCCGACCTTCT 180
Db 309 TCTCTTTACAGGAAGATCTTGGCTGAAAAGTCTTCTTACAAATCCGAATCCGACCTTCT 368
QY 181 ACAGTTTCAGCATCGGGGAAAGTCTTGTGCTGGAACCCAGAGTGTAGTCTCTCATCC 240
Db 369 ACAGTTTCAGCATCGGGGAAAGTCTTGTGCTGGAACCCAGAGTGTAGTCTCTCATCC 428
QY 241 TCAACAGACCAATTTGAGTTCAGTGTAGATCTCCAGAAATTTCCCGAGCATCACTGAT 300
Db 429 TCAACAGACCAATTTGAGTTCAGTGTAGATCTCCAGAAATTTCCCGAGCATCACTGAT 488
QY 301 GTAGTAGTTCAACATGGAAACAGCTAGCAGATTAACACTCAGACAGATGAGTGTAG 360
Db 489 GTAGTAGTTCAACATGGAAACAGCTAGCAGATTAACACTCAGACAGATGAGTGTAG 548
QY 361 CCCTCAAGTAGTCTTACAGGAAGTGTGAAGAGCTGATTTTCTTCATCAGTACAACTA 420
Db 549 CCCTCAAGTAGTCTTACAGGAAGTGTGAAGAGCTGATTTTCTTCATCAGTACAACTA 608

QY	421	CAAGAAGGTTGTAACCTGGAGAGTCTAAACATTAATACTCTCGAAGACAAATTAATT	480
DB	609	CAAGAAGTGGTAAACTGGAGAGTCTAAACATTAATACTCTCTGAAGACAAATTAATT	668
QY	481	GATGAATCTGATAGGATCAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAGAATT	540
DB	669	GATGAATCTGATAGGAICAGAGAGGGGCATCCCTCCACCTGGACTTGGTCAGAGAATT	728
QY	541	TATGAATAGACCCCTTTTGACAACTATCGTCAACACCTTGAATTACAGSTATTACAG	600
DB	729	TATGAATAGACCCCTTTTGACAACTATCGTCAACACCTTGAATTACAGSTATTACAG	788
QY	601	TACAAGAACTCAGGAGGCAATTGACAAGTATGAGGTGGTTCGGAAGCCCTTTCTCGT	660
DB	789	TACAAGAACTCAGGAGGCAATTGACAAGTATGAGGTGGTTCGGAAGCCCTTTCTCGT	848
QY	661	GGTTATGAAAAAATGGTTCCTACTCGTAGTGTACAGSTATCACTTACCGTCAGTGGCT	720
DB	849	GGTTATGAAAAAATGGTTCCTACTCGTAGTGTACAGSTATCACTTACCGTCAGTGGCT	908
QY	721	CTTTGGTCCGAGTCAGCTGCCCTCAATTGGAGATTTCAACAATTTGGACCCCAATGCTGAC	780
DB	909	CTTTGGTCCGAGTCAGCTGCCCTCAATTGGAGATTTCAACAATTTGGACCCCAATGCTGAC	968
QY	781	ATTATGACTCGGAATCAAAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATATGTGGATGCT	840
DB	969	ATTATGACTCGGAATCAAAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATATGTGGATGCT	1028
QY	841	TTCTCCTGCAATTCCTCATGGTGCCAGAGTGAAGATACGATGAGACACTCCATCAGGTGTT	900
DB	1029	TTCTCCTGCAATTCCTCATGGTGCCAGAGTGAAGATACGATGAGACACTCCATCAGGTGTT	1088
QY	901	AAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGTCTCTGATGAAATTCATAT	960
DB	1089	AAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGTCTCTGATGAAATTCATAT	1148
QY	961	AATGGAATCATTATGATCCACCCGAAGGAGAGTATATCTTCCAACACCCACGGCCA	1020
DB	1149	AATGGAATCATTATGATCCACCCGAAGGAGAGTATATCTTCCAACACCCACGGCCA	1208
QY	1021	AAGAACCAAGTCGCTGAGAAATATGATCTCATATTTGGAATGATAGTCCGGAGCCT	1080
DB	1209	AAGAACCAAGTCGCTGAGAAATATGATCTCATATTTGGAATGATAGTCCGGAGCCT	1268
QY	1081	AAATTAACATACGCTGAAATTTAGAGATGAAATCTTCTCGCATATAAAAAGCTTGG	1140
DB	1269	AAATTAACATACGCTGAAATTTAGAGATGAAATCTTCTCGCATATAAAAAGCTTGG	1328
QY	1141	TACAATGCGCTGAAATTTAGGCTATTCAAGACATCTTATTACCGTAGTTTGGTTAT	1200
DB	1329	TACAATGCGCTGAAATTTAGGCTATTCAAGACATCTTATTATGCTAGTTTGGTTAT	1388
QY	1201	CATGTCACAAATTTTTTGCACCAAGCAGCCGTTTTTGGAGCGCCGACGACCTTAAGTCT	1260
DB	1389	CATGTCACAAATTTTTTNGCACCAGCAGCCGTTTTTGGAACNCCGACGACCTTAAGTCT	1448
QY	1261	TTGATTCATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGAGCATTTGTCACAGCCAT	1320
DB	1449	TTGATTCATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGAGCATTTGTCACAGCCAT	1508
QY	1321	GCATCAATAATACTTTAGATGAGCTCAACATGTTTCACTGCACCGATAGTCTTACTTTT	1380
DB	1509	GCATCAATAATACTTTAGATGAGCTGAACATGTTTGACGGCACAGATGTTGTTACTTT	1568
QY	1381	CACCTCGAGCTGGTGGTTATCATTTGGAITGGGATTCGCGCTCTTTAACTATGGAAC	1440
DB	1569	CACCTCGAGCTGGTGGTTATCATTTGGAITGGGATTCGCGCTCTTTAACTATGGAAC	1628
QY	1441	TGGAGGTACTTAGGTATCTTCTCAAAATGCCAGATGGTGGTGGATGGTTCAAAATTT	1500
DB	1629	TGGAGGTACTTAGGTATCTTCTCAAAATGCCAGATGGTGGTGGATGGTTCAAAATTT	1688
QY	1501	GATGGATTTAGATTTGATGGTGTGACATCAATGATGATATTCACCAAGCATATCGGT	1560

1689	Db	 GATGGATTAGATTGGTGTGCACATCAATGATGTAATCTCACCACGGATTATCGGTG	1748
1561	QY	GGATTCACTGGGAACACAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG	1620
1749	Db	GGATTCACTGGGAACACAGGAATACTTTGGACTCGCAACTGATGTGGATGCTGTTGTG	1808
1621	QY	TATCTGATGCTGCTCAACGATCTATTTCATGGGCTTTTCCAGATGCAANTACCAATGGT	1680
1809	Db	TATCTGATGCTGCTCAACGATCTATTTCATGGGCTTTTCCAGATGCAANTACCAATGGT	1868
1681	QY	GAAGATGTTAGCGGAATGCCGACATTTTGTATCCCGTCCAAAGAGGGGGGTGTGGCTTT	1740
1869	Db	GAAGATGTTAGCGGAATGCCGACATTTTGTATCCCGTCCAAAGATGGGGGTGTGGCTTT	1928
1741	QY	GACTATCGGCTGCAATGGCAATTCGTGATAACGGATTGAGTTGCTCAAGAAACGGAT	1800
1929	Db	GACTATCGGCTGCAATGGCAATTCGTGATAACGGATTGAGTTGCTCAAGAAACGGAT	1988
1801	QY	GAGGATTGGAGAGTGGTGATATTTGTTTATACACTGACAAATAGAAGTGGTCGGAAG	1860
1989	Db	GAGGATTGGAGAGTGGTGATATTTGTTTATACACTGACAAATAGAAGTGGTCGGAAG	2048
1861	QY	TGTGTTTCAATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACATAGCAATC	1920
2049	Db	TGTGTTTCAATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACATAGCAATC	2108
1921	QY	TGGCTGATGACAAAGGATATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA	1980
2109	Db	TGGCTGATGACAAAGGATATGATTTTATGGCTCTGGATAGACCGTCAACATCATTA	2168
1981	QY	ATAGATCGTGGGATAGCATTTGCCAAGATGATTAGGCTTTACTATFGGATTAGGAGGA	2040
2169	Db	ATAGATCGTGGGATAGCATTTGCCAAGATGATTAGGCTTTACTATFGGATTAGGAGGA	2228
2041	QY	GAAGGGTACCTAAATTTTCATGGGAATGAATTCGGCCACCTCGAGTGGATTGATTTCCCT	2100
2229	Db	GAAGGGTACCTAAATTTTCATGGGAATGAATTCGGCCACCTCGAGTGGATTGATTTCCCT	2288
2101	QY	AGGCTGAACAACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGAT	2160
2289	Db	AGGCTGAACAACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAATTCAGTTATGAT	2348
2161	QY	AAATGCAGACGGAGATTTCACCTGGGAGATGCAGAAATTTAAGATACCGGGTGCAG	2220
2349	Db	AAATGCAGACGGAGATTTCACCTGGGAGATGCAGAAATTTAAGATACCGGGTGCAG	2408
2221	QY	GAATTTGACCGGCTATGCGATCTTTGAAGATAAATATAGTTTATGACTTCAGAACAC	2280
2409	Db	GAATTTGACCGGCTATGCGATCTTTGAAGATAAATATAGTTTATGACTTCAGAACAC	2468
2281	QY	CAGTTCAATACCAAGAGGATGAAGGAGATAGGATGATTTGTTGAAAAGGAACCTA	2340
2469	Db	CAGTTCAATACCAAGAGGATGAAGGAGATAGGATGATTTGTTGAAAAGGAACCTA	2528
2341	QY	GTTTTGTCTTTAATTTTCACTGCACAAAAGCTATTTCAGACTATCCATAGCTGCTG	2400
2529	Db	GTTTTGTCTTTAATTTTCACTGCACAAAAGCTATTTCAGACTATCCATAGCTGCTG	2588
2401	QY	AAGCCTGGAAAATACAGGTTGCTTGGACTGAGATGATCCATTTTGGTGGCTTCGGG	2460
2589	Db	AAGCCTGGAAAATACAGGTTGCTTGGACTGAGATGATCCATTTTGGTGGCTTCGGG	2648
2461	QY	AGAATTGATCATATGCCGAATATTTTACCTTTTGAAGATGGTATGATGCTCCCTCGT	2520
2649	Db	AGAATTGATCATATGCCGAATATTTTACCTTTTGAAGATGGTATGATGCTCCCTCGT	2708
2521	QY	TCAATTATGGTGTATGACCTTGTAAACACAGCTGCTATGCACTAGTAGACAAGAA	2580
2709	Db	TCAATTATGGTGTATGACCTTGTAAACACAGCTGCTATGCACTAGTAGACAAGAA	2768
2581	QY	GAAGAAAGAAAGAAAGAAAGAAAGCAAGTACACGAGTAGAAGAGTAGTA	2634

Db 2769 GAACAAGAGAAGAAGTAGCTAGCTAGTAGAAGAAGTAGTAGTAAGAAGAA 2822

RESULT 3
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No...6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:belI gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-087-277-3

Query Match 51.8%; Score 1369.8; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 819 TCTGCCAAATAATCTGGATGGTTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 878
Db 1 TCTGCCAAATAATGTGGATGGTTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60
QY 879 TATGGACATCCCATCAGGTGTTAAAGGATTCATTCCTGCTTGGATCAACTACTCTTTACA 938
Db 61 TATGGACATCCCATCAGGTGTTAAAGGATTCATTCCTGCTTGGATCAACTACTCTTTACA 120
QY 939 GCTTCTCTGATGAATTCCTATATTAATGAATACATTATGATCCACCCGAAGAGGAGGTA 998
Db 121 GCTTCTCTGATGAATTCCTATATTAATGAATATATTATGATCCACCCGAAGAGGAGGTA 180
QY 999 TATCTTCCACACCCACGCCCAAGAAACAAAGTCGCTGAGAAATATATGAATCTCATAT 1058

Db 1261 CCCTGAGTGGATTGATTTCCCTAGGCTGAACAACACCTCTCTGTAGTGCCTCAGTAATTC 1320
QY 2139 CGGAACCAATTCAGTTATGATAAATGCAGCGAGATTGACCTGGGAGATCAGAAAT 2198
Db 1321 CGGAACCAATTCAGTTATGATAAATGCAGCGAGATTGACCTGGGAGATCAGAAAT 1380
QY 2199 TTAAAGATACCGT 2211
Db 1381 TTAAAGATACCGT 1393

RESULT 4

US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Klas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: betaII gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is xaa wherein xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is xaa wherein xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is xaa wherein xaa = Pro.
US-09-658-499-3

Query Match 51.8%; Score 1369.8; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 137; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 819 TCTGCCAAATAATGTGATGGTTCTCTCGAATTCCTCATGGGTCAGAGTGAAGATACG 878
Db 1 TCTGCCAAATAATGTGATGGTTCTCTCGAATTCCTCATGGGTCAGAGTGAAGATACG 60
QY 879 TATGGACATCCATCAGGTGTTAAGGATTCATTCCTGTGGATCAACTACTCTTTACA 938
Db 61 TATGGACATCCATCAGGTGTTAAGGATTCATTCCTGTGGATCAACTACTCTTTACA 120

QY 939 GCTTCCTGATGAATTCATATATATGAATACATATATGATCCACCCGAGAGAGAGTA 998
Db 121 GCTTCCTGATGAATTCATATATATGAATACATATATGATCCACCCGAGAGAGTA 180
QY 999 TATCTTCCACACCCGAGGCGGACCAAGTCCCTGAGATATATGAATCTCATAT 1058
Db 181 TATCTTCCACACCCGAGGCGGACCAAGTCCCTGAGATATATGAATCTCATAT 240
QY 1059 TGAATGAGTAGTCCGGAGGCTAAATTAACATCACTAGCTAAATTTAGAGATGAAGTTCT 1118
Db 241 TGAATGAGTAGTCCGGAGGCTAAATTAACATCACTAGCTAAATTTAGAGATGAAGTTCT 300
QY 1119 TCCTCGCATAAAAAGCTTGGGTACAAATGCGCTCAAAATATGCTATTCGAAGAGATTC 1178
Db 301 TCCTCGCATAAAAAGCTTGGGTACAAATGCGGTCAAAATATGCTATTCGAAGAGATTC 360
QY 1179 TTATTACGCTAGTTTGGTTATCATGTCACAAATTTTTTGCACCACGACGCCCTTTTGG 1238
Db 361 TTATTATGCTAGTTTGGTTATCATGTCACAAATTTTTTNGACCAAGCAGCCCTTTTGA 420
QY 1239 AACGCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTTGTGTCT 1298
Db 421 AACNCCGACGACCTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTTGTGTCT 480
QY 1299 CATGGACATTTGTTACAGACCCATGCATCAAAATAAATTAATAGTGAATGATTTGA 1358
Db 481 CATGGACATTTGTTACAGACCCATGCATCAAAATAAATTAATAGTGAATGATTTGA 540
QY 1359 CTGCAACGATAGTTTACTTTCACCTGAGGCTCGTGGTTATCATTTGGATGCGGATTC 1418
Db 541 CGGCACAGATAGTTTACTTTCACCTGAGGCTCGTGGTTATCATTTGGATGCGGATTC 600
QY 1419 CCGCTCTTTAACTATGGAACCTGGAGGTAATAGTATCTTCTCAAAATGCGAGATG 1478
Db 601 CCGCTCTTTAACTATGGAACCTGGAGGTAATAGTATCTTCTCAAAATGCGAGATG 660
QY 1479 GTGTTGGATGCGTTCAAAATTTGATGATTTAGATTTGATGGTGTGACATCAATGATGA 1538
Db 661 GTGTTGGATGCGTTCAAAATTTGATGATTTAGATTTGATGGTGTGACATCAATGATGA 720
QY 1539 TATTCACACGAGTTATCGGTGGGATTCACCTGGGAACACGAGGAATCTTTGGACTCGC 1598
Db 721 TATTCACACGAGTTATCGGTGGGATTCACCTGGGAACACGAGGAATCTTTGGACTCGC 780
QY 1599 AACTGATGTGGATCGTGTGTATCTGATCTGGTCAACGATCTATTCATGCGCTTTT 1658
Db 781 AACTGATGTGGATCGTGTGTATCTGATCTGGTCAACGATCTATTCATGCGCTTTT 840
QY 1659 CCCAGATGCAATTACCATTTGGTGRAGATTTAGCGGAATCGGACATTTCTATTCGCGT 1718
Db 841 CCCAGATGCAATTACCATTTGGTGRAGATTTAGCGGAATCGGACATTTCTATTCGCGT 900
QY 1719 CCAAGAGGGGGTGTGGCTTTGACTATCGGCTGCATATGGCAATTCGTGATAACGAT 1778
Db 901 TCAGATGGGGGTGTGGCTTTGACTATCGGCTGCATATGSCAATTCGTGATAATGAT 960
QY 1779 TGAGTTGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATTTCTATPACACTGAC 1838
Db 961 TGAGTTGCTCAAGAAACGGGATGAGGATGGAGAGTGGGTGATATTTCTATPACACTGAC 1020
QY 1839 AAATAGAGATGGTCCGGAAGAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTTAGT 1898
Db 1021 AAATAGAGATGGTCCGGAAGAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTTAGT 1080
QY 1899 CGGTGATAAAACTATAGCATTTCTGGCTGATGCAAGGATATGATGATTTTATGGCTCT 1958
Db 1081 CGGTGATAAAACTATAGCATTTCTGGCTGATGCAAGGATATGATGATTTTATGGCTCT 1140
QY 1959 GGATAGACCGTCAACATCATTTAATAGATCGTGGGATAGCATTTGCACAGATGATTAGCT 2018
Db 1141 GGATAGACCNCTCAACATCATTTAATAGATCGTGGGATAGCATTTGCACAGATGATTAGCT 1200
QY 2019 TGTAACATGCGATTAGGAGGAGAGGTAACCTAAATTTTCATGGGAATGAATTCGGCA 2078

1620 GTATCTGATCGTGGTCAACGATCTTATTATCATGGCTTTTCCAGATGCAATACCAATGG 1679
1521 TTACTTTGATGCTGGTAAATGATCTAATTCATGACCTTTATCTGAGCGTGAACCAATGG 1580
1680 TGAAGATGTTAGCGGATGCCACATTTTGTTCCTCCGTCACAGAGGGGGTGTGGCTT 1739
1581 TGAAGATGTTAGTGGATGCTTACATTTGCCCTCTCTGTCACGATGGTGGGTAGTTT 1640
1740 TGACTATCGCTGCATATGCGAATTTGCTGATGAACGATGATGCTGCTCAAGAAACGGGA 1799
1641 TGACTATCGGATGCATATGCTGCTGGCTGACAAATGATGATGCTTCTCAAGCAAAAGTGA 1700
1800 TGAGGATGAGAGTGGGTGATTTGTCATACACACACACACACACACACACACACACAC 1859
1701 TGAACCTGGAAGATGGGTGATTTGTCATACACACACACACACACACACACACACACAC 1760
1860 GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGTGATAAACTATAGCAAT 1919
1761 GTGTGTAACCTTATGCTGAAAGTCATGATCAAGCTCTAGTCGGTGTGATAAACTATAGCAAT 1820
1920 CTGGCTGATGGAACGATGATGATTTTATGGCTCTGATGAGACCGTCACATCAAT 1979
1821 TTGGTGTGATGGAACGATGATGATTTTATGGCTCTGATGAGACCGTCACATCAAT 1880
1980 AATAGATCGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2039
1881 CATGATCGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1940
2040 AGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2099
1941 AGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2000
2100 TAGGGTGAACACACACCTCTGATGCTCAGTAATCCCGGAAACCAATTCAGTTATGA 2159
2001 ARAGGTGCCCAAGACTTCCAGTGGTAAGTTTATCCAGGGAATACACAGTTATGA 2060
2160 TAAATGACAGACGGAGATTTGACCTGGGAGATGAGATAATTTAAGATFACCTGGGTTGCA 2219
2061 CAATGTCGTCGAAGATTTGACCTGGGAGATGAGATAATTTAAGATFACCTGGGTTGCA 2120
2220 AGAATTTGACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2279
2121 AGAATTTGATCAGCAATGCAACATCTTGAGCAAAATATCAATTCATGATGATGATGAT 2180
2280 CCAGTTCATATCAGAAAGATGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 2339
2181 CCAGTATATTTCCCGGAACATGAGGAGATGATGATGATGATGATGATGATGATGATGATGAT 2240
2340 AGTTTGTCTTTTAAATTTTCACTGGACAAAGCTATTCAGACTATTCAGACTATTCAGACT 2399
2341 GGTATTTGTCTTCAACTTCCACTGCAACACAGCTATTTTGAATFACCTATTTGGTGTGCTG 2300
2400 GAAGCTGGAAATACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGTGCTGCTGCTG 2459
2301 AAAGCTGGGGTGTATAGGTTGCTTGGACTCAGGCTGATGATGATGATGATGATGATGATGAT 2360
2460 GAGAAATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2519
2361 CAGATTCATCACCAGCGGAGACTTCCAGCGGAGCTGTTCCGATGATATAGGCCATA 2420
2520 TTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2573
2421 TTCATCTCGGTTTATACCAAGCAGAAACATGTCGTCTATGCTCCAGTGGGA 2474

RESULT 6

US-08-941-445A-14

; Sequence 14, Application US/08941445A

; Patent No. 6107060

; GENERAL INFORMATION:

; APPLICANT: Keeling, Peter

; APPLICANT: Guan, Hanping

TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941.445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: mRNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Zea mays
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 91..264
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 265..2487
FEATURE:
NAME/KEY: CDS
LOCATION: 91..2490
US-08-941-445A-14

Query Match 44.6%; Score 1180.4; DB 3; Length 2725;

Best Local Similarity 72.7%; Pred. No. 0;

Matches 1523; Conservative 0; Mismatches 571; Indels 0; Gaps 0;

QY 480 TGATGAATCTATAGGATCAGAGAGGGGATCCCTCCACTGGACTTGGTCAGAAAGAT 539
DB 393 TGATGCTCAAGCTTGACAGAGATGTCAGATGGTCCCCCACCAGCGATGACAAATAAT 452
QY 540 TTATGAATAGACCCCTTTTGCACAAATATCGTCAACACCTTGATTCAGGTATTCACA 599
DB 453 ATTCAGATTCACCCCATGTTGCAAGGCTATAAGTACCATCTTGAGTATCGGTACAGCT 512
QY 600 GTACAGAAATGAGGAGGAGCAATGACAAGTATGAGGTTGGTGGAGGCTTTTCG 659
DB 513 CTATAGAGAAATCCCTTCAGACATGATGACATGAGAGAGGCTTGAGAGGCTTCCCG 572
QY 660 TGGTTATGAAAAAATGGGTTTCACTCGTAGTCTACAGGTATCATCTTACCCTGAGTGGGC 719
DB 573 TAGTATGAGAAGTTTGGATTATGATCCAGCGCGAGGATGATCATATCGAAGATGGGC 632
QY 720 TCTTGGTCCCGAGTCAGCTGCCCTCATTTGGAGATTTCAACAAATGCGGACGCAATGCTGA 779
DB 633 TCCGTGAGCAATTTCTCGAGCATTTGGTGGTGCACGTCAACAACTGGGATCCAAATGCAGA 692

QY	780	CATTAATGACTCGGAATGAATTTGTGTCTGGAGATTTTCTGCCAAATAATGTGGATGG	839
DB	693	TCGTATGAGCAAAAATGAGTTTGTGTGTGGAAATTTTCTGCTTAACAATGCAGATGG	752
QY	840	TTCTCCTGCAATTCCTCATGGTCCAGATCAAGATACGTATGGCACTCCATCAGTGT	899
DB	753	TACATCACCTAATTCCTCATGGATCTGTTAAAGGTGAGAATGGATACTCCATCAGGAT	812
QY	900	TAAGGATTCACATTCCTGTTGGATCAACTACTCTTTACAGCTTCCTCATGAAATTCATA	959
DB	813	AAAGGATTCAAATTCAGCCTGGATCAAGTACTCAGTCAGCGCCCGGAGAAATACCAT	872
QY	960	TAATGGATACATTAATGATCCACCCGAAGAGGAGAGATATATCTTCCAAACACCAACG	1019
DB	873	TGATGGGATTTATATGATCCTCTGAGAGGTAAAGTATGTGTTCAGGCATGCGCAAC	932
QY	1020	AAAGAAACCAAAGTCGTGAGATATATGAATCTCATATTTGGATGAGTAGTCCGGAGCC	1079
DB	933	TAAACGCCAAATCAATGCGGATATATGAACACATGTCGGAATGAGTAGCCCGGAAC	992
QY	1080	TAAATTAACCTATACGTGAATTTAGAGATGAAGTTCTTCCCTCGCATAAAAAGCTTGG	1139
DB	993	GAAGATAAACACATATGTAACITTTAGSGATGAGTCTCCCAAGAATAAAAAAACTTGG	1052
QY	1140	GTACAATGGCGTGCAAAATTAATGGCTATTAAGAGCAATCTTATTAACGTAGTTTGGTTA	1199
DB	1053	ATACAATGCGAGTGCAAAATAATGGCAATCCCAAGAGCACTCATATATATGGAAGCTTGGATA	1112
QY	1200	TCATGTCACAAAATTTTTTCACCAACGACCCCTTTTGGAAACGCCGACCACTTAAGTC	1259
DB	1113	CCATGTAACATAATTTTTTGGCCAAAGTAGTCGTTTGGTACCCCAAGAAATTTGAAGTC	1172
QY	1260	TTTGATTTGATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGCAATGTTTCCACAGCCA	1319
DB	1173	TTTGATTTGATAGACACATGAGCTTGGTTTGTAGTCTCATGGATGCTTCATAGTCA	1232
QY	1320	TGCATCAAAATAATACTTTAGATGACGTGAACATGTTTGATGTCACCGCATAGTTGTACTT	1379
DB	1233	TGGCTCAAGTAATACTCTGATGGGTGAATGGTTTGTATGTTACAGATACACATTACTT	1292
QY	1380	TCACTCTGGAGCTCGTGGTTATCATTTGGATGCGGATCCCGCCTCTTTAACTATGGAAA	1439
DB	1293	TCACAGTGGTCCAGGTGGCCATCAGTGGATGGGATCTCGGCTATTTAACTATGGGAA	1352
QY	1440	CTGGAGGTACTTAGGTATCTCTCAAATGGAGATGGTGGTTGGATCGCTTCAAAT	1499
DB	1353	CTGGGAAGTTTAAAGATTTCTCTCCAAATGCTAGATGGTGGCTCGAGGAATATAAGTT	1412
QY	1500	TGATGGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACACCGAATATPCGGT	1559
DB	1413	TGATGGTTTCCGTTTTTGTGGTGTGACCTCCATGATGTACACTCACACCGGATTAACA	1472
QY	1560	GGGATTCACATGGGAACCTACGAGGAATACTTTGCACTCGCAACTGATGTCGATGCTT	1619
DB	1473	AACAATTTACGGGAACCTTCAATGAGTATTTTGGCTTTGCCACCGATGTAGATGCA	1532
QY	1620	GTATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCAGATGCAATACCAAT	1679
DB	1533	TTACTTGATGCTGGTAAATGATCAATTCATGGACCTTATCCTGAGGCTGTAAACAT	1592
QY	1680	TGAGATGTTTAGCGGAATGCCGACATTTTGATTTCCCGTCCCAAGAGGGGGTGTGGCTT	1739
DB	1593	TGAAGATGTTAGTGGAAATGCCTACATTTGCCCTTCTGTTACGATGGTGGGTAGTTT	1652
QY	1740	TGACTATCGGCTGCATATGCAATTCCTGATAACGGATTTAGTTGCTCAAGAAACGGGA	1799
DB	1653	TGACTATCGGATGCAATGGCTGGCTGACAAATGGATTGACCTTCTCAAGCAAAAGTGA	1712
QY	1800	TGAGGATTCGAGAGTGGGTGATATTTCTCATACACTGCAAAATAGAAAGATGTGCGAAA	1859
DB	1713	TGAAACTTGGAAAGTGGTGAATTTGTGCACACACTGCACAAATAGGAGGTGGTTAGAA	1772
QY	1860	GTGTGTTTCATACCGCTGAAGTCATGATCAAGCTCTAGTCGGTGTATAAAACCTATAGCAT	1919

RESULT 7

RESOLUT /
US-09-257-894-9

; Sequence 9, Application US/09257894

; Patent No. 6376749

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

APPLICANT: Klein, Theodore M

; APPLICANT: Hubbard, Natalie L.

APPLICANT: Lightner, Jonathan E.

6376749el Starches via Modification of

INVENTOR	TITLE OF INVENTION	EXPRESSION OF STARCH BIOSYNTHESIS
BY	BY	BY

	TITLE OF INVENTION:	Enzyme Genes
	NUMBER OF SEQUENCES	OF
1.		
2.		
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100.		

; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS:

ADDRESS: E. I. du Pont de Nemours & Co.,
1007 Market Street,
Wilmington, Delaware

STREET: 1007 Mar
CITY: Wilmington

CITY: Wilmington
STATE: Delaware

STATE: Delaware
COUNTRY: USA

COUNTRY: UZ
ZTP: 19898, ZIP: 19698
: COMPUTER READABLE FORM.

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; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPATIBLE 95
OPERATING SYSTEM: Microsoft Windows 95

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; OPERATING SYSTEM: MFC
; SOFTWARE: Version 7.0A

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2087 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-257-894-9

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Query Match	39.08;	Score 1033;	DB 4;	Length 2087;
Best Local Similarity	73.74;	Pred. No. 1.3e-290;		
Matches 1315;	Conservative 0;	Mismatches 470;	Indels 0;	Gaps 0;
QY	480	TGATGAATCTGTAGGATCAGAGAGAGGGGCATCCCTCCACCTCGACTTGGTTCAGAGAT	539	
DB	303	TGATGCTCAAGCCTTGAACAGAGTTCCAGTGGTCCCTCCACCAAGCATGGACAAAAAT	362	
QY	540	TTATGAATAAGACCCCTTTTGTACAAACTATCGTCAACACCTTGTATACAGGTATTCACA	599	
DB	363	ATTCAGATTTGACCCCATGTTGCAAGGCTATAAGTAGCATCTTCAGTATCGGTACAGCCT	422	
QY	600	GTACAGAAACTGAGGAGGCAATTGACAGTAGTGAAGGTGGTTTGAAGCCTTTTCTCG	659	
DB	423	CTATAGAAGAAATCCGTTTCAGACATTTGATGAACATGAAGGAGGCTTGAAGCCTTCTCCG	482	
QY	660	TGTTATGAAAAAATGGTTCCTCTAGTGTCTACAGGTATCACTTACCGTGAAGTGGC	719	
DB	483	TAGTTATGAGAAGTTTGGATTTAATGCCGCGGAAGGTATCATATCGAAGTGGC	542	
QY	720	TCITGGGCCGATCAGCTGCCCTTCATTTGAGAGATTTCAACAATTTGGACGCAATTCGTA	779	
DB	543	TCCTGGAGCAATTTCTCAGCATTTGGTGGGTGAGTTCAACAACCTGGATCCAAATGCAGA	602	
QY	780	CAATATCACHCGGAATGAATTTGGTGCTCGGAGATTTTCTGCCAATAATGTGGATGG	839	
DB	603	TCGTATGAGCAAAATGAGTTTGGTGTTTGGAAATTTTCTGCCTAACATGCGAGATGG	662	
QY	840	TTCTCTGCAATTCCTCATGGGTCCAGATGAAGATACGTAATGACACTCCATCAGGTGT	899	
DB	663	TACATCACCTATTCTCTATGGATCTCGTTAAAGGTGAGAAATGATCTCCATCAGGAT	722	
QY	900	TAAGGATTCATCTCCTGTGGATCACTACTCTTTACAGCTTCTGTATGAATTCGATA	959	
DB	723	AAAGGATTCAAATCCAGCCTGGATCAAGTACTAGTCAGGCCCCAGGAGAAATACCATTA	782	
QY	960	TAATGGAATACATTATGATCACCCTGAGGAGAGGTATATCTTCCAACACCCACGCCC	1019	
DB	783	TGATGGATTTATATGATCCTCTCGAGAGGTAAAGTATGTGTTCAGGCATGCCAACC	842	
QY	1020	AAAGAACCCAAAGTCGCTGAGATATATGAATTCATATTCATATTCGAATGAGTATCGGAGCC	1079	
DB	843	TAAACGACCAAAATCATTTGGCGATATATGAACACATGTCGGAATGAGTACCGCGGAACC	902	
QY	1080	TAAATTAACATCATACGTGAATTTTACAGATGAAGTTCTCTCCGCAAAAAAGCTTGG	1139	
DB	903	GAGATTAACACATATGTAAACTTTAGGGATCAAGTCTCTCCCAAGAATTAATAAACTTGG	962	
QY	1140	GTACAATGCGCTGCAAAATTAATGGCTATTCAAGACATTTCTTATTACCGCTAGCTTTTGGTTA	1199	

963	ATACATGTCAGTGC	AATAATGGCA	ATTAATGGCA	AGCCTCATATATTATGGAA	GCTTTGGATA	1024
1200	TCAFGTCCAAAATTTTTTTTGACA	CACAGACCGCTTTTGGAAC	CCCCGACGACCTTAAGTC	1259		
1023	CCATGTAACTAAATTTTTTTTGGC	CAAGTAGCTCGTTTTTGGTACC	CCGAAGAATTTGAAGTC	1082		
1260	TTTCATGTATAAAGCTCATCAGCT	AGGAATTTGTTCTCATGGAC	ATTTCTCACAGCCA	1319		
1083	TTTGATTTGATAGACACATGAGCT	GGTTTTGCTTAGTTCATGATGTGGTTCATAGTCA	1142			
1320	TGCATCAAAATAACTTTTAGAT	GGACHTGAACATTTTGATGTC	GCACCGANAGTTTGTACTTT	1379		
1143	TGGCTCAAGTAATCTCTGCA	TGGTTGAATGTTTTGATGGTAC	ACATACACATTAATTT	1202		
1380	TCACTCTGGAGCTCGTGGTTATCA	TTGGATGTGGATTCGCCCTCTTTAACTATATGGAAA	1439			
1203	TCACATGGTGCCAGCTGGCCCAT	CACCTGGATGTGGGATTTCTGGCTATTTAACTATGGGAA	1262			
1440	CTGGAGGTACTTTAGGTATCTCT	CTCAAATGGGAGATGTGTGGATCGCTTCAAAATTT	1499			
1263	CTGGGAAGTTTTAAGATTTCTC	CTCAATGTAGATGGTGGCTCGAGGAATATAAGTT	1322			
1500	TGATGGAATTTAGATTTGATGGT	GTGACATCAATGATGTATATTACACACCGAATATACGGT	1559			
1323	TGATGGTTTTCCGTTTTGATGGT	HGACCTCCATGATGTACACTCACACCGAATTAACAAGT	1382			
1360	GGGATTCACCTGGGAACATACG	AGGAATACTTTGGACTCGCAACTGATGTGATGCTGTGT	1619			
1383	AACATTTACGGGAACITCAAT	CAGTATTTGGCTTTGCCACCGATGATGACAGTGT	1442			
1620	GTATCTGANTGTGCTAACGAN	CHTATTATCATGGGCTTTCCGAGATGCAATTAACCATGG	1679			
1443	TTACTTGATGCTGTAAATGATC	TAATTAATTCATGGACTTTATCCGTGAGCTGTAAACCATGG	1502			
1680	TGAAGATTTAGCGGAATGCCA	CAATTTGTATCCCGTCCAAAGAGGGGGTGTGGCTTT	1739			
1503	TGAAGATCTTTAGTGGGAATG	CCATACATTTGCCCTTCCTGTTACGATGGTGGGTAGGTTT	1562			
1740	TGACTATCGGCTGCATATGGC	AAFTTGTGTGATAACAGGATTCAGTTGCTCAAGAAACGGGA	1799			
1563	TGACTATCGGATGATATGGCT	GTGGCTGACAAATGGATTTGACCTTCTCAAGCAAAAGTGA	1622			
1800	TCAGGATTTGAGAGCTGGTG	NATATTTTCATACACTGACAAATAGAGATGGTCCGAAAA	1859			
1623	TGAACCTTTGGAAGATGGGT	GATATTGTGCACACTGACAAATAGGAGGTGGTTAGAGAA	1682			
1860	GTGTCTTTTCAFPACGCTGAA	AGCTCATGATCAAGCTCTAGTCGGTGATATAAACTATPAGCAAT	1919			
1683	GTGTGTAACCTTATCCTGAA	AGCTCATGATCAAGCAATTAGTCGGCGACAAGACTATTTGGCTT	1742			
1920	CTGGCTGATGGACAAAGATAT	GTATGATTTTATGGCTCTGATAGACCGTCAACATCAATTT	1979			
1743	TTGGTTGATGGACAAGATAT	GTATGATTTTATGGCCCTCGATAGACCTTCAACTCCCTAC	1802			
1980	AATAGATCTGGGTAGCATTTG	CAACAAGATATAGGCTTGTAACATGGGATPAGGAGG	2039			
1803	CATTGATCTGGGATAGCAAT	TACATAGATGATTTAGACTTATCACAATGGSTTTAGGAGG	1862			
2040	AGAAGGGTACCTAAATTTCA	PFGGAATGAATTCGGCCACCTCGAGTGGATTAATTTCCC	2099			
1863	AGAGGGCTATCTTTAATTT	TCATGGGAATAGTTTTGGACATCCTCGAATGGATAGATTTTCC	1922			
2100	TAGGGCTGAACAACACCTCT	CTGATGGCTAGTAATCCCGGAACCAATTCAGTTATGA	2159			
1923	AAGAGGTCCGCAAGACCTT	CCAAGTGGTAAGTTTATTCCAGGGGANTTAACAACAGTTATGA	1982			
2160	TAAATTCAGACGAGAGATTG	CACCTGGGAGATGCAAGATATTTAAGATACCGTGGGTGCA	2219			
1983	CAAAATGCTCGAAGATTTG	ACCTGGGTGATGACAGATACTTTAGGTATCATGTGATGCA	2042			
2220	AGAAATTTGACCGGCCATNG	CAGTATCTTTGAAGATTAATAATACGATTT	2264			
2043	AGAGTTTGATCAGCAATGCA	ACATCTTTGACCAAAATATGAATTT	2087			

RESULT 8

US-09-257-894-8/C

; Sequence 8, Application US/09257894

; Patent No. 6376749

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

; APPLICANT: Klein, Theodore M.

; APPLICANT: Hubbard, Natalie L.

; APPLICANT: Lightner, Jonathan E.

; TITLE OF INVENTION: No. 6376749el Starches via Modification of

; TITLE OF INVENTION: Expression of Starch Biosynthesis

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: E. I. du Pont de Nemours and Company

; STREET: 1007 Market Street

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows 95

; SOFTWARE: Version 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/257,894

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/091,052

; FILING DATE: JUNE 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Majarian, William R.

; REGISTRATION NUMBER: 41,173

; REFERENCE/DOCKET NUMBER: BB-1066-A

; TELEPHONE: 302-992-4926

; TELEFAX: 302-773-0164

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2165 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-09-257-894-8

Query Match 39.0%; Score 1031.4; DB 4; Length 2165;
Best Local Similarity 73.6%; Pred. No. 4e-290;
Matches 1314; Conservative 0; Mismatches 471; Indels 0; Gaps 0;

QY	480	TGATGATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACTGGTTCAGAAAT	539
DB	1785	TGATGCTCAAGCCCTTGAACAGAGCTCGAGTGGTCCCCCACCAGCGATGACAAAT	1726
QY	540	TTATGAATAGACCCCTTTTGCAAACTATCGTCAACACCTTGATACAGGATTACA	599
DB	1725	ATCCAGATGACCCCATGTGTGACGGCTATAGTACCAATCTTGGATCGGTACAGCCT	1666
QY	600	GTACAGAACTGAGGAGGCAATTCAGAGTATGAGGGTGGTGTGGAAGCCCTTCTCG	659
DB	1665	CTATAGAAGATCCGTTTCAGACATTTGATGACATGAGGAGGCTTGGAGCCCTTCTCCG	1606
QY	660	TGTTTATGAAAAATGGTTTCTACTCCTAGTGTACAGTATCACCTTACCGTTCAGTGGGC	719
DB	1605	TACTTATGAGAGTTTGGATTAAATGCCAGCGGGAAGTATCACATATCGAATGGGC	1546
QY	720	TCTTGTGCTCCAGTACGCTGCCCTCATTTGGAGATTTCAACAATTTGGAGCGCAATCTGA	779
DB	1545	TCTTGGAGCATTTTCTGACAGCATTTGGTGGTGTACGTTCAACAACTGGGATCCAAATGCAGA	1486

QY	780	CATTATGACTCGGAATGAATTTGGTCTCTGGAGATTTTCTGCCAAATAATCTGGATGG	839
DB	1485	TCGTATGAGCAAAATGAGTTGGTCTTTGGAAATTTTCTGCCAAATAATCTGGATGG	1426
QY	840	TTCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGTATGATGGACATGCCATGGTGT	899
DB	1425	TACATCACCTATTCTCTCATGGATCTCGTGTAAAGGTGAGATGGATCTCCATCGGAT	1366
QY	900	TAAAGATTCCATTCTCTGCTTGGATCAACTACTCTTTACAGCTTCTTGATGAATTTCA	959
DB	1365	AAAGATTCAATTCAGCCTCGGATCAAGTACTCAGTGCAGGCCGCCAGGAATAATACCA	1306
QY	960	TAAATGGAATACATTAATGATCCACCGAGAGAGAGAGGTATATCTTCCAAACCCAGGC	1019
DB	1305	TGATGGGATTTTATTAATGATCTCTGAAAGAGTTAAAGTATGTTTCAGGCATGCGAAC	1246
QY	1020	AAAGAAACCAAGTCGCTGAGAAATATGAATCTCATATTTGGAATGATGATGTCGAGCC	1079
DB	1245	TAAACGACCAAAATCATTCGGGATATATGAACACATGTCGGAATGAGTAGCCCGAAC	1186
QY	1080	TAAATTAACACTCAATGCTGAATTTAGAGATCAAGTTCTTCTCCCAATAAAAGCTGG	1139
DB	1185	GAGATTAACACATATGTAACCTTTAGGGATGAGTCTCCCAAGATAAAAGAACTGG	1126
QY	1140	GTAATCGCTGCAAAATATGGCTATTCAAGAGCAATCTTATTACGCTAGTTTGGTTA	1199
DB	1125	ATACAATGCAGTGCAAATATGGAATCCAAAGAGCACTCATATTAAGAGCTTTGGATA	1066
QY	1200	TCATCTCAAAATTTTTCACCAAGAGAGCGGTTTGGAGCGCCGAGAGCTTAAGTC	1259
DB	1065	CCATGTAACATAATTTTTCGCCAAAGTAGTCTGTTTGGTACCCAGAGAAATTTGAATC	1006
QY	1260	TTTGATTCATAAAGCTCATGAGTAAAGTATGTTCTCTCATGGACATGTTTCACAGCA	1319
DB	1005	TTTGATTCATAGAGCACAATGAGCTGGTTGCTAGTCTCATGGATGGTTTCATAGTCA	946
QY	1320	TGCATCAAAATATCTTTAGATGGACTGAACATGTTTGACTGCACCGATAGTTTACTT	1379
DB	945	TGCGTCAAGTAAATATCTCTGGATGGTTGAATGGTTTTCATGATGATACACATTAAT	886
QY	1380	TCATCTGGAGCTCGTGGTTATCATGATGGATGGATTCGCCCTCTTTACTATGGA	1439
DB	885	TCAGTGGTCCAGTGGCCCACTGATGGATGGGATTCGCTGCTATTTAACTATGGAA	826
QY	1440	CTGGAGGACTTACTTAGGTATCTCTCAAAATGCGAGATGGTGGTGGATGCTTCAAT	1499
DB	825	CTGGGAAGTTTAAAGATTTCTCTCTCAATGCTAGATGGTGGCTCGAGGAATATAAGT	766
QY	1500	TGATGGATTTAGATTTGATGGTGTGACATCAATGATATATTCACCACGATTTATCGT	1559
DB	765	TGATGGTTTCCGTTTGTGATGGTGAATCTCATGATGATGATGATGATGATGATGAT	706
QY	1560	GGGATTCACATGGGAACCTACGAGGATATCTTTGGACTCGACACTGATGATGATGAT	1619
DB	705	ACATTTACCGGGAACCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT	646
QY	1620	GTAATGATGCTGTGCAACGATCTTATTCATGGCTTTTCCAGATCAATTCACATGG	1679
DB	645	TTACTTGAATGCTGTAATGATCTAATTCATGAGCTTATCTGAGGCTGTACCAATGG	586
QY	1680	TGAAGATGTTAGCGGAATCCGACATTTTGTATTCCTGCTCCAAAGAGGGGCTGTGCT	1739
DB	585	TGAAGATGTTAGTGAATGCTATATTTGCCCTTCTCTGTCACGATGATGATGATGAT	526
QY	1740	TGACTATCGCTCATATGCAATTCCTGATAACGATGATGATGATGATGATGATGATGAT	1799
DB	525	TGACTATCGATGCAATGCTGCTGGCTGCAAAATGATGATGATGATGATGATGATGAT	466
QY	1800	TGAGATGAGAGATGGGTGATATTTGTTCATACACTGACAAATAGAGATGTCGGA	1859
DB	465	TGAACCTTGAAGATGGGTGATATTTGTGCACACTGACAAATAGAGGTTGGTTAGAA	406

Db 2124 ATATACAGCCTGGACCCCAAGCTGGAGATATTCAGAGACCAATTCAGGTACCGGATGAAA 2065
QY 598 CAGTACAAGAACTGAGGAGGCAATTCACAAGTATGACAGGTGGTGTGGAGGCTTTCT 657
Db 2064 AGATTCTAGACAGAAAGCATCAATGAAAGAAATGAGGGAAGTCTTGAATCTTTTCT 2005
QY 658 CGTGGTTTGAATAAATGGTTTCACTCGTCTAGTACAGGTATCACTTACCCTGAGTGG 717
Db 2004 AAGGCTATTGGAATTTGGGATTAATACAAATGAGGATGGAATCTATATCTGTAATGG 1945
QY 718 GCTCTTGGTCCCAAGTACGCTGCCCTCATTTGGAGATTTCAACAATTTGGGAGCAAAATGCT 777
Db 1944 GCACCTGCTCGCAGGAGGAGAGCTTATTGCTGACTTCAATGACTGGAATGCTGCAAA 1885
QY 778 GACATTATGACTCGGAATGAAATTTGGTCTGGGAGATTTTCTGCCAAATATCTGAT 837
Db 1884 CATAAGATGAGAGGATTAATTTGGTGTGTTGGTCAATCAAAAT--TGACCATGTCAA 1828
QY 838 GGTTCCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGT 897
Db 1827 GGGAAACCTGCCATCCCTCAAAATCCAAAGTTAAATTTGCTTTCTACATGGTGAGTA 1768
QY 898 GTTAAGATTCATTCCTGCTGGATCACTACTCTTTACAGCTTCTGATGAAT---- 953
Db 1767 TGGGTTGATCGTATTCAGCATTTGATTGTTATCGGACTGTTGATGCCCTTAAATTTGGA 1708
QY 954 --TCCATATAATGAATACATATGATCCACCCCAAGAGAGAGGTATATCTTCCAACAC 1011
Db 1707 GCTCCCTATGATGGTGTCAATGGGATCCCTGCTCTGCTCTGCTGCTGCTGCTGCTGCT 1648
QY 1012 CCAGGCCAAGAACCAAGTCCGCTGAGAAATATGAAATCTCATATTTGGAATGAGTAGT 1071
Db 1647 CCTCGGCTTCAAGGCTGCTGCTCCAGGTATCTPATGAAGCCATGAGGTATGAGTGGT 1588
QY 1072 CCGAGGCTTAAATTAATCACTCATAGTGAATTTAGAGATGAAGTCTTCTCCGCAATRAA 1131
Db 1587 GAAAGACGAGTAAACATATAGGAAATTTGCAGACAATGTTGCGCACGATAGGA 1528
QY 1132 AAGCTTGGGTACATGGCTGCAAAATATGCTATTCAGAGCAATCTTATTAAGCTAGT 1191
Db 1527 GCAATTAACACACACAGTTCAGTTGATGCGAGTTATGGAGCATTCGTACTATGCTTCT 1468
QY 1192 TTTGGTTATCATGTCACAAATTTTTCACACAGAGCGGCTTTTGGAAACGCGGACGAC 1251
Db 1467 TTCGGTACCATGTGACAAATTTCTTTCGGGTTAGCAGCAGATCAGGCACACAGAGAC 1408
QY 1252 CTTAACTCTTGATGATAAGCTCATGAGCTAGGAAATTTGTTCTCATGAGCATGCT 1311
Db 1407 CTCAAATATCTTGTGATAAGGCACACAGTTTGGGTTTGGAGTTCTGATGAGTGTGTC 1348
QY 1312 CACAGCCATGCATCAAAATTAATTTAGATGGACTGAAATGTTTG-----ACTGC 1362
Db 1347 CATAGCCATGCAAGTAATATGTCACAGATGTTTAAATGGCTATGATGTTGGACAAAGC 1288
QY 1363 ACCGATGTTGTTACTTTCATCTGGAGCTCGTGGTTATPACTTGGATGGGATTCGCGC 1422
Db 1287 ACCCAAGAGTCCCTATTTTCATCGCGGAGATAGAGGTTATCAAACTTTGGGATAGTCGG 1228
QY 1423 CTCCTTAACTATGGAACCTGGAGGCTATTAGGTATCTTCTCTCAATCGGAGATGGTGG 1482
Db 1227 CTGTCAACTATGCTAACTGGAGGATTAAGGTTTCTTCTTAACCTGAGATTTGG 1168
QY 1483 TTGATGCTGTTCAAAATTTGATGATTTAGATTGAGTGTGACATCAATGATGATATT 1542
Db 1167 TTGGATGATTCATGTTTGAATGCTTCCGATTTGATGGATTTACATCAATGATGATCAT 1108
QY 1543 CACACGAGTATCGGTGGATTCATCTGGACACACAGGATATCTTTGGCTCGCACT 1602
Db 1107 CACCATGATCAATGTGGGTTTACTGGAACCTACAGGAATATTTCAAGTTTGACACA 1048
QY 1603 GATGGATGCTGTTGTTGATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTCCCA 1662
Db 1047 GCTGTGGAGCAGTGTGTTTACATGATGCTTGCAAAACCATTAATGCACAAACTCTGCCA 988

QY 1663 GATGCAATTAACCATTTGTTGAGAGATGTTAGCGGAATGCGGACATTTTGTATTCCCGTCAA 1722
Db 987 GAAGCAACTCTTGTGCTGAAGATGTTTCAGGCATGCGGTCCTTTGCCGCCAGTTGAT 928
QY 1723 GAGGGGGTGTGGCTTTGACTATCGCTGCAATGCTGATGCTGATAAAACGATTTGAG 1782
Db 927 GAAGTGGGTGGTGTGACTATCGCTGCAATGCTGATGCTATCCCTGATAGATGATGAC 868
QY 1783 TTGCTCAAGAAACGGGATG---GGATTGGAGAGTGGTGTATATTTGTCATPACACTGACA 1839
Db 867 TACCTGAAGATAAAGATGACTCTGAGTGGTGCATGCTGATGCTGATAAGCATACTTACT 808
QY 1840 AATAGAAGATGGTCGGAAGTGTGTTTCACTACCTGAAAGTGTATGATCAAGCTCTAGTC 1899
Db 807 AACAGGAGATATCTGAAAAATGCAATCGCATATGCTGAGAGCCATGATCACTCTATTGCT 748
QY 1900 GGTGATTAACATATAGCATCTGCTGATGACAGAGGATATGATGATTTTATGCTGCTG 1959
Db 747 GGCACAAAACATTTGCTGCTGATGACAGAGGAAATGTCACCTGGCATGTCACAC 688
QY 1960 GATAGACCGTCAACATCAATTAATAGATCGTGGATAGCAATTCACAAAGATGATAGGCTT 2019
Db 687 TTGAGCCTGCTTCACTTACAAATGATCGAGGATTCACATCCAAAGATGATCACTTC 628
QY 2020 GTAACATGGGATGAGGAGAGGTTACCTAAATTTTCATGCGGAAATGAATTCGGCCAC 2079
Db 627 ATCAATGGCCCTGGAGGTGATGGCTTACTTGAATTTATGGGAAATGATTTGGTGCAC 568
QY 2080 CTTGAGTGTGATTTTCCCTAGGCTGCAACACACCTCTCTGATGGCTCAGTAAATCCCC 2139
Db 567 CCAGAAATGGATTTGCTTCCCAAGAA----- 541
QY 2140 GGAACCAATTCAGTTATGATAAATGACAGCGAGATTTGACCTGGGAGATCCAGAAAT 2199
Db 540 GGGACAACTGGAGTATGATAAATGACAGACAGTGGAGCTTTGTGGACACTGATCAC 481
QY 2200 TTAGATACCGTGGGTTCGAGAAATTTGACCGGCTATGACGATCTTTGAAGATAAAT 2259
Db 480 TTGCGGTACAAGTACATGCTGCTTACCAAGCGATGAATCGGCTCGATGAGATTT 421
QY 2260 GAGTTTATGACTTCAGAACACCCAGTTTCAATATCACAAAGGATGAAGGAGATAGGATGAT 2319
Db 420 TCTTCTCTTCTGCTCAAGCAGATGCTCAGGACATGAGGATGAGGAAAGCTATT 361
QY 2320 GTATTGAAAAGGAAACCTAGTTTGTGCTTAAATTTTCACTGGCAAAAAGCTATCA 2379
Db 360 GTCTTTGAAGCTGGAGATTTACTTTTGTGTTTCAATTTCCATCCCAAGAAACTTACGAG 301
QY 2380 GACTATCGATAGCCCTGCTGAGGCTGGAATATACAGTTGCTTGGCTTGGACTCAGATGAT 2439
Db 300 GCGTCAAGTGGGATGCGATTTGCTGCGGAAATACAGATGAGCTGCTGCTGCTGCTGCT 241
QY 2440 CCACATTTTGTGGCTTCGGGAGAAATGATCATATAATCGCAATATTTTCACT 2491
Db 240 CTGGTCTCGGTGGACATGGAAGATTTGCCACGAGCTGATCACTTACGT 189

RESULT 11

US-09-257-894-24
; Sequence 24, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company

1837 GGGAAACACTGGAGCTATGATAAATGACAGCAGACAGTGGAGCCTGTGGACACTGATCAC 1896
2200 TTAAGATACCGTGGGTGCAAGAAATTTGACCGCCTATGCAAGTATCTTGAAGATAATAT 2259
1897 TTCCGGTACAAAGTACATGAATGCGTTTGACCAAGCGATGAATGCGCTCGATGAGAGATTT 1956
2260 GAGTTTATGACTTCAGAACACCACTGATCATATCAGGAAAGGATGAAGGAGATAGGATGATT 2319
1957 TCCTTCCCTTCGTCGTCAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAGGTTATT 2016
2320 GTATTTGAAAAGGAAACCTAGTTTGTCTTTAAATTTTCACTGGGACAAAAGCTATTCA 2379
2017 GTCTTTGAACGTGGAGATTAGTTTGTCTTTTCAATTTCCATCCCAAGAAACCTTACGAG 2076
2380 GACTATCGCATACCTGCTCCCTGAAGCCCTGGGAAATACAAAGTTGCTTTGGACTCAGATGAT 2439
2077 GGTACAAAGTGGATGCGATTGCTCGGGGAAATACAGATAGCCCTGGACTGATGCT 2136
2440 CCACCTTTTGGTGGCTCGGAGAAATGATCAATAAGCCGAAATTTCACT 2491
2137 CTGCTCTCGTGACATGGAAGAGTTGGCCACGACGCTGGATCACTTCAGT 2188

RESULT 12
US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winber and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; NAME/KEY: transit_peptide
; LOCATION: 2..190
; FEATURE:

; NAME/KEY: mat_peptide
; LOCATION: 191..2467
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..2470
; US-08-941-445A-16

Query Match 23.7%; Score 628.4; DB 3; Length 2763;
Best Local Similarity 59.7%; Pred. No. 9.2e-173;
Matches 1177; Conservative 0; Mismatches 741; Indels 54; Gaps 5;

QY 538 ATTATGAATAGACCCCTTTTCACAAACTATCGTCAACACCTTGATTCAGCTATCA 597
DB 251 ATATACGACCTGGACCCCAAGCTGGAGATATTCAGGACCAATTCAGTACCGGATGAAA 310
QY 598 CAGTACAAAGAACTGAGGGAGGCAATTCACAAGTATGAGGGTGGTTGGAGCCCTTTTCT 657
DB 311 AGATTCTAGACGAAGAAGGATCAATTCGAAGAAATGAGGAAGTCITGATCTTTTCT 370
QY 658 CGTGGTTATGAAAAATGGGTTTCACGCTAGTGTCTACAGATATCACTTACCGTAGTGG 717
DB 371 AAAGGCTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACCTGTATATCGTAATGG 430
QY 718 GCTCTTGGTCCCGACGCTGCGCTCATCTGGAGATTTCAACAATTTGGAGCGCAATGCT 777
DB 431 GCACCTGCTGCGCAGAGGACAGCTTATTTGGTGACTTCAATGATGAGTGGATGGTGCRAAC 490
QY 778 GACATTATGACTCGGAATGAATTTGGTCTGGAGATTTTCTGCCAAATTAATGTGGAT 837
DB 491 CATRAAGATGGAAGAGGATAAATTTGGTGTGGTTCGATCAAAAT---TGACCATGTCAAA 547
QY 838 GGTCTCTGCAATTCCTCATGCTCGAGTGAAGATACGATAGGACACTCCATCAGGT 897
DB 548 GGGAAAGCTGCCATCCCTCACAATTCCAAGTTTCAAAATTCCTTCTACATGGTGGAGTA 607
QY 898 GTTAAGGATTCCTTCTGCTTGGATCAACTACTCTTTTACAGCTTCCCTGATGAAAT---- 953
DB 608 TGGTTGATCTATTCAGCAATGATTCGCTATGCGGACTGTGATCCCTCTAAATTTGGA 667
QY 954 --TCCATATAATGGAATACATTAATGATCCACCGAAGAGGAGAGATATATCTTCCAAAC 1011
DB 668 GCTCCCTATGATGGTGTTCATTGGATGCTCTCTGCTCTGAAAGGTACACATTTAAGCAT 727
QY 1012 CCACGGCCAAAGAACCAAGTCTGAGATATATGATCTCTATTTGATTTGATGAGTAGT 1071
DB 728 CTTGGGCTTCAAAGCCTGCTGCTCCAGTATATGAGCCCATGATGATGATGATGATGAT 787
QY 1072 CCGGAGCCTAAATTAACCTCATAGCTGAATTTTAGAGATGAAGTTCTTCCCTCGCATAAA 1131
DB 788 GAAAAGCCAGCAGTAAGCAGATATAGGGAATTTGCAGACATGTTGTTCCAGCATACGA 847
QY 1132 AAGCTTGGGTACATGGCTGCAATATGATGCTATTCAGAGCATTTCTTATTACGCTAGT 1191
DB 848 GCAATAACTACACACAGTTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT 907
QY 1192 TTTGGTTATCATGTCAAAATTTTTCACCAAGCAGCGCTTTTGGAAACCGCAGAC 1251
DB 908 TTCGGGTACCATGTGACAAATTTCTTGGGTTAGCAGCAGATCAGGACACACAGAGGAC 967
QY 1252 CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGACATTTGTT 1311
DB 968 CTCAAATATCTTTGATAAGGCACACAGTTTGGTTTGGAGTCTGATGATGATGTTGTC 1027
QY 1312 CACAGCCATGATCAAAATTAATCTTAGATGAGCTGAACATGTTTG-----ACTGC 1362
DB 1028 CATAGCCATGCAAGTAAATGTCACAGATGGTTTAAATGGCTATGATTTTGGACAAAGC 1087
QY 1363 ACCGATAGTGTCTACTTTCACTCTGAGCTCGTGTATATGATGATGATGATGATGATGAT 1422
DB 1088 ACCAAGAGTCTCTATTTTCAATGCGGAGATGAGAGTTATCAATTTGGGATAGTCTGG 1147
QY 1423 CTCTTTAACTATGGAACACTGGAGGACTTGGTATCTTCTCAAAATGCGAGATGGTGG 1482

Db 1148 CTGTTCAACTATGTAACCTGGAGGTATTAAGGTTTCTCTTTCTAACCCTGAGATATTGG 1207
QY 1483 TTGGATCGGTTCAAAATTGATGGATTTAGATTGATGGTGTGACATCAATGATGATATT 1542
Db 1208 TTGGATGAATTCATGTTGATGGCTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1267
QY 1543 CACACGAGTATATCGGTGGGATTCACGTGGGAACCTACGAGGAATACTTTGGACTCGCAACT 1602
Db 1268 CACCATGGTATCAATGTTGGGTTTACTTGGAACTACGAGGAATACTTTGAGTTGGACACA 1327
QY 1603 GATGTGATGCTGTTGTGATCTGATGCTGGTCAACGATCTATTCATGAGCTTTTCCCA 1662
Db 1328 GCTGTGATGAGTTGTTGATGATGCTGGGATGCGGATTTGTTGATTCCTCGTCCAA 1722
QY 1663 GATGCAATACCAATGCTGAGATGTTAGCGGAATGCGGATTTGTTGATTCCTCGTCCAA 1722
Db 1388 GAGCAACTGTTGTTGCTGAAGATGTTTCAGGCGATGCGGTCCTTTGCGGCGCAATGAT 1447
QY 1723 GAGGGGGTGTGCTTTGCTATCGCTGCTATGCAATGCTGATGAATAACGGAATGAG 1782
Db 1448 GAAGTGGGTTGGTTGATCTATCGCTGCTGCAATGCTATCCCTGATGATGATGATGAC 1507
QY 1783 TTGCTCAAGAAACGGGATGA--GGATGAGAGTGGGTGATATGTTCTATACACTGACA 1839
Db 1508 TACCTGAAGAATAAAGATGACTCTGAGTGGTGCATGGTGAATAGCGCATCTTTGACT 1567
QY 1840 AATAGAAGTGGTGGGAAAGTGTGTTCTATAGCTGAAAGTCAATGATCAAGCTCTAGTC 1899
Db 1568 AACAGGAGATATCTGAAATGCTGATGCTGATGCTGAGAGCCATGATCATCTATTGTT 1627
QY 1900 GGTGAATAAATACTAGCATCTCTGCTGATGCAAGGATATGATGATTTTATGGGCTG 1959
Db 1628 GCGGACAAACTATGCTATCTCTGCTGATGCAAGGATGCTGATGCTGATGCTGATGCT 1627
QY 1960 GATGACCGCTCAACATCAATTAATGATGCTGAGGATGCTGATGCTGATGCTGATGCT 2019
Db 1688 TTCCAGCCTGCTTCACTACATCAATGATGAGGATGCTGATGCTGATGCTGATGCT 1747
QY 2020 GTAACTATGATGATGAGGAGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 2079
Db 1748 ATCAATGCTGCTGAGGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1807
QY 2080 CTTGAGTGGATGATTTCCCTAGGCTGAAACACACCTCTCTGATGCTGATGCTGATGCT 2139
Db 1808 CCAGAATGATGATGCTTCCAGAGAA-----1834
QY 2140 GGAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2199
Db 1835 GGAACCAATTCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1894
QY 2200 TTAAGATACGCTGGGTTGCAAGATTTGACCGGCTATGCTGATGCTGATGCTGATGCT 2259
Db 1895 TTCCGCTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1954
QY 2260 GAGTTTATGATCTCAGAACACCACTGATGATGATGATGATGATGATGATGATGATGAT 2319
Db 1955 TCTTCTCTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 2014
QY 2320 GTATTTGAAAAGGAACCTAGTTTGTCTTTTAAATTTTCACTGGAACAAAGCTATTCA 2379
Db 2015 GTCTTTGAACTGGAGATTTAGTTTGTCTTTTCAATTTCCATCCCAAGAAACTTACGAG 2074
QY 2380 GACTATCGCATGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAT 2439
Db 2075 GGTCTCAAAAGTGGGATGCGATTTGCTGCGGAAATACAGAGTACGCTGCTGATGCT 2134
QY 2440 CCACCTTTTGGTGGCTTCGGGAGATTTGATCAATGCGGAAATTTTCACCT 2491
Db 2135 CTGGCTTCGGTGGAGATGGAAGAGTTGCCACGACGTGGATCCTTACGT 2186

RESULT 13

US-09-257-894-12

; Sequence 12, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lighner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2772 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 49..2580
; US-09-257-894-12

Query Match 23.7%; Score 628.4; DB 4; Length 2772;
Best Local Similarity 59.7%; Pred. No. 9.2e-173;
Matches 1177; Conservative 0; Mismatches 741; Indels 54; Gaps 5;

QY 538 ATTTATCAATACACCCCTTTTCACAAATATGTCACAACTTGTGATTCAGTATATCA 597
Db 364 ATATAGACCTGGACCCCAAGCTGGAGATATTAAGGACCAATTCAGGTACCGATGAA 423
QY 598 CAGTACAAGAACTGAGGAGGCAATGACAAGTATGAGGCTGTTGGAGCCTTTCT 657
Db 424 AGATTCTAGACGAGAAAGATCAATTAAGAAATGAGGAAAGTCTGATATCTGATGG 483
QY 658 CGTGGTTATGAAAATATGGGTTTCTACTCGTGTAGTCTACAGGTATCACTTACCGTGTGG 717
Db 484 AAAGGCTATTGAAATTTGGGATTAATACAAATGAGATGGAATCTGTATATCTGATGG 543
QY 718 GCTCTTGGTCCGACGTGAGTCCCTCAATTTGGAGATTTCAAAATTTGGGACGCAATGCT 777
Db 544 GCACCTGCTGCGCAGGAGGAGAGCTTATTTGGTGAATTAATGAGTGAATGCTGCAAC 603
QY 778 GACATATGACTCGGAATGAATTTGGTGTCTGAGATTTTCTGCAATATATGATGAT 837
Db 604 CATAGATGAGAGAGATTAATTTGGTGTGCTGATCAAAAT---TGACCAATGCAAA 660

QY		838	GGTCTCCTCGAATTCCTCATCCGGTCCAGAGTGAAGATACGTTATGGACACTCCATCAGGT	897
Db		661	GGGAACCCPGCCATCCCTCACAAATCCAAATTCAAATTTCAATTTCCGCTTTCTACATCGTGGAFTA	720
QY		898	GTTAAGSATTCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCCTGATGAAAT----	953
Db		721	TGGGTTGATCGTAATCCACAGATTGATCGTTAIGCGACTGTTGATGCCCTCTAAATTTGGA	780
QY		954	--TCCATAATATGGAATCATTATGATCAACCOCGAGAGAGAGAGGTATATCTTCCAACAC	1011
Db		781	GCTCCCCTATGATGGTGTTCATTTGGGATCCCTCCTGCTTCGTGAAGSGTACACAATTTAAGCAT	840
QY		1012	CACGCGCCRAAGAACCARAAGTCGGTGAGAATATATGAAATCAATTCGAATGAGTAGCT	1071
Db		841	CTCGGCCCTTCAAGGCCTGCTGCTCCAGCTATCTATGAAGCCCATAGTAGTATGAGTGGT	900
QY		1072	CCGGAGCCTHAAAATTAACATCATACGTGAAATTTTAGAGATGAAGTTCTTCTCGCAPAAAA	1131
Db		901	GAAGAACCCAGCAGTAAGACATATAGGAAATTTGCAGACAAATGTTGTGCCAGCATACGA	960
QY		1132	AAGCTTGGGTACAAATCGGCTGCNAAATATATGGCTATTTCAAGACCAATTCITATTACGCTAGCT	1191
Db		961	GCAAAATAACTACAAACACAGTTCAGTTTGATGGCAGTTATGGAGCAATTCGTACTAATGCTCT	1020
QY		1192	TTTGGTTATCATGTCACAAATTTTTTTTGGACCAAGCAGCCGTTTTTGGAAAGCCGCGACAG	1251
Db		1021	TTGGGTACCATGTGACAAATTTCTTTTGGTTAGCAGCAGATCAGSCACACACAGAGGAC	1080
QY		1252	CTTAAGTCTTTGATGATTAAGCTCAIAGCTAGGAAATTTGTTGTTCTCATGACATGTTT	1311
Db		1081	CTCAAAATATCTTTGATGAAGGCACACAGTTTGGGTTTTCGAGTTCTCGATGATGTGTCT	1140
QY		1312	CACAGGCATGCATCAAAATAATACTTTAGATGGACTGAACATGTTTG-----ACTGC	1362
Db		1141	CATAGCCATGCAAGTAAATGTCACAGATGGTTTAATGGCTATGATGTGGACRAAGC	1200
QY		1363	ACCGATAGTTGTTTACTTTCACTCTGGAGCTCGTGGTTTATCATNTGGATGTGGGATCCCGC	1422
Db		1201	ACCCAAAGATGCCATTTTCATGCGGGAGATAGAGTTATCATAAACTTTGGGATAGTCGG	1260
QY		1423	CTCTTTAACTPATGGAACATGGGAGTACTTAGTATCTTCTCTCAATCGAGATGGTGG	1482
Db		1261	CTGTTCAACTATGCTAACGTGGGAGGTATTAAGGTTTCTCTTCTAACCTGAGATATGG	1320
QY		1483	TTGGATCGCTTCAAAATTTGAIGATTTAGATTTGATGGTGTGACATCAATATGATATTT	1542
Db		1321	TTGGATGAATTCATGTTGATGGCTTCGGAATTTGATGGAGTTACATCAATGCTGTATCAT	1380
QY		1543	CACACGGATATCGGTGGGATTCACGTGGAACTACGAGAAATACHTTTGACTCGCAACT	1602
Db		1381	CACCATGGTATCAATGTGGGGTTTACTTGGAACTCCACAGAAATTTTCAGTTTGGACACA	1440
QY		1603	GATGTGGATGCTGTTGTGATCATGATGCTGGTCAAGGATCTTATTCATGSGGCTTTTCCCC	1662
Db		1441	GC GTGGATGCAGTTGTTTACATGATGCTTGCRAAACCATTAATGACAAACACTCTTGCCA	1500
QY		1663	GATGCAATTPACCATTTGGTGAAGATGTTTAGCGGAATGCCGACATTTTGTATTCCTGCCAA	1722
Db		1501	GAAGCAACTGTTGTGCTGAAGATGTTTTCAGGCATGCCGTCCTTTTSCGCGCCAGTTGAT	1560
QY		1723	GAGGGGGTGTGGCTTTGACTATCGGCTGCATATGGCAATTCGCTGATAAAGGATTGAG	1782
Db		1561	GAAGTGGGGTGTGGGTTTGACTATCGCCTGGCAATGGCTATCCCTGATAGATGGATTGAC	1620
QY		1783	TTGCTCAAGAAACGGGAATGA---GGATTTGGAGAGTGGGTGATATTTGTCATACACTGACA	1839
Db		1621	TACTGAAGAAATAAAGATGACTCTGAGTGGCTGATGGGTGAATAAGCAATACCTTTGACT	1680
QY		1840	AATAGAAGATGGTCGGAAGAGTGTGTTTCATAGCTCAAGAGTCATGATCAAGCTCTAGTC	1899
Db		1681	AACAGGAGATATCTGAAAAATGCATCGCATATGCTAGAGCCCATGATCAGTCTATTTGTT	1740
QY		1900	GGTGATAAAACTATAGCATTTCTGGCTGATGGCAAGGATATGATGATTTTATGGGCTCTG	1959

Db	1741	GGGACAAAAC	TAATGCA	TTCCCTGATGGACAAGGAATGTACACTGCAATGTCAGAC	1800
Qy	1960	GATAGACCGTCAACATC	ATTAATAGATCGTGGGATAGCATTTGGCACAAAGATGATTAGGCTT	2019	
Db	1801	TTGCAGCCTGCTTCACTAC	CAATATGATCGAGGATTGCAC	TCCAAAAGATGATTCAC	1860
Qy	2020	GTAACTATGGGATTAGGAGGAGAGG	TACTAAATTTTCATGGAATGAATTCGCCCCAC	2079	
Db	1861	ATCACAATGCCCTTGGAGTGTAG	CTGCTCAATTTTATGGGAATAGTTTGGTTCAC	1920	
Qy	2080	CCGTGAGTCGATTGATTTCCCTAGGCT	TGAACAACCTCTCTGATGCTCAGTAATACCCC	2139	
Db	1921	CCAGATGGATTGACTTTCCAGAA	-----	1947	
Qy	2140	GGAAACCAATTCAGTTA	TATGATAAATCGACACGGAGATTTGACCTGGGAGATCGAGAAATAT	2199	
Db	1948	GGGAACAACCTGGAGCTATG	ATAATGACAGACAGCTGGAGCCCTTGTGGACACTGATCAC	2007	
Qy	2200	TTAAGATACCGTGGTTTGC	AAAGATTTTGACCGGCTATGCAGTATCTTTGAAGATAAATAI	2259	
Db	2008	TTGGGGTCAAGTACATG	GAATGCGTTTGGACCAACGCGATGAATGGGCTCGATAGAGATTT	2067	
Qy	2260	GAGTTTATGACTTCAGAACAC	CCAGTTCATATCACGAAAGGATGAAGAGATAGGATGATT	2319	
Db	2068	TCCTTCCTTTCTGTCGTCA	AAAGCAGATGTCAGCGACATGAACGATGAGGAAAAGTTATT	2127	
Qy	2320	GTAATTCGAAAAGAAAC	CTTAGTTTTTTCCTTTAAITTTTCACTGGACAATAAAGCTATTCA	2379	
Db	2128	GTCTTTGAACGTGGAGATTT	TAGTTTTTGTATTTTCAATTTCCATCCCAAGAAACCTTACGAG	2187	
Qy	2380	GACTATCGCATAGCTCGCT	GAAGCCGGAATAATACAAAGTTGCTTTGGACTCAGATGAT	2439	
Db	2188	GGCTACAAAGTGGGATG	CGGATTTGCCCTGGGAATACAGATAGAGCTCTGATGCT	2247	
Qy	2440	CCACTTTTGGTGGCTTC	GGGAGAAATGATCATAAATGCCGAATATTTTCACTT	2491	
Db	2248	CTGGTCTTCGGTGGACAT	TGGAAGAGTTTGGCCACGACGTGGATCACTTCAAGT	2299	

RESULT 14

US-08-104-158-1
; Sequence 1, Application US/08104158
; Patent No. 6215042
; GENERAL INFORMATION:
; APPLICANT: Willmitzer, Lothar
; APPLICANT: Sonnwald, Uwe
; APPLICANT: Rossmann, Jens
; APPLICANT: Mueller-Roeber, Bernd
; APPLICANT: Visser, Richard Gerardus Franciscus
; APPLICANT: Jacobsen, Evert
; TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
; CAUSE CHANGES IN THE CARBOHYDRATE COMPOSITION AND THE
; CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
; TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
; TITLE OF INVENTION: CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
; NUMBER OF SEQUENCES: 2
; ADDRESS: Ostrolenk, Faber, Gerb & Soffen
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/104,158
; FILING DATE: 13-AUG-1993
; CLASSIFICATION: 800
; PRIORITY DATA:

APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: EA-1996 PCT (951-91)
TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2909 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHEtical: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Solanum tuberosum cv. Desiree

STRAIN: Desiree

DEVELOPMENTAL STAGE: growing tuber

TISSUE TYPE: tuber

CELL TYPE: total tuber

IMMEDIATE SOURCE:

LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)

FEATURE:

NAME/KEY: CDS

LOCATION: 2..1699

OTHER INFORMATION: /note= "for Branching enzyme I

OTHER INFORMATION: (partial) truncated protein; 97,11 % identity to

OTHER INFORMATION: active potato branching enzyme"

Query Match 23.3%; Score 617.2; DB 4; Length 2909;
Best Local Similarity 60.08; Pred. No. 1.7e-169;
Matches 1185; Conservative 0; Mismatches 733; Indels 58; Gaps 7;

QY	548	TAGACCCCTTTTGACAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGA	607
Db	165	TGGATCCAACTTTGGAACCTTATCTAGATCACTTCACACACAGATGAAGATATG	224
QY	608	AACCTGAGGGAGCAATTGACAAATGACAGGTATGAGGTGTTGGAGCCCTTTCTCGTGGTATG	667
Db	225	ATCAGAAATGCTCATTGAAATATATGAGGACCCCTTGAGGAATTTGCTCAAGTTAT	284
QY	668	AAAAATGGGTTTCACTCGTAGTGTCTACAGTATCACTTACCGTACGTGGGCTCTTGGT	727
Db	285	TAAATTTGGATTCAACAGGAAGATGGTTCATAGTCTATCGAATGGGCTCCTGCTG	344
QY	728	CCAGTCAGTCCCTCATTTGGAGATTTCAACAAATTTGGAGCGCAAAATGCTGACATATGA	787
Db	345	CTCAGGAAGCAGAGATTTGGCGATTTCAATGTTAGGAACGGTTCTTAACACATGATG	404
QY	788	CTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCAATATATGGATGGTTCCTCTG	847
Db	405	AGAAGACCAAGTTTGGTGTGGAGTATAGATTCC---TGATGTTGACAGTAAGCCAG	461
QY	848	CAATTCCTCATGGTCCAGAGTGAAGATAGTATGGACACTCCATCAGGTGTTAAG---G	904
Db	462	TCATTCACACAACTCCAGAGTTAAGTTCTGTTCAACATGGTAATGGATGGGTAG	521
QY	905	ATTCCATTCCTGTTGGATCAACTACHTCTTTTACAGCTTCC-----TGATGAATTCAT	958
Db	522	ATCGTATCCCTGCTTGGATTAAGTATATCCACTCCAGACGCCAAGTTTTCAGCCCAT	581
QY	959	ATAATGGAATACATATATGATCCACCCGACAGAGAGGATATATCTTCCAAACCCAGGC	1018
Db	582	ATGATGGTGTCTACTGGGACCCACCACCTTTAGAAAAGGTACCACTTCAAAATACCTCGCC	641

QY	1019	CAAGAAACCAAAAGTCGCTGAGAAATATGAAATCTCATATGTAATAGTAGTCCGAGC	1078
Db	642	CTCCCAACCCCGAGCCCAAGAACTACAGACACATGTCGSCATGSCAGCTCTGAGC	701
QY	1079	CTAAAAATTAACATCATACGTGAATTTAGAGATGAAGTTCTTCTCGCATAAAAAGCTTG	1138
Db	702	CAGTGAATTCGTATCGTGAGTTTGCAGATGATTTTACCTCGGATTAAGGCAATA	761
QY	1139	GGTCAATGGCTGCAAAATATGCTATTCAAGAGCATCTTATTACGCTAGTTGGTT	1198
Db	762	ACTATAATACCTCTCCAGTTGAGGCCAATAATGAACATCTTACTATGATCATTTGGAT	821
QY	1199	ATCATGTCACAAAATTTTTCACCAAGCAGCCGTTTGGAAAGCCGACGACCTTAAGT	1258
Db	822	ATCATGTTACAACTTTTTCGCTGTGACCAATAGATATGAAACCCGAGGACCTTAAGT	881
QY	1259	CTTTGATTTGATAAAGCTCATGAGCTAGGAATTTGTTCTCTATGACATATGTTCAAGCC	1318
Db	882	ATCTGATAGATAAAGCACAATAGCTTGGGTTTACAGGTTCTGTGTGATGTATTCAGTC	941
QY	1319	ATGCATCAATAAATATCTTTAGATGAGCTGAACATGTTTGAATGCACCGATAGTCT	1374
Db	942	ATGCAAGCAATAATGTCATCTGATGCTTCATGCTTATGATTTGGCAAGTTCTCAG	1001
QY	1375	-----TACTTTCATCTCTGAGCTCGTGGTTATCATTTGGATTTGGATTTCCGCCCTTTTA	1429
Db	1002	AATCCTACTTTTCATGCTGAGAGCGAGGTACCAATAGTTTGGGATGACGAGCGTTCA	1061
QY	1430	ACTATGAAACTGGGAGCTATGATCTCTCAATTCGAGATGGTGGTGGATG	1489
Db	1062	ACTATGCCAATTTGGAGGTTCTTCTGTTTCCATTTTCAACATGAGGTGGTGGTGAAG	1121
QY	1490	CGTTCAAAATTTGATGATTTAGTTGATGGTGTGACATCAATGATGATATTTCCACCAG	1549
Db	1122	AGTATAACTTTGACGATTTTCGATTTGATGGAATAACTTCTATGCTGTATGTTCAATG	1181
QY	1550	GATTATCGGTGGGATTTCACTGGGAACTACGAGGAATATTTGGACTCCCAATGATGG	1609
Db	1182	GAATCAATATGGGATTTACAGGAACTATAATGATGATTTTTCAGGAGCTACAGATGTTG	1241
QY	1610	ATGCTGTGCTATCTGATGCTGTCACAGCATCTTATCAATGGGCTTTTCCCAATGCAA	1669
Db	1242	ATGCTGTGCTATTTAATGTTGGCAATAATGATGATTTCAAGATTTTCCCAACGCA	1301
QY	1670	TIACCAATTTGTAAGATTTTACGCGAATGCGGACATTTTGTATTTCCCTCCCAAGAGGG	1729
Db	1302	CTGTTATTTGCGAAGATGTTTCTGTTATGCGGGGCTTAGCGGCTGTTTCTGAGGAG	1361
QY	1730	GTGTTGGCTTTGATCTCGGTCGATATGCGCAATTTGATGATGATGATGATGATGATGATG	1789
Db	1362	GAATTTGTTTGTATTCAGGCTTGGCAATGCGCAATCCAGATAGTGGATGATGATGATG	1421
QY	1790	AGAAACGG---GATGAGGATTTGAGAGTGGGTGATATTTTATACACTGACAAATAGAA	1846
Db	1422	AGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1481
QY	1847	GATGGTGGGAAAGTGTGTTTATACGCTGAAAGTCAATGATGATGATGATGATGATGATG	1906
Db	1482	GATATACAGAGAAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1541
QY	1907	AACTATAGCATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1966
Db	1542	AGCAATTTGATTTCTCTTATCAAAAGAGATGATGATGATGATGATGATGATGATGATG	1601
QY	1967	CGTCAACATCATTAATAGATCGTGGGATGATGATGATGATGATGATGATGATGATGATG	2025
Db	1602	ATGCTTCTCTGTTGTTGATGAGGAATTCGCTTGGCAAGATGATGATGATGATGATGATG	1661
QY	2026	ATGGGATTTAGGAGGAAAGGTAAGTAAATTTTCAATGGAATGATGATGATGATGATGATG	2085
Db	1662	ATGGCTTTGGAGGAGGAGGTAAGTAAATTTTCAATGGAATGATGATGATGATGATGATG	1721


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Db      1210  TTTGATCAATTCATGTTTATGCGCTTCGGATTTCAGTTCATCAATCTATCAT 1269
QY      1543  CACCACGGATTATCGGTGGGATTCACCTGGGAATACCTTGGACTCGCAACT 1602
Db      1270  CACCATGGTATCAATGTGGGTTTACTGGAATACCAAGGAATATTCAGTTGGACACA 1329
QY      1603  GATGTGGATGCTGTGTGATCTGATGCTGCTCAACGATCTTATTCATGGCTTTCCCA 1662
Db      1330  GCTGTGATGAGTTGTTACATGATGCTTGCACCAATTTAATGCACAACTTTGCCA 1389
QY      1663  GATGCAATTAACATTCGTGAAGATGTTAGCGGATGCCGACATTTTGTATTCCTCCGTCAA 1722
Db      1390  GAAGCAACTCTGTGCTGAAGATGTTTCAGGCATGCCGGTCCTTTCGGGCCAGTTGAT 1449
QY      1723  GAGGGGGTGTGGCTTGGCTTGGCTGCTGATGCGCAATTCGTGATAAACGGATTGAG 1782
Db      1450  GAAGGTGGGTGGGTTGGCTTGGCTGCTGCGCAATGCTATCCCTGATAGATGGATTGAC 1509
QY      1783  TTGCTCAAGAAACGGGATGA---GGATTGGAGAGTGGTGATATTTGTTTCATACACTGACA 1839
Db      1510  TACCTGNAGATAAAGATGACTCTGAGTGTGATGGTGAATAGGCGCATACTTTGACT 1569
QY      1840  AATAGAGATGGTGGGAAAGTGTGTTTACAGCTGAAAGTTCATGATCAAGCTCTAGTC 1899
Db      1570  AACAGGAGATATACTGAAAAATGCATGCGATATGCTGAGAGCCATGATCACTATTTGTT 1629
QY      1900  GGTGATAAACTATAGCATCTGGCTGATGCGCAAGGATATGATGATTTTAIGGCTCIG 1959
Db      1630  GCGCAAAACTATTGCAITTCCTGATGGCAAGGAAATGACACTGGCAITGTCAGAC 1689
QY      1960  GATAGACCTCAACATCAATATAGATGCTGGGATAGCATTCACAGATGATTAGCCTT 2019
Db      1690  TTGCAGCCTGCTTCACCTACCAATGATCGAGGGATTCACCTCCAAAGATGATTCACCTC 1749
QY      2020  GTAACATAGGATAGGAGAGAGGTTACCTAAATTCATGGGAATGAATTCGGCCAC 2079
Db      1750  ATCACAATGSCCCTTGGAGGTGATGCTACTTGAATTTATGGGAATGAGTTGGTCAC 1809

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OM nucleic - nucleic search, using sw model

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Perfect score: 2646
Sequence: 1 ATGGTGTATACACTCTCTGG.....AAGTAGTAGTAGAAGAGAA 2646

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1369.8	51.8	1393	9	US-10-254-534-3
3	1317.4	49.8	2418	9	US-09-938-842A-872
4	1290	48.8	2577	9	US-09-938-842A-337
5	1167.2	44.1	3039	10	US-09-792-127-3
6	1166.6	44.1	2559	10	US-09-792-127-1
7	578.2	21.9	2994	9	US-10-084-817-92
8	576.6	21.8	2955	9	US-09-918-624B-30
9	576.6	21.8	2955	10	US-09-880-107-2148
10	257.8	9.7	602	10	US-09-770-149-955
11	136	5.1	604	10	US-09-925-300-453
12	114.6	4.3	441	10	US-09-770-444-893
13	104.8	4.0	601	9	US-10-025-380-304
14	104.8	4.0	601	10	US-09-922-217-304
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16	88.8	3.4	204	10	US-09-878-574-12567
17	88.6	3.3	1877	10	US-09-974-300-653
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19	75.8	2.9	2193	9	US-09-738-626-1354

c 20	75.8	2.9	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 21	74.6	2.8	310	9	US-10-102-524-1616	Sequence 1616, Ap
c 22	68.2	2.6	543	10	US-09-815-343-373	Sequence 373, App
c 23	66.8	2.5	184	10	US-09-864-761-20375	Sequence 20375, A
c 24	66.8	2.5	276	10	US-09-864-761-20595	Sequence 20595, A
c 25	66.8	2.5	489	10	US-09-864-761-3607	Sequence 3607, Ap
c 26	66.8	2.5	90650	9	US-10-175-523-80	Sequence 80, Appl
c 27	66.6	2.5	16299	9	US-10-175-523-64	Sequence 64, Appl
c 28	65.8	2.5	288	9	US-09-728-444-165	Sequence 165, App
c 29	65.8	2.5	305	10	US-09-864-761-19262	Sequence 19262, A
c 30	65.8	2.5	496	10	US-09-864-761-2534	Sequence 2534, Ap
c 31	65.8	2.5	6944	9	US-10-172-086-111	Sequence 111, App
c 32	65.8	2.5	225883	9	US-10-175-523-57	Sequence 57, Appl
c 33	65.8	2.5	1691139	9	US-10-067-514-1	Sequence 1, Appli
c 34	65.4	2.5	419	10	US-09-864-761-6432	Sequence 6432, Ap
c 35	65	2.5	659158	9	US-09-771-208-20	Sequence 20, Appl
c 36	64.2	2.4	157	10	US-09-864-761-21717	Sequence 21717, A
c 37	64.2	2.4	301	10	US-09-864-761-17047	Sequence 17047, A
c 38	64.2	2.4	462	10	US-09-864-761-3829	Sequence 3829, Ap
c 39	64.2	2.4	471	10	US-09-864-761-2776	Sequence 2776, Ap
c 40	64	2.4	576	10	US-09-815-343-924	Sequence 924, App
c 41	63.6	2.4	232	10	US-09-864-761-19928	Sequence 19928, A
c 42	63.6	2.4	312	10	US-09-864-761-22972	Sequence 22972, A
c 43	63.4	2.4	483	10	US-09-864-761-1384	Sequence 1384, Ap
c 44	63.2	2.4	261	10	US-09-864-761-19524	Sequence 19524, A
c 45	63.2	2.4	261	10	US-09-864-761-25517	Sequence 25517, A

ALIGNMENTS

RESULT 1
US-10-254-534-1
; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:belI gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:


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Qy 1801 GAGGATGGAGAGTGGGTGATATGTTTCATACACTGACAAATAGAAATGCTCGGAAAG 1860
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RESULT 2

US-10-254-534-3

; Sequence 3, Application US/10254534

; Publication No. US20030046730A1

; GENERAL INFORMATION:

; APPLICANT: EK, Bo

; APPLICANT: KHOSNOODI, Jamshid

; APPLICANT: LARSSON, Clas-Tomas

; APPLICANT: LARSSON, Hakan

; APPLICANT: LARSK, Lars

```
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCJ/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
; US-10-254-534-3
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Best Local Similarity 98.9%; Pred. No. 0;
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Db	601	CCGCTCTTTAACTATGGAAACTGGGAGGTACTTAGTATCTCTCMAATCGGAGATG	660
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Db	661	GTGGTTGGATTCGGTTCAAAATTTGATGGAATTTAGATTGATGGTGTGACATCAATGATGA	720
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Db	961	TGAGTTCCTCAAGAAACGGGATGAGGATTTGGAGAGTGGGTGATATTGTTTCATACACTGAC	1020
Qy	1839	AAATAGAGATGTCGCGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT	1898
Db	1021	AAATAGAGATGTCGCGAAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGT	1080
Qy	1899	CGGHTATAACATATAGCATCTGGCTGATGGAGCAAGGATATGATGATTTTATGGCTCT	1958
Db	1081	CGGTGATAAACAATATAGCATCTGGCTGATGGAGCAAGGATATGATGATTTTATGGCTCT	1140
Qy	1959	GGATAGACCGTCAACATCATTATAGATCTGGGATAGCATTCGACAAAGATGATTAGGCT	2018
Db	1141	GGATAGACCNCTCAACATCATTATAGATCTGGGATAGCATTCGACAAAGATGATTAGGCT	1200
Qy	2019	TGTAACATATGGATTTAGGAGGAGAGGGTACCTAAATTTCAAGGAATGAATTCGGCCCA	2078
Db	1201	TGTAACATATGGATTTAGGAGGAGAGGGTACCTAAATTTCAAGGAATGAATTCGGCCCA	1260
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Db	1261	CCCTGAGTGGATGATTTCCCTAGGGCTGAACACACCTCTCTGATGGCTCAGTAATCCC	1320
Qy	2139	CGGAACCAATTCAGTTTATGATAAATGCACACGAGATTTTGACTGGGAGATGCAGAATA	2198
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Qy	2199	TTTAAAGATACCGT	2211
Db	1381	TTTAAAGATACCGT	1393

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RESULT 3
US-09-938-842A-872
; Sequence 872, Application US/09938842A
; Patent NO. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 872
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

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Query Match	49.8%	Score 1317.4	DB 9	Length 2418
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DB	216	TGATGATGATCCAGAGAGTTCCTCAGAGATNTTTGATCTAGAAAGTCCAAACAT		
QY	444	GTCTAAACCAFTAAATACCTCTGAGAGACAAATTTATGATCAATCTGATA---		
DB	276	TACTGAGGCACTAAGAAGAGAACCAAAACAATCAACGTTGTCAAGGAGAGAGG		
QY	501	AGAGAGGGGATCCCTCCACCTGCACITGGTCAGAGAATTTATGAATATGACCC		
DB	336	ACCAAGAATAGTTCCTCCCAACCGGTGATGCCAAGAAATTTATGAGATGACCC		
QY	561	GACAAACTATCGTCAACACCTPTGATTACAGSTATTCACAGTACAAAGAACTGAG		
DB	396	ACGAACCTTACAACAAATCATCTTGATTTACCGTTATGACAGATATAAAGATTGCG		
QY	621	AATTGACAAGTATGAGGCTGGTTTGGAGCGCTTTCTCGTGGTTATGAAAATA		
DB	456	AATAGACAAGTATGAGGCTGGTCTTGAGGCATTTCTCTCGTGGCTATCAAAGTT		
QY	681	CACTCGTAGTCTCAGAGTATCACTTACCGTGAGTGGGCTCTTGGTCCCAAGTC		
DB	516	TTCCGCGAGTATGCCGCTTAACCTTATAGAGATGGGCGCTCGAGCTAAGGCT		
QY	741	CCTCATTTGGAGATTTCACAAATTCGGACGCAAAATGCTGACATATGACTCGA		
DB	576	ACTTATCGGAGATTTCACAACTGGAAATCTTAATGACAGATATCATGACTCGGA		
QY	801	TGGTCTCTGGGAGATTTTCTGCGCAAAATAATGTGGATGGTTCTCTCGCAATTC		
DB	636	TGGTCTTTGGGAGATCTTTTGGCCCAACAACACATGATGGTTGCGCTGCAATTC		
QY	861	GTCCAGAGTGAAGATAGATATGGACATCCATCAGTGGTTTAAAGATTCCATTC		
DB	696	CTCACGTGAAGATTGGTATGGATATCTCCATCTGGCAATTAAGACATCAATTC		
QY	921	GATCAACTACTCTTTACAGCTTCCTGATGAATTCATATAATGGAATACATATTA		
DB	756	GATCAAGTCTTCGGTGGAGCTCCAGGTGAATGCCATTTCAATGGCAATATCA		
QY	981	ACCCGAGAGGAGAGGTATATCTTCCACACCCACCGGCCAAGAAACCAAGT		

816 TCCAGAGAGGAGAGATGATGTTTCAACATCTCTCAACCAAGAGACCTAAGTCGCTAAG 875
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876 GATTATGAAGACACATGTTGGCATGAGTAGCAGCGAACCATGCTCAATAGTATGCTAA 935
1101 TTTTAGAGATGAAGTCTTCTCTCGCATAAAAAGCTTGGGTACATGGCTGCAAAATAT 1160
936 CTTTAGAGATGATGTTCTCCCGCATCAAAAGCTTGGATATAGTGTGTCAAAATAT 995
1161 GGCTATTCAAGAGACATCTTATTACGCTAGTTTTGGTTATCATGTCACAAATTTTTTGC 1220
996 GGCCATACAAAGAACATCAUATTATGCCAGCTTTGGGTACCATGTCACAACTTTTTGC 1055
1221 ACCAAGCAGCGTTTTCGAGCGCCGAGGACCTTAAGTCTTTGATGATGAAGCTCATGA 1280
1056 CCCAAGCAGTCGCTGTGGGACCCGAGAGAACTAAAATCACTAGATAGAGCTCACGA 1115
1281 GCTAGGAATTGTTCTCTCATGGACATGTTTACAGCCATGTCATCAAAATATATCTTTAGA 1340
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1401 TCATTGATGAGGATTCGCCCTCTTAACTATGGAACCTGGAGCTAGTATGATCT 1460
1236 CCATTGATGAGGATTCGAGACTTTTCAATTAATGGAGCTGGGAAGTATTAACGATATCI 1295
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1581 GGAATCTTTGAGTCCCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1640
1416 CGATATCTTTGAGTGGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1475
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1761 AATTGCTGATAACGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1820
1596 CATAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1655
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1656 CATCATTTACACACTTACCAACAGAGAGTGTGATGATGATGATGATGATGATGATGATG 1715
1881 TCATGATCAAGCTCTAGTGGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1940
1716 TCAGATCAAGCTCTTGTGGTGAATAAACAATTTGCTTCTGATGATGATGATGATGATGATG 1775
1941 GTATGATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2000
1776 GTATGATTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1835
2001 GCACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2060
1836 GCACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1895
2061 GGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2120
1896 GGAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1955

2121 TGATGGCTCAGTAATCCCGAAACCAATTCAGTTATGATTAATGCAGACGAGATTGA 2180
1956 TGATGGTAGCTGATTCCTGGCAACAATTTTCAGTTATGACAAATTCGCGCCGAGATTGA 2015
2181 CCTGGGAGATGAGAAATTTTAAGATACCGTGGGTTGCAAGAAATTTGACCGGCCATGCA 2240
2016 TCTTGGGATGAGATTAATTCAGATACCGGGACTACAAAGAAATTTGATCAGGCAATGCA 2075
2241 GTATCTTGAAGATAAATATGATTTATGACTTCAGAACACCACTTCATATCAGCAAGGA 2300
2076 ACATCTTGAAGAGATTAAGTTTATGACTTCGAGCACCACCAATTCATATCAGCAAGGA 2135
2301 TGAAGGAGATGAGATGATTTATTTGAAAAAGAAACCTAGTTTGTCTTTAAATTTTCA 2360
2136 CGAAGCAGATAGATTAATCGTATTCGAAAGAGGTGATCTCGTCTTTGCTTTAACTTTCA 2195
2361 CTGACAAAAAGCTTATTCAGATACGATTCGATAGCCTGAGCCTGGAACCTGGAATACAGGT 2420
2196 CTGGACCAAGCAGCTACTTTGATTCGCAATTTGCTTCCAAAGCCTGGAATATAGAT 2255
2421 TGCCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATTTGATCATATACCGGA 2480
2256 CGTATTTGACTCGGACGATCTCTTTTGGTGGATTAATAGGCTCGATCGCAAGGCAGA 2315
2481 ATATTACCTTTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2540
2316 GTACTTCACTTATGATGCTTATAGGACGACGACCTGCTCTTCATGGTCTATGACCC 2375
2541 TTGTAACACAGCAGTGGTCTATGCACTAGTAGACAAAGA 2579
2376 GTGTAGAACCCCGTGGTTTATGCTTTAGCAAAACACGA 2414

RESULT 4

US-09-938-842A-337
; Sequence 337, Application US/09938842A
; Patent No. US2002160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Krieps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

Query Match 48.8%; Score 1290; DB 9; Length 2577;
Best Local Similarity 76.1%; Pred. No. 0;
Matches 1590; Conservative 0; Mismatches 500; Indels 0; Gaps 0;

QY 503 AGAGGGCATCCCTCCACCTGGACTTGGTCAGAGATTTATGAAATAGACCCCTTTTGA 562
Db 443 AGAGGAAGATTTCCACCTCCCTGGAGATGGGAAGAAATATATGACATTTGATCTTATGTTGA 502
QY 563 CAAACTATCGTCAACACTTGTATTACAGGTATTACAGGTATGCGCAAGAACTCAGGAGCA 622
Db 503 ACAGTCATCTATCATCTTGTATCCGATATGGCAGTACAGAAACTCGGTGAAGAA 562

QY	623	TTGACAAGTATGAGGGTGGTTTGGAAAGCCCTTTTCCTCGTGGTTATGAAAAAATGGGTTTCA	582
Db	563	TTGACAAGAATGAAGTGGTTTGGAGGCAATTTCTCGTGGTTATGAAATATTTGGCTTCA	622
QY	683	CTCGTAGTGTACAGGTATCACTTACCGTGAGTGGCTCTTTGGTGGCCAGTCAGCTGCC	742
Db	623	CTCGAAGCGCACTGATATCACTTACGGGAATGGCACCGGAGCTAGGCAGCATCAC	682
QY	743	TCATTTGGAGATTTCAACAAATTTGGAGCGCAAAATCTGCACATTAATGATTCGSAATGAATTTG	802
Db	683	TGATCGGAGATTTTAATAACTTGAATTCGGAATCTGATGTATGCGTTCGGAACGACTTTG	742
QY	803	GTCTCTGGGAGATTTTCTGCCCCAAATAAATCTGGATGGTCTCTCTGCAATTCCTCATGGGT	862
Db	743	GTGTGTGGGAAATATTTCTGCCAAATAAATGCTGATGGCTCACACAGCAATTTCCCCATGGCT	802
QY	863	CCAGATGAAGATACATATGGACACATCCATCAGTGTTAAGGATTCATCTCTGCTTTGGA	922
Db	803	CCGGTGTGAAGATCCGCATGGATACCCCATCTGGTATTAAGAGATCCATTCACAGCTTGA	862
QY	923	TCAACTACCTTTACAGCTTCCGATGAATTCATATCCATATATGAAATACATATATGATCCAC	982
Db	863	TCAAGTATCTGTCCAGCACCTGGCGAGATCCCATATATGAGGATATATATGAGCCCTC	922
QY	983	CCGAAGAGGAGAGGTATATCTTCCACACCCACGGCCGAAGAAACCAAGTCTCGCTGAGAA	1042
Db	923	CTGAGGAGGATAAATATGCTTCAACACATCTCTGTCCTCAAGAAACCCACATCGCTCGTA	982
QY	1043	TATATGAATCTCATATTTGAAATGAGTAGTCCGAGGCTTAAATTAATCATCATGCTGAAT	1102
Db	983	TATATGAATACATTTGGAATGAGTAGTAGCGAACCNAAGATTAATATACATATGCCAAT	1042
QY	1103	TTAGATGAAGTTCTTCCCTCGCATAAAAAGCTTGGGTACATGCGCTGCAAAATATGG	1162
Db	1043	TTAGAGATGATGTACTTCCCGTATAAAAAGCTAGGCTATATGCTGTGCAGATATGG	1102
QY	1163	CTATTCAGAGCAATCTTATTAACGCTAGTTTTGGTATATCATGTACAAATTTTTTTGCAC	1222
Db	1103	CCATTCAGAGCATGCTACTATGCCAGCTTTTGGGTATCATGTGACAAATTTTTTGCAC	1162
QY	1223	CAAGCAGCGTTTGGNACCCGAGACCTTAAGTCTTTGATTTGATTAAGCTCATGAGC	1282
Db	1163	CTAGCAGCCGTTTGGAACACCTGATGACCTTAATCTTTGATAGCAAAAGCTCATGAGC	1222
QY	1283	TAGGAATTTGTTCTCATGGACATTTTCCACAGCCATGCATCAAAATATATCTTTAGATG	1342
Db	1223	TAGTCTGGTTTCTCATGGAATATGTGCACAGCCATGCATCAAAAACACACTGGAATG	1282
QY	1343	GACTGACATGTTTACTGCACCGATAGTTTACTTTTCACTCTGGAGCTCTGGTTATC	1402
Db	1283	GCTCGGACATTTTGTATGTGACTGATGGTCAATATTTCCACTCTGATCGGTGGTATC	1342
QY	1403	ATTGGATGTGGGATTTCCGCTCTTAATCATGGAACATGGGAGGTACTTAGTATCTTC	1462
Db	1343	ATTGGATGTGGATTTCTCGTCTTTCATTTACGGAAGCTGGGAAGTCTTAGATATCTTC	1402
QY	1463	TCTCAATCGGAGATGGTTGGATCGGTTTCAAAATTTGATGATTTAGATTTGATGGTG	1522
Db	1403	TTTCCACGCGAGATGGTGGCTGGAAGAATACAAAGTTTGTATGGGTTTCAAGATTTGATGGTG	1462
QY	1523	TGACATCAATGATGTATATTCACACAGGATTAATCGGTGGATTCACCTGGGAACACTACGAGG	1582
Db	1463	TGACTTCCATGATGTACATCATCATGAGCTGCAGGTTCGAATTTACTGGGAATTCATG	1522
QY	1583	AATACTTTGACTCGCAACTGATGTGGATCTCTTGTATCTCATGCTGGTCAACGATC	1642
Db	1523	AGTACTTTGGATATTTCTACTGATGTTGACGCTGTGGTCTATCTAATGCTGGTGAACGATT	1582
QY	1643	TTATTCATGGCTTTTCCAGATGCCAATTACCATTGGTGAGATGTTAGCGGAATGCCGA	1702
Db	1583	TGATTCATGGCTATACCCCTGAGGCTATTTGTTTCGCGGAAGATGTTAGCGGAATGCCAG	1642
QY	1703	CATTTTGTATTTCCGCTCAAGAGGGGGGTGTGGCTTTGACTATCGGCTGCATATGSCAA	1762

[illegible]

```

RESULT 5
US-09-792-127-3
: Sequence 3, Application US/09792127-3
: Patent No. US2002002713A1
: GENERAL INFORMATION:
: APPLICANT: Allen, Steve
: APPLICANT: Beckles, Diane M.
: APPLICANT: Butler, Karla
: APPLICANT: Pearlstein, Rich
: TITLE OF INVENTION: Starch Branch
: FILE REFERENCE: BB1439 US NA
: CURRENT APPLICATION NUMBER: US/09-
: CURRENT FILING DATE: 2001-02-23

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; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-3

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Query Match	44.1%	Score 1167.2	DB 10	Length 3039
Best Local Similarity	72.0%	Pred. No. 7.6e-312		
Matches 1523	Conservative 0	Mismatches 593	Indels 0	Gaps 0
QY	481	GATGAATCTGATAGGATCAGAGAGAGGGGCATCCCTCCACCTGGACATTTGGTCAGAAATTT	540	
Db	474	GAATCAATCTAGAGGGAGAAATTTACGATTTCTGCCACCACCGGAAATGGACACAATA	533	
QY	541	TATGAATAAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTTACAGTATTCACAG	600	
Db	534	TACGAGATTGACCCACGCTCCGAGACTTTAAGTACCATCTTGGATTCAGATATAGCCATA	593	
QY	601	TACAAGAACTGAGGGAGGCAATTGACAAGTATGAGGCTGGTTTGGAGCCTTTTCTCGT	660	
Db	594	TACAGGAGATAAGTTTCAGACATTTGATGAACAGGAGGAGCATGGATGATTTTCCCGC	653	
QY	661	GGTTATGAAAAATGGTTTTCACCTCGTAGTGCTACAGGTATCATCTTACCCTGGAGTGGCT	720	
Db	654	GGTTACGAGAAGTTTGGATTTATGGCAGCGCTGAAGGTATCATCTTACCAGAAATGGCT	713	
QY	721	CTTGGTCCCAAGTCAGTGCCTTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTGAC	780	
Db	714	CCTGGAGCAGATCTGCAGCATTTAGTTGGCGACTTCAACAATTTGGGATCCAAATGCGAGAC	773	
QY	781	ATTATGACTCGGAATGAATTTGGTGCTGGGAGATTTTCTGCGAAATAATATGGATGGT	840	
Db	774	CATATGAGCAAAAATGACCTTGGTGTTTGGAGATTTTCTGCGCAAAATGCGAGATGGT	833	
QY	841	TCCTCTGCAATTCCTCATGGTCCAGAGTCAAGATAGTATGACACTCCATCAGATGGTT	900	
Db	834	TCGCCACCAATTCCTCACGGCTCACGGGTGAAGTGAGATGAGATCTCCATCTGGGATA	893	
QY	901	AAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCATAT	960	
Db	894	AAGGATTCATTCCTGCTGGATCAAGTACTCCGTGCAGACTCCAGGAGATATACCATAC	953	
QY	961	AATGGAAATACATATGATCCACCGGAGAGGAGGTATATCTTCCACACCCACAGGCCA	1020	
Db	954	AATGGAAATATTTATGATCTCCCGAAGAGGAGGATGATGATTTCAAGCATCTCAACCT	1013	
QY	1021	AGAAACCAAGTCGCTGAGAATATATGAATCTCATATGGATGAGTAGTCGGAGCCT	1080	
Db	1014	AAACGACCAAAATCATTCGGATATATGAACACATGTTCGATGAGTAGCCCGGAACCA	1073	
QY	1081	AAATTTAATCATACGTGAATTTTAGAGATGAAGTTCTTCTCTGCAATAAAAAAGCTTGG	1140	
Db	1074	AAAGTCAACACATATGCAAACTTCAGGGATGAGGTGCTTCCAAAGATTTAAAGACTTGG	1133	
QY	1141	TACAATGCGCTGCAATTTATGGCTATTCAAGACATTCATTATTACGCTAGTTTGGTTAT	1200	
Db	1134	TACAATTGCACTGCAAAATATGGAATTTCCAAAGACACTCATPACTATGGAAGCTTTGGGTAC	1193	
QY	1201	CATGTCACAAATTTTTTGCACCAAGCAGCGCTTTTGGAAAGCCCGCAGACCTTAAAGTCT	1260	
Db	1194	CATGTTACCAATTTCTTGACCAAGTAGCCGTTTTGGGTTCGCCCAAGGATTTAAATCT	1253	
QY	1261	TTGATTTGATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGTGACATTTGTTCCAGGCAT	1320	
Db	1254	TTGATTTGATAGACTCACGAGCTTGCGTTGGTTGTCTCATGTGATGTTGTTTCACGTCAC	1313	
QY	1321	GCATCAAAATAACTTTAGATGGACTGACATGTTTTCAGTCGACCGGATAGTTGTTACTTT	1380	
Db	1314	CGCTCAAAATAACCTTTGACCGGGTTGAATGGTTTGTGATGGCAGGATACACATTTACTTC	1373	

1381	QY	CAC	TC	TG	GAG	CTCG	TG	TAT	C	A	P	T	G	A	T	G	G	A	T	T	C	C	G	C	C	T	T	T	A	A	C	A	T	A	T	G	A	A	A	C	1441
1374	DB	CAT	GC	G	G	T	T	C	A	C	G	G	G	C	A	T	C	A	C	T	G	A	T	G	G	G	A	T	T	C	C	G	T	G	T	T	T	A	A	C	1433
1441	QY	TGG	G	A	G	T	A	C	T	A	G	T	A	T	C	T	C	T	C	A	A	T	C	C	G	A	G	A	T	G	G	T	G	G	A	T	G	G	T	C	1500
1434	DB	AAG	A	G	A	G	T	T	A	A	G	T	T	C	T	A	C	T	T	C	A	T	G	C	A	A	G	A	T	G	G	T	G	G	A	T	A	A	G	1493	
1501	QY	GAT	G	A	T	T	A	G	A	T	T	G	A	T	G	T	G	A	C	A	T	A	A	T	A	T	T	C	A	A	T	A	T	T	C	A	A	T	C	1560	
1494	DB	GAT	G	G	T	T	C	G	A	T	T	C	G	A	T	G	G	C	G	A	C	T	C	A	A	T	A	T	T	C	C	A	T	A	T	T	C	A	1553		
1561	QY	GG	A	T	T	C	A	C	T	G	G	A	C	T	A	C	T	G	G	A	T	A	C	T	T	T	G	G	A	T	G	G	A	T	G	G	A	T	C	1620	
1554	DB	ACC	T	T	T	A	C	A	G	A	G	T	A	C	A	A	T	T	T	T	G	G	C	T	T	T	G	G	C	T	T	T	T	T	T	T	T	T	C	1613	
1621	QY	TAT	C	T	G	A	T	G	T	G	T	C	A	A	C	A	T	T	T	T	C	A	T	G	G	G	T	T	T	T	T	T	T	T	T	T	T	T	C	1680	
1614	DB	TAC	T	T	G	A	T	G	A	T	A	T	C	A	A	T	T	C	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	1673	
1581	QY	GA	A	T	G	T	T	A	G	C	G	A	A	T	T	T	G	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	1740	
1674	DB	GA	A	T	G	T	T	A	G	C	G	A	A	T	T	T	G	C	C	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	C	1733	
1741	QY	GAC	T	A	T	C	G	G	T	G	C	A	T	A	T	G	G	A	A	T	T	G	C	T	A	A	A	C	G	A	T	T	T	T	T	T	T	T	C	1800	
1734	DB	GAC	T	A	T	C	G	C	T	A	C	A	T	A	T	G	G	T	G	C	G	A	C	A	A	T	T	T	T	T	T	T	T	T	T	T	T	T	C	1793	
1801	QY	GAG	A	T	T	G	G	A	G	T	G	G	T	G	A	T	T	T	T	A	C	A	C	T	A	C	A	A	A	T	A	A	A	T	A	A	A	T	C	1860	
1794	DB	GA	A	T	T	G	G	A	G	T	G	G	T	A	T	T	T	G	C	A	C	A	C	A	A	A	A	A	A	T	A	A	A	T	A	A	A	T	C	1853	
1861	QY	TGT	T	T	T	C	A	T	A	C	G	T	G	A	A	A	T	C	A	T	A	G	T	C	T	A	G	T	G	A	T	A	A	A	T	A	A	A	T	C	1920
1854	DB	TGT	T	T	T	A	C	T	A	G	T	G	A	A	A	T	C	A	T	A	G	T	C	T	A	G	T	G	A	T	A	A	A	T	A	A	A	T	C	1913	
1921	QY	TGG	C	T	G	A	T	G	G	A	A	T	A	T	T	T	T	T	T	T	A																				

1585 TCGGGCATCCTGAATGGATAGACTTTCCAAAGAGGCCCAACAGTACTTCCAAAGTGGTAAGT 1644
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2132 TAATCCCGGAAACCAATTCAGTTATGATAAATGACAGCGAGATTTGACCTGGGAGATG 2191
2191
1645 TCATCCCGGAAACCAACAGATTCAGCAAAATGCCGTGGAAGATTTGACCTGGGTAAGT 1704
1704
2192 CAGAATATTAAGATACCGTGGTTGCAAGAAATTTGACCGGCTATGAGTATCTTGAAG 2251
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1705 CAGAAATTTCTTAGGTATCATGTATGACAGCAATTTGATCAGCAATGCAAGTCTTGAAG 1764
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2252 AFAAATATGAGTTTATGACTTCAGAACACCACTTCATATCAGAAAGGATGAGGAGATA 2311
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1765 AAAAATATCGTTTATGATACATCAGAACCACTACGTATCTCGGAAACATGAGGAAGTA 1824
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2312 GGATGATGTTATTTGAAAAGAAACCTAGTTTGTGCTTTAAATTTTCACTGCAGCAAAA 2371
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1825 AGGTATCGTGTGTTGAAAAGGGGACTTGGTATTTGTGTTCACTTCCACTGGAGTAGTA 1884
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2372 GCTATTCAGACTATTCGCATAGCTGCTGCTGAAGCCTGGAAATACAAAGTTGCTTGGACT 2431
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1885 GCTATTTGCACTACCGGTGCGCTCTTTAAAGCCTGGGAAGTACAAAGTGGTCTTAGACT 1944
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2432 CAGATGATCCAGCTTTTGGTGGCTTCGGGAGAAATGATCATATATCCGAATATTCACCT 2491
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1945 CGGACGCTGGACTCTTTGGTGGATTTGGTAGGATCCATCACACTGCAGACGACGTCATT 2004
2004
2492 TTGAAGGATGTTATGATGATGCTGCTGCTTCAATTTATGTTGTTATGCTTGTAAACAG 2551
2551
2005 CTGACTGCCACATGACAAAGGCCCTCCATTTCTGATGTTACACTCCTAGCAGAACCT 2064
2064
2552 CAGTGGCTATGCTAGTACGAAAGAAAGAAAGAAAGAAAGAAAG 2596
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2065 GTGTGTCTATGCTCCATGAACATAACAGCAAGTGCACATACG 2109
2109

RESULT 7

US-10-084-817-92
; Sequence 92, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Nuchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 92
; LENGTH: 2994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CH1
US-10-084-817-92

Query Match 21.9%; Score 578.2; DB 9; Length 2994;
Best Local Similarity 57.5%; Pred. No. 62e-149;
Matches 1164; Conservative 0; Mismatches 813; Indels 48; Gaps 5;
5;
544 GAAATAGACCCCTTTTGACAAACTATGTCACCAACCTTGATTAACAGTATTCACAGTAC 603
603
215 GAGATCGACCCGTACTTGAAGCCCTACGCGCTGGACTTCCAGCGCAGGTATAAGCAGTTT 274
274
604 AAGAACTAGGGAGGCAATTGACAGTATGAGGGTGGTTTGGAGGCTTTTCGTGGGT 663
663
275 AGCCAAATTTTGAAGAACTTTGGAGAAATGAAGGTGGTATTTGATAAGTTTCCAGAGCG 334
334

664 TATGAAAAAATGGGTTTCTACTCGTACTGTACAGGTATCACTTTACCGT---GAGTGGGCT 720
720
335 TATGAATCATTTGGCGTCCACAGATGCTGTGATGGTGTGTTATTAFACTGCAAGAAATGGCC 394
394
721 CTTGGTCCAGTCACTGCCCTCATTTGGAGATTTCAACAATTTGGACGCAAAATGCTGAC 780
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395 CCGGAGCAGAGGAGGATTTCTTACTGGAGATTTAAATGGTGGAAATCCATTTTCTGAT 454
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781 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCAAAATATATGGATGGT 840
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455 CCATACAAAAAAGTGGATTAAGAAATGGAGCTGTATATCCCAACAAAGCAGATATAA 514
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841 TCCTCCGAATTTCTCATGCTGGTCCAGAGTCAAGATACAGTATGAGCACTCCATCAGGTG-- 898
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515 TCTGTACTCGTCTCATGCTGATGATCCAAATTAAGAGTAGTTATTACTAGTAAAGCGGAG 574
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809 GGATACACTGCTATTCAGTTGATGCAATCATGAGAGTCTTACTATGCCAGCTTGTG 868
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1198 TATCATGTCACAAATTTTTCACCAACAGCAGCCGTTTGGAGCCGCGCCAGCCTTAAG 1257
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929 GAACCTGGTAGACACAGCTCATTCATGCTGATCATAGTCTCTTAGATGGTACACAGC 988
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1318 CATGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1377
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989 CATGCTTCAAAAATTCAGCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1048
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1378 TTTCACTCTGGAGCTCGTGGTTATCATTTGGATGTTGGGATTCGCGCTCTTTAACTATGA 1437
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1438 AACTGGAGTACTTAGGTATCTCTCTCAAAATGCGAGATGTTGATGCTGCTCAAA 1497
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1109 AGCTGGAGTCTTAAGATCTCTCTCTCAAAATGCGAGATGTTGATGCTGCTCAAA 1168
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1498 TTTGATGATTTAGATTTGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1557
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1229 CAAGGTTTCTCAGGTGATTAAGTGAATTTTCCGAGCTACAAGTATGATGATGATGATGAT 1288
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1618 GTGATCTGATGCTGGTCAACAGTCTTATTCATGGCTTTTCCAGAGTCAATTAACAT 1677
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1349 GCTGAGGATGATCAGGAATGCCAGCTCTGTGCTCTCAATTTCCAGGGAGGGGGTGGT 1408
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1738 TTTCACTATCGCTGCTGATATGCTGATTAACAGGATTTGATGATGATGATGATGATGAT 1794
1794

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1409 TTTGACATATCGACTAGCCATGGCAATTCAGATAAGTGGATTACGCTACTTAAAGAGTTT 1468
1795 CGGATGAGATGGAGAGTGGGTGATATTTGTTCAATACACTGACAAATAGNAGATGGTCG 1854
1469 AAAGATGAAGCTATGGGATGGGATATATATACACGCTTCAACAAACAGCGCTACCTT 1528
1855 GAAAGTGTGTTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATA 1914
1529 GAAAGTGCATGCTTATGACAGAGCCATGATCAGCAATGGTTGGGATAAGTCGCTG 1598
1915 GCATTCGTGCTGATGSAAGAGATATATGATGATTTATGGCTCTGGATAGACCGTCAACA 1974
1589 GCATTTGGTGTGATGGATGCGGAATGTATACAAACATGATGAGTGCCTGACTCCCTTACT 1648
1975 TCATTATAGATCGTGGATAGCAATTCGACAGAGATGATTAGGCTGTGAACCTATGGGATTA 2034
1649 CCAGTTATGATCGTGGATACAGCTTCATATAAATGATGACTCAATTACCGATGGGCTT 1708
2035 GGAGGAGAAGGTTACCTAAATTTTCATGGGAAATGAATTCGGCCACCGCTGAGTGGATTGAT 2094
1709 GGTGGAGAAGGCTATCTCAATTTTCATGGGTAATGAATTTGGGCATCCCTGAATGGTTAGAC 1768
2095 TTCCTAGGGCTGAACAAACACCTCTCTGATGGCTCAGTAATCCCGCGAAACCAATTCAGT 2154
1769 TTCCTCAAGAAA-----GGAAATAATCAGAGT 1795
2155 TATGATAAATCGACAGCGAGATTGACCTGGGAGATCGAGAAATATTTAAGATACCGTGGG 2214
1796 TACCATTTATGCCAGCGGCGAGTTTCATTTAACTACGACGACCTTCTTCGCTACAAGTTC 1855
2215 TTGCAAGAAATTTGACCGGCTATGACGATATCTTGAAGATAAATATGATGTTTATGACTTCA 2274
1856 CTAATAATTTTGACAGGATATGAATAGATTGGAAGAAAGATATGTTGGCTTGCAGCT 1915
2275 GAACACAGCTTCATATCAGAAAGGATGAGGAGATAGGATGATGTTGTTTGAAGAGGA 2334
1916 CCACAGGCTACGTGAGTGAAGAAACATGAAGGCAATAAGATCATTTGCTTTTGAAGAGCA 1975
2335 AACCTAGTTTTGCTTTTAAATTTTCACTGGCAAAAGCTATTCAGAGCTATCGGATAGCC 2394
1976 GGTCTTCTTTTCACTTTTCACTTCCATCCACAGAGAGCTACACTGACTACCGATTGGA 2035
2395 TGCCGTAAGCCTGGAATAACAGGTGGCTTTGGACTCAGANGATPCCACTTTTGGTGGC 2454
2036 ACAGCAATGCGAGGAAATTCAAAATTTGCTAGATTGCTAGATTGAGATGCGAGCGGAATATGGAGG 2095
2455 TTGCGGAGAAATGATCAATGCGGAATATTTCACTTTGAAGGATGGTATGATGATCGT 2514
2096 CATCAGAGACTGGACCAAGCAGCTGACTTTTTTTCTGAGGCTTTTGAACATAATAGGCGT 2155
2515 CCTCGTTCAATTATGGTGTATGACCTTGTAAAACAGCAGTGGTC 2559
2156 CCTATCTCTTTTGGTGTACATTCACAGAGAGTGGCCCTCATC 2200
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RESULT 8

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US-09-918-624B-30
; Sequence 30, Application US/09918624B
; Publication No. US20030113720A1
; GENERAL INFORMATION:
; APPLICANT: Scheye, Xiao Min
; APPLICANT: Sornasse, Thierry
; TITLE OF INVENTION: CDNAS EXPRESSED IN ADIPOCYTE DIFFERENTIATION
; FILE REFERENCE: PA-0033 US
; CURRENT APPLICATION NUMBER: US/09/918,624B
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/222,470
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PERL Program
; SEQ ID NO 30
; LENGTH: 2955
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
; US-09-918-624B-30

Query Match
Best Local Similarity 57.4%; Pred. No. 1.7e-148;
Matches 1163; Conservative 0; Mismatches 814; Indels 48; Gaps 5;

544 GAAATAGACCCCTTTTTCAGAAAATATCTCGTCAACACTTGTATACAGTATTCACAGTAC 603
187 GAGATCGACCGCTACTTTGAAGCCCTTACGCCCTGGACTTCCAGCGCAGGTATAAGCAGTTT 246
604 AAGAAATCAGGAGGCAATTCACAAGTATGAGGTGTTTGGAGCCCTTTCTCGTGGT 663
247 AGCCAAATTTGAAGAACATTTGGAGAAATGAAGTGGTATGATGAATTTTCCAGAGC 306
664 TATCAAAAATTTGGTTTTCACTCGTAGTCTACAGATATCATTACCTTACCGT---GAGTGGCT 720
307 TATGAATCATTTGGCGTCCACAGATGCTGCTATGGTGGTTTTATCTCCAAAAGAAATGGGCC 366
721 CTTGCTGCCAGTACGCTGCCCTCATTTGGAGATTTCAACAAATGGGACGCAAAATCTCGAC 780
367 CCGGAGCAGAGAGGAGTTTCTTACTGGAGATTTTAAGGTTTGAATCCATTTTCGTAC 426
781 ATTATGACTCGGAATGAATTTGGTCTCTGGGAGATTTTCTGCCCCAAATAATGTGGATGCT 840
427 CCATACAAAACACTGGATATGGAATGGGAGCTGTATATCCCAACCAAGCAGATAAA 486
841 TCTCCTGCAATTCCTCATGTTGGTCCAGAGTGAAGTACGTATGGAACACTCCATCAGGTG-- 898
487 TCTGTACTCGTGCCTCATGGAATCCAAATTAAGGTAGTTTATTACTAGTAAAGCGAGAG 546
899 -TTAAGGATTCCTTCCTGTTGGATCACTACTCTTTACAGCTTCTCTGATGAAATTCCTCA 957
547 ATCTGTATTCGTTTACCGTGGGCAAGTATGTTGGTTTGGTGAAGGTGATTAATGTGAAT 606
958 TATATGGAATACATTAATGATCCACCCGGAAGAGAGAGTATATCTTCCACACCCACGG 1017
607 TATGATTGATACACTGGGATCC-----AGAACACTCATATGATTTAAGCATTTCCAGA 660
1018 CCAAGAAACCAACTGCTGAGATATATGAATCTCATATTTGGAATGAGTAGTCCGGAG 1077
661 CCAAGAAAGCCAGGAGCTTGAAGATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720
1078 CCTAAAATTAACCTCATGCTGAATTTTAGAGATGAAGTCTCTCCCTCGCATATAAAAGCTT 1137
721 GGAAAGTAGCTTCTTTAATAACATTTTACATGCAATGTACTACCAAGATCAAGGCCCT 780
1138 GGGTACAATGGCTGCCAAATTTATGGCTATTTCAAGAGCATCTTATTAGCTAGTTTGGT 1197
781 GGATCAACTGCTTCACTGATTTGCAATCATGAGCAGATGCTTACTATGCCAGCTTTGCT 840
1198 TATCATGTCACAAATTTTTCACCAAGCAGCCGCTTTGGAAACCCGACACCTTAAG 1257
841 TACCAATCACAAGCTTCTTTGACGCTTCCAGCCGTTATGGAAACCTTGAAGAGCTTACAA 900
1258 TCTTTGATTGTAAAGCTCATGAGCTAGGAATTTGTTCTCTCATGACATTTGTTCCACAGC 1317
901 GAACTGGTAGACAGAGCTCATTCATGGGTATCATAGTCTCTTAGATGTGTACACAGC 960
1318 CATGATCAAAATTAATTAATTTAGATGAGTGAACATGTTTGAATGACCGCATAGTTGTTAC 1377
961 CATGCTTCAAAAATTTACAGCATGATTTGAATATGTTTGAATGGGACAGATTCCTTGTTAT 1020
1378 TTTCACTCTGGAGCTGGTGTATCATTTGGAATGTTGGATTCCTGCTTTTAACATGGA 1437
1021 TTTTATCTGGACCTAGAGGAGCTCATGATCTTTGGATGAGAGATGTTTGTCCCTACTCC 1080
1438 AACTGGGAGTACTTAGGTATCTTCTCTCAATGCGAGATGCTGTTGGTGTGATGCTTCAAA 1497
```

Db 1081 AGCTGGGAAGTTTAAAGATTCCTCTGTCAACAATAAGATGGTGGTGAAGAATATCGC 1140
QY 1498 TTTGATGATTTAGATTTGATGGTGTGACATCAATGATGATATATCAACCACCGATATCG 1557
Db 1141 TTTGATGATTTGATGGTGTGATGCTGTAGTCTCATCTTATCATCAACCATGGATGGGT 1200
QY 1558 GTGGGATTCACGTGGGAACCTACAGGAATCTTTGGACTCGCAACTGATGATGATGCTGT 1617
Db 1201 CRAAGTTTCTCAGGTGATTTACAGTGAATATTTCCGGACTACAGTAGATGAAGATGCT 1260
QY 1618 GTGTATCTGATCTGGTCAACAGATCTTATTCATGGGCTTTTCCAGATGCAATATCAAT 1677
Db 1261 ACTTACCTCATCTGGCAATCATTTGGTTCACACGCTGTGCCGATTCCTATACAAATA 1320
QY 1678 GGTGAAGATGTTAGCGGAATCCGACATTTTGTATTCCTGGTCCAGAGGGGGTGTGGC 1737
Db 1321 GCTGAGGATGTATCAGGAATGCCAGCTCTGTCTCTCCAATTTCCAGGGAGGGGTGGT 1380
QY 1738 TTTGACTATCGGCTCATATGGCAATTCGTGATAAAGGATTTGCTCA--AGAA 1794
Db 1381 TTTGACTATCGACTAGCCATGCCAATTCAGATAAGTGGATTCAGTACTTAAAGATTT 1440
QY 1795 CGGGATGAGGATTTGGAGATGGGTGATATTTGTATACACTGACAAATAGAAGATGGT 1854
Db 1441 AAGATGAAGACTGGCAATGGCGATATAGTATACAGCTCACAAACAGGCGCTACCTT 1500
QY 1855 GAARAGTGTGTTATAGCTCAAGATCATGATCAAGCTCTAGTCCGTGATGATGATGAT 1914
Db 1501 GAAAGTGCATTTGCTATGACAGAGCCATGATGATGATGATGATGATGATGATGATG 1560
QY 1915 GCATTTCTGGCTGATGACAAAGATATGATGATGATGATGATGATGATGATGATGATG 1974
Db 1561 GCATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
QY 1975 TCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2034
Db 1621 CCAGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
QY 2035 GGAGGAGAGGTACTTAAATTTCAATGGAATGATGATGATGATGATGATGATGATGAT 2094
Db 1681 GGTGAGAGGCTATCTCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1740
QY 2095 TTCCCTAGGCTGAACAACACCTCTGTATGCTCAGTAAATCCCGGAAACCAATTCAGT 2154
Db 1741 TTCCCAAGAA-----GGAAATATGAGAGT 1767
QY 2155 TATGATAATGCAGACGGAGATTTGACCTGGGAGATGCAGATAATTTAAGATACCTGGG 2214
Db 1768 TACCATTTATGACAGCGCGAGTTTCATTTAACTGACGACGACCTTCTCGCTACAGTTC 1827
QY 2215 TTGCAAGATTTGACCGGCTATGAGTATCTTGAAGATAATATGATGATGATGATGAT 2274
Db 1828 CTAAATAATTTGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1887
QY 2275 GAACACAGTTTCAATATCAGAAAGATGAAGGAGATAGATGATGATGATGATGATGATG 2334
Db 1888 CCACAGGCTACGTGAGTGAAACATGAAGCAATAGATGATGATGATGATGATGATGAT 1947
QY 2335 AACCTAGTTTGTCTTAAATTTTCACTGGCAAAAAGCTATTCAGACTATGCGATAGCC 2394
Db 1948 GGTCTCTCTTTTCAATTTCACTTCCATCCAGCAAGAGCTACACTGACTACCGAGTTGA 2007
QY 2395 TGCCCTGAGCTGGGAAATACAGGTTCGCTGGACTCAGATGATGATGATGATGATGAT 2454
Db 2008 ACAGACTTGCAGGGAAATCAAAATTTGCTAGATTCAGATGATGATGATGATGATGAT 2067
QY 2455 TTCCGGAGAAATGATCAATGCCGAATATTTCACTTTTGAAGATGATGATGATGATG 2514
Db 2068 CATCAGACTGGACCACAGCACTGACTTTTTTCTGAGGCTTTTGAACATAATGGGCT 2127
QY 2515 CCTCGTTCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2559
Db 2128 CCTATTCTCTTTTGGTGTACATTCAGACAGAGTGGCCCTCATC 2172

RESULT 9

US-09-880-107-2148
: Sequence 2148, Application US/09880107
: Patent No. US20020142981A1
: GENERAL INFORMATION:
: APPLICANT: Horne, Darci T.
: APPLICANT: Vockley, Joseph G.
: APPLICANT: Scherf, Uwe
: APPLICANT: Gene Logic, Inc.
: TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
: FILE REFERENCE: 44921-5028-WO
: CURRENT APPLICATION NUMBER: US/09/880,107
: CURRENT FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: US 60/211,379
: PRIOR FILING DATE: 2000-06-14
: PRIOR APPLICATION NUMBER: US 60/237,054
: PRIOR FILING DATE: 2000-10-02
: NUMBER OF SEQ ID NOS: 3950
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2148
: LENGTH: 2955
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

Query Match 21.8%; Score 576.6; DB 10; Length 2955;
Best Local Similarity 57.4%; Pred. No. 1.7e-148;
Matches 1163; Conservative 0; Mismatches 814; Indels 48; Gaps 5;
QY 544 GAAATAGACCCCTTTTGACAAACATATCGTCAACACCTTGATFACAGGTATTCACAGTAC 603
Db 187 GAGATCGACCCGCTACTTGGAGCCCTGAGGCTTCCAGCGAGGTATACAGCAGTTT 246
QY 604 AAGAAGCTGAGGAGGCAATGACAAAGTATGAGGTGGTTCGAAAGCCTTTTTCGTGGT 663
Db 247 AGCCAAATTTTGAAGAACATTTGGAGAAATGAGGTGGTATGATAAGTTTTCCAGAGGC 306
QY 664 TATGAAAAATGGTTTTCACCTCGTAGTGTACAGGTATACATTACCTGTTTTCAGTGGGT 720
Db 307 TATGATCATTTTGGGCTCCAGAGTGTGCTGATGTTTATCTTACCCAAGAAATGGGCG 366
QY 721 CTGTGTCACCTGACCTGCTCATTTGGAGATTTCAACAAATTTGGACCAATGCTGAC 780
Db 367 CCGGAGCAGAGGAGTCTTTCTTACTGGAGATTTAATGGTGGATCCATTTTCGTAC 426
QY 781 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATATCTGGATGT 840
Db 427 CCATACAAAAAATGGAATATGAAAAATGGAGCTGATATCCCAAGCAGATAAA 486
QY 841 TCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGTATGGACACTCCATCAGGTG-- 898
Db 487 TCTGACTCGTCCCTCATGGATCCAAATTAAGAGTAGTTATTACTAGTAAAAAGCGAGAG 546
QY 899 -TTAAGGATTCCTCTGCTGATCAACTACTCTTTACAGCTTCTCTGATGAAATCCA 957
Db 547 ATCTGTATCGTATTTCCACCGTGGCAAGATATGTTCTGTAAGGTGATATATGTAAT 506
QY 958 TATAATGGAATACATATGATCCACCGAGAGAGAGTATATCTTCCAAACACCGAG 1017
Db 607 TATGATGGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAGCATTTCCAGA 660
QY 1018 CCAAGAAACCAAGCTCGCTGAGATATATGATCTCATTTTGGATGAGTAGTCCGGAG 1077
Db 661 CCAAGAAACCGAGGCTAAGAAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720
QY 1078 CCTAAATTAACATACGTGAATTTTATGAGATGAGTTCTTCTCTCGATTAAGAGTTT 1137
Db 721 GGAAGTAGCTTCATTAACATTTTACATGCAATGTACTACCAAGATCAAGGCTTT 780

QY 1138 GGTACAAATGCGCTGCAAAATATATGGCTATTCAGAGCAATCTTATTACGCTAGTTTGGT 1197
Db 781 GGATACAACTGCATTCAGTTGATGGCAATCATGAGCATGCTTACTATGCCAGCTTGGT 840
QY 1198 TATCATGTCAAAATTTTTCACCAAGAGCCGTTTGGNACCCGACGACCTTAAG 1257
Db 841 TACCAAATCAAAAGCTTCTTTCAGCTTCCAGCCGTTATGGAACACCTGGAAGAGTACAA 900
QY 1258 TCTTTGATGTATAAGCTCATGAGCTAGGATGTTGTTCTCATGACAAATGTTTCACAGC 1317
Db 901 GAACCTGGTAGACACAGCTCAITCCATGGTATCATAGTCCCTTTAGATGTGTACACAGC 960
QY 1318 CATGCATCAAAATATACCTTAGATGAGTGAACATGTTGACTGCACCGATAGTTGTTAC 1377
Db 961 CATGCTTCAAAATATACGACAGATGATGATATGTTGATGGACAGATCCCTGTTAT 1020
QY 1378 TTCTACTCTGGAGCTCGTGGTTATCATTTGGATGTGGGATTCGCCCTCTTAACTATGA 1437
Db 1021 TTTCTATCTGGACCTTAGAGGACATCATGCTTTGGGATAGGAGATGTTTGCCCTACTCC 1080
QY 1438 AACTGGGAGTACTTAGTATCTTCTCTCAATGCGAGATGGTGGTTCGATCGCTTCAAA 1497
Db 1081 AGCTGGGAAGTTTAAAGATCTCTCTGTCAAACATAAGATGGTGGTGTGAAGAAATATGCG 1140
QY 1498 TTTGATGATTTAGATTTGATGGTGTGACATCAATGATGTATATTCACACGGATATCG 1557
Db 1141 TTTGATGATTTGCTGTTGATGGTGTACGTCATCTTCCGTCATGAGATGTTTGCCCTACTCC 1200
QY 1558 GTGGGATTCACCTGGGAACCTACGAGGAATCTTTGGACTCGCAACTGATGTGGATGCTGTT 1617
Db 1201 CAAGTCTTCTCAGTGATTCAGTGAATATTTCCGACTACAAATGATGAGATGCCCTGG 1260
QY 1618 GTGATCTGATGCTGGTCAACGATCTTATTCATGGGCTTTTCCAGATGCAATTAACCAT 1677
Db 1261 ACTTACCTCATGTTGGCAATCATTTGCTTCACAGCTGTGTCCGATTTCTATAACAATA 1320
QY 1678 GGTGAGATGTTAGCGGAATGCGGACATTTGTATTCGTCACAGAGGGGGTGTGGC 1737
Db 1321 GCTGAGATGATATCAGGAATGCCAGCTCTGTGCTCTCCAATTTCCAGGGGAGGGGGTGT 1380
QY 1738 TTTGACTCTGCTCATATGGCAATTCGTGATAAAGGATGAGTTGCTCA---AGAAA 1794
Db 1381 TTTGACTATCGACTAGCCATGCCAATTCAGATAGTGGATTCAGCTACTTAAAGATTT 1440
QY 1795 CGGATAGGATGAGTGGAGTGGTGTATTTGTCATACACTGACAAATAGAAAGATGGTG 1854
Db 1441 AAAGATGAAGCTGGAACATGGCGATATAGTATACAGCTCACAAACAGGCGCTACCTT 1500
QY 1855 GAAAGTGTGTTTCATCGCTCAAAATCATGATCAGCTAGTCGCTGATGATAAACTATA 1914
Db 1501 GAAAGTGCATTTGCTTATGCGAGAGCCATGATCAGGCAATGGTTGGGGATAGTCGCTG 1560
QY 1915 GCATTCGCTGATGACAAAGGATATGATGATTTTATGGCTCTGGATAGACCGTCAACA 1974
Db 1561 GCATTTTGGTTGATGATGCGGAATGTATCAACATGAGTGTCTGACTCTTTTACT 1620
QY 1975 TCATTAATAGATGTTGGATGACATTCGACAGATGATGAGCTTGTAACTATGGGATTA 2034
Db 1621 CCAGTATATGATGCTGGAATACAGCTTCATAAAATGAUCCGACTATTACGATGGGCTT 1680
QY 2035 GGAGGAGAAGGTACTTAATTTTCATGGGAATGAATTCGGCCACCCTGAGTGGATTCAT 2094
Db 1681 GGTGGAGAAGGCTATCTCAATTTTCATGGGATGAATTTGGGCATCTCCAAATGTTAGAC 1740
QY 2095 TTCCCTAGGGTGAACAACACCTCTCTGATGGCTCAGTAATCCCGGGAACCAATTCAGT 2154
Db 1741 TTCCCAAGAAA-----GGAAATATCAGAGT 1767
QY 2155 TATGATAATGCAGACCGAGATTTGACCTGGGAGATGCAGAAATATTTAAGATACCGTGGG 2214
Db 1768 TACCATTATGCGAGCGGAGTTTCATTTAACTGACGACGACCTTCTTCGCTTACAAGTTC 1827
QY 2215 TTGCAAGATTTTGCCGGCCTATGACAGTATCTTGAGATAAATATCAGTTTATGACTTCA 2274

Db 1828 CTAAATAATTTTGACAGGGATATGAATAGATTGGAGAAAGATATGGTTGGCTTCACGT 1887
QY 2275 GAACACCACTTCATATCACGAAGGATGAAGAGATAGGATGATGATTGTTTGAAGAAAGGA 2334
Db 1888 CCACAGGCTCTAGTGTAGTGAAGAAACATGAAGCAATAGATCATTCGTTTGAAGAGGA 1947
QY 2335 AACCTAGTTTTGTCTTTAAATTTCACTGGACAAAGCTATTCAGACTATCGCATAGCC 2394
Db 1948 GGTCTCTTTTCATTTTCACTTCCATCCAAAGAGAGCTACACTACTACCGAGTTGA 2007
QY 2395 TCCCTGAAGCTGGGAAATACAAAGTTGCTTGGACTCGACTAGATCCACTTTTGGTGGC 2454
Db 2008 ACAGCATTTGCCAGGAAATTCAAAATTTGCTAGATTTCAGATGCGAGCGAAATATGAGGG 2067
QY 2455 TTCGGGAGAATTTGATCATTAATCCGAATATTTCACTTTTGAAGGATGGTATGATCAT 2514
Db 2068 CATCAGAGACTGGACACAGCACTGACTTTTCTGAGGCTTTTGAACATAATGGCCT 2127
QY 2515 COTCTTCAATTTATGGTGTATGCACCTTGTAAACAGAGAGTGGTC 2559
Db 2128 CCTATTCTCTTTTGGTGTACATTCACAGCAGAGTGGCCTCATC 2172

RESULT 10
US-09-770-149-955/c
; Sequence 955, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:

; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Any
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770,149
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 955
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-09-770-149-955
Query Match 9.7%; Score 257.8; DB 10; Length 602;
Best Local Similarity 75.1%; Pred. No. 9.3e-61;
Matches 322; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

QY 2151 CAGTTATGATAATTCACAGAGGAGATTTGACCTGGGAGATGAGATATTTAAGATACCG 2210
Db 602 CAGTTATGATAATTCACAGAGATTTGATCTGGGATGAGATATTTAAGATACCG 543
QY 2211 TGGGTTGCAAGAAATTTGACCGGCTATGAGTATCTTGAAGATAAATATGAGTTTATGAC 2270

Db 542 CGGACTACAAGATTGATCAGCAATGCAACATCTTGAAGAGAAATACGGTTTATGAC 483
QY 2271 TTCAGACACAGATTCATATACCAAGAGATCAAGGAGATAGGATGATGATTGAAAA 2330
Db 482 TTCGGAGACCAATTCATATACCAAGAGATCAAGGAGATAGGATGATGATTGAAAA 423
QY 2331 AGGAACACCTAGCTTTTGTCTTAAATTTTCACCTGGCAAAAGCTATTCAGACTATCGCAT 2390
Db 422 AGGTGAICTGCTCTTGTCTTAACTTTTCACCTGGCAAGAGCTATTCAGACTATTCAGCAT 363
QY 2391 AGCCTGCCGAGCTGGAAAAATACAGAGTTGCTTGGACCTAGATGATCCACCTTTTGG 2450
Db 362 TGGTTCCTCCAGCCTGGAAAAATATAGATCGTATTTGGACTCGGAGCATCCCTTTGG 303
QY 2451 TGGCTTCGGGAGAAATGATCAATATGCGGATATTTTCACCTTGAAGGATGGTATGATGA 2510
Db 302 TGGATTCAAATAGGCTCGATCCCAAGGCGAGAGTACTTCACTTATGATGGCTTATAGGACGA 243
QY 2511 TCGTCCCTCGTTCAATTAATGTTGATGCAACCTTGTAAGACAGCAGTGGTCTATGCACTAGT 2570
Db 242 ACGACCTTGCTCTTCTGCTTATGCAACCTGATAGAACCCGCGTGTATGCTTTATGCTTTAGC 183
QY 2571 AGACAAGA 2579
Db 182 AAACACGA 174

RESULT 11

US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453
; LENGTH: 604
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (517)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (540)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (567)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (593)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-300-453

Query Match 5.1%; Score 136; DB 10; Length 604;
Best Local Similarity 58.8%; Pred. No. 4.6e-27;
Matches 254; Conservative 1; Mismatches 17; Indels 6; Gaps 1;
QY 903 GGATTCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAAATTCATATAA 962
Db 47 GTATCGATTTCACCGTGGCAAGATGTTGGTTCGTGAAGGTGATATGGAATTATGA 106

QY 963 TGGAAATACATTAATGATCCACCCGAAAGAGAGAGAGTATATCTTCCCAACACCCAGGCCAAA 1022
Db 107 TTGGATACACTGGGATCC-----AGAACACTCATATGAGTTTAAAGCATTTCCAGACAAA 160
QY 1023 GAAACCAAGTCGCTGAGAAATATATGAATCTCATATTTGGAATGAGTAGTCCGAGACCTAA 1082
Db 161 GAAGCCAGGAGCTTAAGAAATTTAATCTCATCTGGAATTTCTTCCCATGAAGGAAA 220
QY 1083 AATTAACATCATAGCTGAATTTTAGAGATGAAGTTCTTCTCGCATATAAAAAAGCTTGGSTA 1142
Db 221 AGTACCTTCTTATAAACATTTTACATGCAATGTACTACCAAGATCAAGAGCTTTGGATA 280
QY 1143 CAATCGGCTGCAAAATATGGCTATTCAAGAGCATTTTATTACGCTAGTATTTGGTATCA 1202
Db 281 CAACATGCAATTTAGTTGATGGCAATCATGAGCATGCTTACTATGCGAGCTTTGGTTACCA 340
QY 1203 TGTCAAAATTTTTTGCACCAAGCAGCGGTTTTTGAAGCCCGGAGGACCTTAAGTCTTT 1262
Db 341 AATCAAGCTTCTTTTGCAGCTTCCAGCGGTTATGGAACACCTGAAGAGCTACAAAGAACT 400
QY 1263 GATTGATAAAGCTCATGAGCTAGGAATTTGTTCTCATGGACATTTTCACAGCCATGC 1322
Db 401 GGTAGACACAGCTCATTTTCATGGGTATCATAGTCTCTTAGATGTGTACAGCCATGC 460
QY 1323 ATCAATAATAC 1334
Db 461 TTCAAAAAATTC 472

RESULT 12

US-09-770-444-893
; Sequence 893, Application US/09770444
; Patent No. US2002023280A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krickler, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 893
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-893

Query Match 4.3%; Score 114.6; DB 10; Length 441;
Best Local Similarity 67.2%; Pred. No. 3.1e-21;
Matches 162; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:27:32 ; Search time 3588.65 Seconds

(Without alignments)

11941.316 Million cell updates/sec

Title: US-10-056-454A-14_COPY_145_2790

Perfect score: 2646

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_estfun:*

15: em_estom:*

16: gb_gss:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_other:*

25: em_gss_pro:*

26: em_gss_rod:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1177.6	44.5	2766	11 AY109521	AY109521 Zea mays
2	1122.6	42.4	2732	11 AY109532	AY109532 Zea mays
3	615.8	23.3	3012	11 AY105679	AY105679 Zea mays
4	564.4	21.3	2738	11 AK009815	AK009815 Mus muscu
5	482.2	18.2	728	14 BU008463	BU008463 QGH7K17.Y
6	473	17.9	713	14 BQ986883	BQ986883 QGF10L08.

7	436.2	16.5	689	13 BI308555	BI308555 RST529965
8	436	16.5	801	10 BE198628	BE198628 HVSMEH008
9	424.2	16.0	678	10 AY939010	AY939010 AV939010
10	414.6	15.7	731	10 BE602527	BE602527 HVSMEH009
11	407	15.4	717	14 BU005876	BU005876 QGG9F08.Y
12	406.2	15.4	713	13 BM526229	BM526229 sal38f02
13	397.6	15.0	825	12 BF065047	BF065047 HV_CEB002
14	393.2	14.9	695	14 BQ240494	BQ240494 TaE05016F
15	385.4	14.6	621	12 BG521671	BG521671 13-3 Stev
16	384	14.5	650	10 BE427534	BE427534 PSR7153 I
17	381.4	14.4	646	9 AU238577	AU238577 AU238577
18	377.6	14.3	651	12 BG526727	BG526727 63-11 Ste
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20	372.8	14.1	569	10 AV442128	AV442128 AV442128
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22	369.6	14.0	576	10 AW244197	AW244197 687050F06
23	367.8	13.9	571	13 BI469105	BI469105 sal07e09
24	366.6	13.9	560	14 BM885252	BM885252 sal97a08
25	366.6	13.9	575	13 BI425610	BI425610 sah59a11
26	361.4	13.7	589	10 AW596011	AW596011 si96g03.Y
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36	340	12.8	516	14 BQ253050	BQ253050 sao05e05
37	337.2	12.7	569	13 BJ233506	BJ233506 RJ233506
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39	332.8	12.6	568	14 BQ240653	BQ240653 TaE05014F
40	327.8	12.4	509	12 BG651974	BG651974 sad72d10
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44	307.6	11.6	751	13 BI920158	BI920158 EST540093
45	306.4	11.6	898	14 BQ716536	BQ716536 AGENCOURT

ALIGNMENTS

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AY109521.1	VERSION	AY109521.1	GI:21213273			
HTC.	KEYWORDS	HTC.				
Zea mays.	SOURCE	Zea mays.				
Zea mays	ORGANISM	Zea mays				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC						
clade; Panicoideae; Andropogoneae; Zea.						
1 (bases 1 to 2766)						
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,						
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.						
Maize Mapping Project/DuPont Consensus Sequences for Design of						
Overgo Probes						
Unpublished (2002)						
2 (bases 1 to 2766)						
Coe,E.C.						
Direct Submission						
Submitted (25-APR-2002) Maize Mapping Project, University of						
Missouri, Columbia, MO 65211, USA						
Location/Qualifiers						
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/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BAGs in conjunction with the Maize Mapping Project"

BASE COUNT 715 a 546 c 689 g 718 t 98 others
ORIGIN

Query Match		44.5%	Score 1177.6;	DB 11;	Length 2766;
Best Local Similarity		70.8%;	Pred. No. 1.2e-257;		
Matches 1486;		Conservative 0;	Mismatches 612;	Indels 0;	Gaps 0;
QY	506	GGGCGATCCCTCCACCTGGACTTGGTCAGAGATTATGAAATAGACCCCTTTTGACAA	565		
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QY	566	ACTATCGTCAACACCTTGATTACAGGTATTACACACTACAGAACTGAGGAGGCAATTG	625		
DB	423	GGTTTCGGGGTCACCTTGACTACCGATACAGTGAATATAGAGATTAGCTGCGGTATTG	482		
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QY	686	GTAGTGCTACAGGTATCACTTACCGTGAGTGGCTTCTTGGTGCCCGACGTACGTCGCCCA	745		
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DB	603	TAGTGACTTCAACAACCTGGAACCAACCAATGCTGATGCTATGCGCAGAAATGAGTACGCG	662		
QY	806	TCTGGGAGATTTTCTGCCAATTAATGTGGATGTTCTCTCCCTGCAATTCCTCATGGGTCCA	865		
DB	663	TTTGGGAGATTTTCTGCTCAACATGCTGATGTTGCTCCCTGCTATTTCTCTATGGCTCAC	722		
QY	866	GAGTGAAGATACGTATGACACTCCATCAGGTGTTTAAGGATTTCCATTCCTGCTTGATCA	925		
DB	723	GTGTAAGATACGATGGACACACCACTGCTGTTGTAAGGATTTCCATTCCTGCCGGAATCA	782		
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DB	783	AGTTTCTGTGCGAGCTCCAGGTGAAATACCATACCAACGGTATATATTATGACCCACCTG	842		
QY	986	AAGAGGAGGTATATCTTCAACACCCACCGCCCAAGAAACCAACCAAGTCGCTGAGAAAT	1045		
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QY	1046	ATGAATCTCATTTGGAATGAGTATGTCGGAGCTTAAATTTAACTCATACCTGAAATTTTA	1105		
DB	903	ATGAATCACATGTTGGAATGAGTACCGCGGAACCAAGATAATACATATGCTAACTTCA	962		
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DB	1023	TCCAGGAACACTCTTATTATCCAGCTTGGGTACCATGTTTACGAANNNNNNNGCCCCCA	1082		
QY	1226	GCAGCGGTTTGGACGCGCCGACGACCTTAAAGTCTTTGATGATTAAGCTCATGAGCTAG	1285		
DB	1083	GTAGCGGTTTGGGACTCCAGAGACCTAAAAATCTTATTGATAAAGCGCATGAGCTTG	1142		
QY	1286	GAATTTGTTCTCATGACATTTGTCACACCCATGATCAATTAATTAATTTAGATGAC	1345		
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QY 1920 CTGGCTGATGACGACAGGATATGATGATTTATGCTCTGATAGACCGTCAACATCAATT 1979
Db 1843 TTGGTTGATGACGACAGGATATGATGATTTATGCTCTGATAGACCGTCAACATCAATT 1902
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VERSION AY105679.1 GI:21208757
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays.
REFERENCE 1 (bases 1 to 3012)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 3012)
AUTHORS Coe, E.C.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
FEATURES Location/Qualifiers
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assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project."
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2171 TGTCTTGAACGTGGAGATTAGTTTGTTCATTTTCAATTTCCATCCCAAGAACTTACGA 2230
2379 AGACTATCCATGCTGCTGAGCCTGGAACCTGGAATAAAGGTTGCTTGGACTCAGATCA 2438
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FEATURES

source

Location/Qualifiers

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/cultivar="L. serriola"

/cultural D:SCIT TOI
/db yref="taxon:4236"

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TAG_TISSUE-flowers post-fertilized
TAG_SEQ-TCGTCAGCCG"

a	132 c	146 q	214 t
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ORIGIN

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Querry	Index	Best Local similarity	79.0%: pred.	No. 3.5e-97;

Best local similarity	563	Conservative	0	Mismatches	150	Indels	0	Gaps	0
Matches	563	Conservative	0	Mismatches	150	Indels	0	Gaps	0

676 GGTTTCACTCGTAGTGCTACAGGTATCACATTACCGTGAGTGGGCTCTTGGTGCCCACTCA 735

A vertical ruler with markings from 0 to 75 cm. The markings are in centimeters, with major ticks every 10 cm and minor ticks every 1 cm. The ruler is oriented vertically with the 0 mark at the top and the 75 mark at the bottom.

Db
1 GGTTTCACTCGAAGCAAACAGGTATCACTTATAGAAATGGGCACCTGGGGCAAAGTCT 60

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Db 61 GCTTCACTTATTGGAGATTTCACACAACTGGAAATCCAAATGCTGATGTTATGACCCGGAAT 120

QEE

QY 796 GAATTGGTGTCTGGGAGATTTTCTGCCAAATAAAGTGGATGGTCTCCGCAATTCCT 839

180

DB
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ATGCTGGTGTTCAGGATTCCATTCCCT 915

QY
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[illegible]

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100

976 GATCCACCCGAAGAGGAGAGGTATATCTTCCAACACCCACGGCCAAAGAAACCAAGTCG 1035

Db 301 GATCCCCACAAGAGGAAATAACGTGTTTCAACATCCAAGACCAAGAAGCCGAAATCT 360

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FEATURES	SOURCE
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QGG9F08, mRNA sequence.
ACCESSION
VERSION
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SOURCE
ORGANISM
Lactuca sativa.
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 717)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig685f1, see http://cgpdb.ucdavis.edu/
for details.
Plate: QGG9 row: F column: 08.

FEATURES
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Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
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233 a 122 c 155 g 206 t 1 others

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QY 882 GGACATCCATCAGGTCTTTAAGGATTCATCTCTGCTTGGATCAATCTCTTACAGCT 941
Db 439 GGATACGCCATCTGGCATTTAAAGACTCGATCTGCTTGGATCAAGTTTTCAGTACAAGC 498
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QY 1002 CTTCCAAACACCCAGCGGCAAAACCAAGTCGCTGAGATATATGATGATGATGATGATGATGAT 1061
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RESULT 12
BM526229
LOCUS
DEFINITION
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Gm-cl059-4491 5' similar to TR:Q9XIS5 Q9XIS5 BRANCHING ENZYME 1
PRECURSOR ;, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Glycine max
soybean.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
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,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
BM526229
BM526229.1 GI:18731047
EST.
BM526229
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 573)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wyllie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers

Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Public Soybean EST Project
Unpublished (1999)

TITLE JOURNAL COMMENT

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 421.

FEATURES source

1. 573
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/db_xref="taxon:3847"
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BASE COUNT 169 a 110 c 126 g 167 t 1 others
ORIGIN
Query Match 15.4%; Score 406.2; DB 13; Length 573;
Best Local Similarity 81.8%; Pred. No. 5.7e-82;
Matches 468; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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QY 952 ATTCCATATATGAATACATTATGATCCACCCGAGAGAGAGGTATCTTCCACAC 1011
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Db 1 ATTCCATACAGCGGATATCTATGATCCCGAGAGAGAGAAATATGTTTCAACAT 60

QY 1012 CCACGGCCAAAGAACCAAGTCGCTGAGATATATGAATCTCATATTTGGAATGAGTAGT 1071
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Db 61 CCACAGCCAAAGAGACCAAAATACATAGATATATGATGATGATGATGATGATGATGAT 120

QY 1072 CCGAGGCTAAATTAATCTACTAGTGAATTTAGAGATGAAGTCTTCCTCGCATAAA 1131
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QY 1132 AAGCTTGGGTACATGCGCTGCAAAATTTATGCTATTCACAGCATTTTATTACGCTAGT 1191
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Db 181 AGCTTGGCTATATGCTGTCAGATATGCGTATCCAGAACATCTTTATTATGCCAGC 240

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QY 1252 CTTAAGCTTTGATTGATGAAGCTCATGAGCTAGGAATGTTGTTCTCATGGACATGTT 1311
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QY 1312 CACAGCCATCATCAATATATCTTTAGATGGAGTGAACATGTTTACCTCCACCGATG 1371
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QY 1432 TATGGAACCTGGAGGTACTTAGTATCTCTCAATCGGAGATGGTGGATGG 1491
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Db 481 TATGGAAGCTGGGAAGTTCTTAAGGTATCTTCTGAATGCACGATGGTGGTGA 540

QY 1492 TCAAAATTGATGATTTAGATTGATGTGT 1523
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Db 541 TACNAGTTGATGGATTTCGATTGATGTGT 572

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RESULT 13 LOCUS

BF065047

DEFINITION
HV_CEB0022L05f Hordeum vulgare seedling green leaf EST library
HV_CEB0022L05f, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare.
Hordeum vulgare.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 825)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi,
D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla6) seedling
leaf cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 594
Seq primer: AATTACCTCCTCACTAAAGG
High quality sequence stop: 732.
Location/Qualifiers
1. 825

FEATURES

source

/organism="Hordeum vulgare"
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/clone="HV_CEB0022L05f"
/library HV_CEB0022L05f
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
C.I. 16151 (Mla6) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate 5874 (AVR-Mla6
) of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;
uninoculated leaves were harvested 20 hr post-inoculation
(Wei, Wise). In the TJ Close lab at the University of
California, Riverside, total RNA was prepared from each
sample pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give pBluescript SK(-) cDNA
phagemids (Choi, Close). Phagemids were plated and picked
at the Clemson University Genomics Institute (CUGI) (Begum
, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 00:19:16 ; Search time 5591 Seconds
(without alignments)
4341.216 Million cell updates/sec

Title: US-10-056-454A-15_COPY_49_882
Perfect score: 4465
Sequence: 1 EKSSYNSEPRSTVAASGV.....EEEEEEVAAVEVVVEE 834

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-UNITS=bits -START=1 -END=1 -MATRIX=blosom62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: gb.in.*
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5: gb.ov.*
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7: gb.pl.*
8: gb.pr.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	4465	100.0	2992	8	STU011890
2	4465	100.0	3033	6	A58164
3	4372.5	97.9	2523	8	STU011889
4	4358.5	97.6	2578	6	A58169
5	4339	97.2	2493	8	STSBEI
6	4334	97.1	2576	6	A58166
7	4320	96.8	3074	6	AR123355
8	4297	96.2	2982	8	STU011888
9	4274	95.7	2563	6	AX256072
10	4269	95.6	3003	6	A58162
11	4268.5	95.6	3231	6	A58168
12	4225	94.6	2529	6	A58167
13	4220.5	94.5	2955	8	STU011885
14	4161.5	93.2	2975	6	A58163
15	3535.5	79.2	3123	8	AB071286
16	3363	75.3	3090	6	A92164
17	3347.5	75.0	3549	6	PSSBEIGEN
18	3320	74.4	2517	8	AB042937
19	3318.5	74.3	3360	8	AB029548
20	3309.5	74.1	2542	8	ATU22448
21	3281.5	73.5	2913	6	A92162
22	3266	73.1	2577	6	AX412751
23	3266	73.1	2577	6	AX412752
24	3249	72.8	2668	8	ATU18817
25	3239	72.5	3015	6	E14723
26	3236	72.5	3015	6	AB023498
27	3236	72.5	2364	6	E14724
28	3184.5	71.3	2795	8	ZMU65948
29	3166	70.9	2970	8	AF286319
30	3160	70.8	2970	8	TASBA2
31	3149	70.5	2853	8	TAG66376
32	3136	70.2	2726	8	AF338432
33	3130.5	70.1	2554	8	AF064560
34	3096	69.3	2919	6	E08183
35	3092	69.2	2918	8	RICBCE3
36	3021.5	67.7	2725	6	AR106495
37	3021.5	67.7	2725	8	MZEGUICTRN
38	3002	67.2	2780	8	AF064561
39	2496.5	55.9	104364	8	AC006919
40	2489.5	55.8	7020	8	ATSBE21
41	2462	55.1	1393	6	AR123356
42	2387.5	53.5	102897	8	ATF17C15
43	2165	48.5	3128	6	A46462
44	2159	48.4	2493	8	SIY08786
45	2156	48.3	2843	8	MESBERNA

ALIGNMENTS

RESULT 1

STU011890 2992 bp mRNA linear PLN 07-APR-1999
LOCUS Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
DEFINITION A-6.
ACCESSION AJ011890.1 GI:4584512
VERSION SBEII gene; starch branching enzyme II.
KEYWORDS Solanum tuberosum.
SOURCE Solanum tuberosum.
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 2992)
AUTHORS Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M.,
Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
TITLE A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2992)
AUTHORS Jobling, S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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Best Local Similarity: 100.00% Mismatches: 0
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DB: 8 Gaps: 0

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QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThr 40
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QY 61 AlaSerGlnLeuLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
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QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
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Db 1004 AGAGTGAAGATACCTATGGACATCCATCAGTGTGTAAGGATTCATTCCTGCTGTGATC 1063
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
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Db 1064 AACTACTCTTTACAGCTTCCTGTGATGAAATTCATATGATGAATACATATGATGACCC 1123
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US-10-056-454a-15_copy_49_882 (1-834) x A58164 (1-3033)

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DEFINITION Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
A-5.
ACCESSION AJ011889
VERSION AJ011889.1 GI:4584510
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum.
REFERENCE 1
AUTHORS Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M.,
Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
TITLE A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
JOURNAL Unpublished
AUTHORS Jobling, S.A.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
FEATURES
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DEFINITION Sequence 19 from Patent WO9634968.
ACCESSION  A58169
VERSION     A58169.1  GI:3713894
KEYWORDS   .
SOURCE     unidentified.
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 2578)
AUTHORS    Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
            Sidebottom, Christopher M. and Westcott,R.J.
TITLE      IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL    Patent: WO 9634968-A 19 07-NOV-1996;
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QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
DB 2101 CTTGAAGATAAATATGATGATTTATGACTTCAGAACACCACTCATATCAGAAAGGATGAA 2160
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
DB 2161 GGAGATGAGTGAATGATTTGAAAGAAACCTAGTTTGTCTTTAAATTTTCACCTGG 2220
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
DB 2221 ACAAAAGCTATTACAGACTACGCATAGCTGCCTGAAGCTTGGAAATACAGGTTGCC 2280
QY 761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
DB 2281 TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATAATGCCGAAT 2340
QY 781 PheThrPheGlyTyrTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
DB 2341 TTCACCTTGAAGGATGGTATGATGATCGTCTCGTTCAATATGGTGTATGACACCTAGT 2400
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
DB 2401 AGAACAGCAGTGGTCTATGCACACTAGTAGACAAA-----GAAGAGAGAGAGAGAA 2448
QY 821 GluGluValAlaAlaValGluGluValValValGluGluGlu 834
DB 2449 GAAGAGCTAGCAGTAGTAGAAGAACTAGTAGTAGAAGAGAA 2490

RESULT 6

A58166
LOCUS A58166 2576 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 16 from Patent WO9634968.
ACCESSION A58166
VERSION A58166.1 GI:3713891
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 2576)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.

TITLE IMPROVEMENTS IN OR RELATING TO PLANT SEARCH COMPOSITION

JOURNAL Patent: WO 9634968-A 16 07-NOV-1996;

NAT STARCH CHEM INVEST (US)

COMMENT Other publication AU 5509996 961121.

FEATURES Location/Qualifiers

source 1. 2576

/organism="unidentified"

/db_xref="taxon:32644"

BASE COUNT 770 a 462 c 615 g 729 t

ORIGIN

Alignment Scores:

Pred. No.:	0	Length:	2576
Score:	4334.00	Matches:	818
Percent Similarity:	98.56%	Conservative:	4
Best Local Similarity:	98.08%	Mismatches:	11
Query Match:	97.07%	Indels:	2
DB:	6	Gaps:	1

US-10-056-454A-15_COPY_49_882 (1-834) x A58166 (1-2576)

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DB 66 GAAAGGCTTCTTACAAATCCGAATCCGACCTTCTACAGTTGAGATCGGGAAGTC 125
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThr 40
DB 126 CTGTGCTGGAACCCAGAGTAGTCTCTCATCCCTCAACAAACCAATTTGAGTTCAC 185
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
DB 186 GAGACATCTCCAGAAATTCGCCAGCATCAACTGATGATAGATGATTTCAACAATGGAAC 245
QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer 80
DB 246 GCTAGCCAGATTAACCTGAGACGATGACGTTGAGCCGTCAGAGTATCTTACAGGAGT 305
QY 81 ValGluLeuLeuAspPheAlaSerSerLeuGlnGluGlyLysLeuGluGlu 100
DB 306 GTTGAAGAGCTGGATTTTCTCATCACTCAACATCAAGAAGGTGTTAACTGAGGAG 365
QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
DB 366 TCTAAAACATTAATCTCTCGAAGAGACAAATTTATGATGAATCTGATAGATCAGAG 425
QY 121 ArgGlyLeuProProGlyLeuGlyGlnLysIleValGluLeuAspProLeuLeuThr 140
DB 426 AGGGGCAATCCCTCCACCTGGACCTGGTCAGAGAAATTTATGAAATAGACCCCTTTGACA 485
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
DB 486 AACTATCGTCAACACCTTGATTTACAGGTATTACAGTATCAAGATCAAGAACTGAGGAGCAAT 545
QY 161 AspLysThrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
DB 546 GACAAGTATGAGGTGGTTTGGAAAGCTTTTCTCGTGTGTTATGAAATAATGGTTTCACT 605
QY 181 ArgSerAlaThrGlyIleThrTyrArgGluThrAlaLeuGlyAlaGlnSerAlaAlaLeu 200
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QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
DB 666 ATTGAGATTTCAACAATTTGGGAGCAAAATGCTGACATTTATGACTCGGAATGAAATTTGGT 725
QY 221 ValTrpGluIlePheLeuProAsnValAspGlySerProAlaIleProHisGlySer 240
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QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaThrIle 260
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QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspPro 280
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QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
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QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
DB 1024 AGAGATGAAGTCTTCTTCGCATATAAAAGCTGGGTACAAATGGCTCAAAATATGCT 1083
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
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QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
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QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnThrLeuAspGly 400
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QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
DB 1264 CTGACATGTTTGAGCGCACCGCATGTTGTTACTTTCCTCTGAGAGCTCGTGGTATCAT 1323
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DB 1324 TGGATGAGGATTCCTCCGCTTTTAACTATGAAACTGGAGGACTTATGATATCTTCTC 1383
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DB 1384 TCAATGCGAGATGTTGTTGATGAGTTCAAATTTGATGATTTAGATTTGATGTTG 1443
QY 461 ThrSerMetMetTyrIleHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
DB 1444 ACATCAATGATGATATCTACCCAGGATTCGGTGGGATTCACGCGGAACCTACAGGAA 1503
QY 481 TyrPheGlyLeuAlaThrAspValAlaValValTyrLeuMetLeuValAsnAspLeu 500
DB 1504 TACTTGGACTCGCAACTGATGATGCTGTTGTTGATCTGATGCTGCTCAACGATCTT 1563
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DB 1564 ATTCATGGGCTTTTCCAGATGCAATTTACCATGCTGAAGATGTTAGCGGAATGCCGACA 1623
QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
DB 1684 GCTGATAAATGATTTAGTTCAGTTCAGAAACCGGATGAGGATTTGAGAGTGGGTGATAT 1743
QY 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
DB 1744 GTTCATACACGACAAATAGAGATGGTGGGAAAGTGTGTTTCACTGCTGCAAGTATCAT 1803
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetThr 600
DB 1804 GATCAAGCTCTAGTGGGTGATAAATCTAGCAATTTCTGCTGCTGATGCAAGATATGAT 1863
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
DB 1864 GATTTTATGGTCTGATAGACCGCAACATCAATTAATAGATCGTGGGATAGCATGTCAC 1923
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1924  AAGATGATTAGCTTTGTAACCTATGGGATTAGGAGAGAGGTTACATAATTCATGGGA 1983
641   AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 560
1984  AATGAATTCGGCCACCCTAGTGGATTGATTTCCCTAGGCTGGAACACACCTCTCTGAT 2043
661   GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
2044  GACTCAGTAATTCGGGAACCAATTCAGTTATGATAAATGATGAGACGAGGATTTGACCTG 2103
681   GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
2104  GGAGATGAGATAATTTAAGATACCGTGGGTGCAAGAAATTTGACCGGCTATGCAGTAT 2163
701   LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
2164  CTTGAAGATAAATGAGTTATGACCTCAGAACACCACTGTTTATATCATACGAAAGATGAA 2223
721   GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
2224  GGAGATAGATGATGATTTGTAATTTGAAAGAGAAACCTAGTTTGTCTTAAATTTTCACTGG 2283
741   ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
2284  ACAAAGCTATTCAGACTATCGCATATCGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 2343
761   LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGlnTyr 780
2344  TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAATGATCAATGCGCCAAATAT 2403
781   PheThrPheGluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCys 800
2404  TTCACCTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2463
801   LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGluGlu 820
2464  AGAACAGAGTGGTGTATGCACTAGTAGACAAA--GAAGAAGAAGAAGAAGAAGAAGA 2520
821   GluGluValAlaAlaValGluGluValValValValValValValValValValValVal 834
2521  GAACAAGTAGCAGTAGTAGAGAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2562

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RESULT 7

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LOCUS       AR123355
DEFINITION  Sequence 1 from patent US 6169226.
ACCESSION   AR123355
VERSION     AR123355.1 GI:14108321
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.

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REFERENCE 1 (bases 1 to 3074)
AUTHORS Ek, B.; Kiosnoodi, J.; Larsson, C.-T.; Larsson, H. and Rask, L.
TITLE Starch branching enzyme II of potato
JOURNAL Patent: US 6169226-A 1 02-JAN-2001;
FEATURES location/Qualifiers
1..3074
/organism="unknown"

BASE COUNT 902 a 558 c 712 g 896 t 6 others
ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 3074
Score: 4320.00 Matches: 812
Percent Similarity: 97.96% Conservative: 5
Best Local Similarity: 97.36% Mismatches: 13
Query Match: 96.75% Indels: 4
DB: 6 Gaps: 1

US-10-056-454a-15_COPY_49_882 (1-834) x AR123355 (1-3074)

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393  CTTGTGCTTGAACCCAGAGTGATAGCTCCTCATCTCAACAGACCAATTTGAGTTCACT 452
41  GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
453  GAGACATCTCCAGAAATTTCCCCAGCATCACTGATAGTAGTAGTTCAACAATGGAACAC 512
61  AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
513  GCTAGGCAGATTAAACTGAGAACGATGACGTTGAGCCCTCAAGTCAATCTTACAGAAAT 572
81  ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyLysLeuGluGlu 100
573  GTTGAAGAGCTGGAATTTGCTTTCATCACTACAACTACAAAGAGGTGTTAACTGGAGAG 532
101  SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
633  TCTAAACATTAATTAATCTTCTGAAGAGACAATTAATGATCAATCTCATAGGATCAGAG 692
121  ArgGlyIleProProGlyLeuGlnLysIleTyrGluIleAspProLeuLeuThr 140
693  AGGGCATCCCTCCACCTGGAGCTTGTGAGAAGATTATGAATAGACCCCTTTTGACA 752
141  AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
753  AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAAGAACTGAGGGGCAAT 812
161  AspLysTyrGluGlyGlyLeuGluAlaPheSerArgTyrGlyLysMetGlyPheThr 180
813  GACAAATATGAGGGTGGTGGAGCTTTTCTCGTGGTTATCAAAAATGGGTTTCACT 872
181  ArgSerAlaThrGlyIleThrTyrArgGluTyrAlaLeuGluValAlaGlnSerAlaLeu 200
873  CGTAGTGTACAGGTATCACCTACCGTGGTGGCTTCTGGTGGCCAGTACAGTCCCTTC 932
201  IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
933  GTCTGGGAGATTTTCTGCCAAATATGTGGATGTTCTCTGCAATTTCTCATGGTCC 1052
241  ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
1053  AGAGTGAAGATACGTATCGACACTCCATCAGTGGTGAAGATTCAATCTCTGCTGGATC 1112
261  AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
1113  AACTACTCTTTACAGCTTCTCTGATGAAATTCATATATGAATATATATATGATCACC 1172
281  GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
1173  GAAGAGGAGAGGTATATCTTCAACACACCGCCGCAAAACCAACCAACCTCGCTGAGA 1232
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321  ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
1293  AGAGATGAAGTCTTCTCTCGCATAAAAAGCTTGGTACATATGCGGTGCAATTTATGCT 1352
341  IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
1353  ATTCAAGAGCATCTTATTTATGCTAGTTTGGTTATGCTATGCTACAAAATTTTNGCAC 1412
361  SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380

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see result 3

res 1

late

late

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Db 1593 TGGATGCGGATTCGCGCTCTTTAACTATGGAACCTGGGAGGTACTTAGTACTCTTC 1652
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RESULT 8
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DEFINITION      Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE
A-4.
ACCESSION      AJ011888
VERSION      AJ011888.1 GI:4584508
KEYWORDS      SBEII gene; starch branching enzyme II.
SOURCE      Solanum tuberosum.
ORGANISM      Solanum tuberosum.
REFERENCE      1 (bases 1 to 2982)
AUTHORS      Jobling,S.A., Schwall,G.P., Westcott,R.J., Sidebottom,C.M.,
Debet,M., Gidley,M.J., Jeffcoat,R. and Safford,R.
TITLE      A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 2982)
Jobling,S.A.
TITLE      Direct Submission
JOURNAL      Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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BASE COUNT 888 a 529 c 703 g 862 t
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Best Local Similarity: 96.52% Mismatches: 17
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Db: 8 Gaps: 1

US-10-056-454A-15_COPY_49_882 (1-834) x STU011888 (1-2982)

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Qy	21	LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr	40
Db	344	CTTGTGCTGGAATCCAGAGTGATAGTCCATCCATCCATCAACAGATCAATTTAGTTCGCT	403
Qy	41	GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis	60
Db	404	GAGACATCTCCAGAAAATTCGCCAGCATCAACTGATGTAGATAGTTCAACAATGGAACAC	463
Qy	61	AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer	80
Db	464	GCTAGCCAGATTAAACTGAGACGATGACGTTGAGCCGTCAAGTGATCTTACAGGAAGT	523
Qy	81	ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyLysLeuGluGlu	100
Db	524	GTTCAAGAGCTGGATTTTGCTTCATCACTACAACTACAAGAAGTGGTAAACTGGAGGAG	583
Qy	101	SerLysThrLeuAsnThrSerGluGluThrIleleAspGluSerAspArgIleArgGlu	120
Db	584	TCTAAAACATTAATACTCTGAAGAGACAAATTAITGATGAATCTGTAGATCAGAGAG	643
Qy	121	ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr	140
Db	644	AGGGGATCCCTCCACCTGGACTTGGTCAGAGATTTATGAATAGACCCCTTTTGACA	703
Qy	141	AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle	160
Db	704	AACTATCGTCAACACCTTGATTACAGGTATTACAGTACAAGAACTCAGGAGGCAATT	763
Qy	161	AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr	180
Db	764	GACAAGTATGAGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAGAATGGGTTTCACI	823
Qy	181	ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu	200
Db	824	CGTAGTGCTACAGTATCACTTACCGTGAGTGGCTCTCTGGTGGCCAGTCAGCTGCCCTC	883
Qy	201	IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly	220
Db	884	ATTGGGATTTCAACAATTTGGAGCGCAATTCIGACTTTATGACTCGGAATGAATTGGT	943
Qy	221	ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer	240
Db	944	GTCTGGGAGATTTTCTGCCAAATAATGTGGATGGTTCTCTCGCAATTCCTCATGGGTCC	1003

Qy	241	ArgValLysIleLeuArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle	260
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Qy	261	AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro	280
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Qy	281	GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle	300
Db	1124	GAGAGGAGAGGTATATCTTCCACACCCACGCCCAAGAAACAAAGTCGGTGGAATA	1183
Qy	301	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320
Db	1184	TATGAATCTCATATTGGAATGAGTAGTCGGAGCCTAAATTAACATCATACGTGAATTTT	1243
Qy	321	ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleAla	340
Db	1244	AGAGATGAAGTTCTTCTCGCATAAAAGCTTGGGTACAAATCGCGTGCAAAATTAGGCT	1303
Qy	341	IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro	360
Db	1304	ATTCAAGAGCATTTCTTATATGCTAGTTTGGTTATCATGTGCACAAATTTTTCACCA	1363
Qy	361	SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu	380
Db	1364	AGCAGCCGTTTTGGAAACCCCGACGACCTTAACTGTTGATTGATAAAGCTCATGAGTA	1423
Qy	381	GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly	400
Db	1424	GGAATGTTGTTCTCATGTGACATGTTTACAGCCATGCAATCAAAATAACTTTAGATGA	1483
Qy	401	LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis	420
Db	1484	CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCCTCTCGAGCTCGTGGTTATCAT	1543
Qy	421	TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu	440
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Qy	441	SerAsnAlaArgTyrTrpIleuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal	460
Db	1604	TCAATGGAGATGTTGGTGGATGAGTTCAAATTTGATGATTTAGATTTGATGGTGTG	1663
Qy	461	ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu	480
Db	1664	ACATCAATGATGTGTACTCACACCGATTATCGGTGGGATTCACATGGAACCTACGAGAA	1723
Qy	481	TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu	500
Db	1724	TACTTTGACGTCGCAACTGATGGATGCTGTGTGTATCTGTATCTGCTCAACGATCTT	1783
Qy	501	IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr	520
Db	1784	ATTCAATGGCTTTTCCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACA	1843
Qy	521	PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetalIle	540
Db	1844	TTTTGTGTTCCGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGCAATT	1903
Qy	541	AlaAspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIle	560
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Qy	561	ValHisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGlnSerHis	580
Db	1964	GTTTCATACACTGACAAATAGAGATGGTCGGAAGAGTGTGTTTCATACCCCTGAAGTCA	2023
Qy	581	AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr	600
Db	2024	GATCAAGCTCTAGTCGGTGATAAACTATAGCATTCCTGGCTGATGGAGCAAGGATATGAT	2083
Qy	601	AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis	620

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Qy
Db 241 ArgValLysLeuArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
Db 801 AGAGTGAAGATACGTATGGACACCTCCATCAGTGTTAAGGATTCCTCCTGGATC 860
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Db 1881 GATTTATGGCTCTGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATTCAC 1940
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DEFINITION Sequence 12 from Patent WO9634968.
ACCESSION A58162
VERSION A58162.1 GI:3713887
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE unclassified.
1 (bases 1 to 3003)
AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
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TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
JOURNAL Patent: WO 9634968-A 12 07-NOV-1996;
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FEATURES Location/Qualifiers
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/db_xref="taxon:32644"
BASE COUNT 895 a 535 c 706 g 867 t
ORIGIN

Alignment Scores:

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Best Local Similarity:	96.29%	Mismatches:	18
Query Match:	95.61%	Indels:	5
DB:	6	Gaps:	1

US-10-056-454A-15_COPY_49_882 (1-834) x A58162 (1-3003)

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QY	41	GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis	60
Db	407	GAGACATCTCCAGAAATTCGCCAGCATCAACTCATGTAGATAGTTCAACAATGSAACAC	466
QY	61	AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer	80
Db	467	GCATGCCAGATATAAAGCTGAGACGATGACGTTGAGCCGTCACAGTATCTTACAGGAAGT	526
QY	81	ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGluGlyGlyLysLeuGluGlu	100
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QY	141	AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle	160
Db	707	AACTATCGTCAACACCTTGATTAACAGCTATTACAGTACAAGAAACTCAGGAGGCAATT	766
QY	161	AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr	180
Db	767	GACAGATGAGGGTGGTTTGGAGCTTTTCTCGTGGTATGAAGAATGGGTTTCACT	826
QY	181	ArgSerAlaThrGlyIleThrTyrArgGluTyrAlaLeuGlyAlaGlnSerAlaAlaLeu	200
Db	827	CGTAGTGCTACAGGTATCACTTACCGTGAGTGGGCTCTGGTGCCAGTCAGCTGCCCTC	886
QY	201	IleGlyAspPheAsnAsnThrAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly	220
Db	887	ATTGGGGATTCAACAAATGGGAGCAATGCTGACTTTATGACTCGGAATGAATTTGGT	946
QY	221	ValTyrGlnIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer	240
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QY	241	ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTyrIle	260
Db	1007	AGAGTCAAGATACGTATGGACATCCATCAGGTGTTAAGGATTCCTTCCTGCTGGATC	1066
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Db	1067	AACTACTCTTTACAGCTCTCTGATGAATTCATATATGAATGATATATATGATCCACCC	1126
QY	281	GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle	300
Db	1127	GAAGAGGAGAGGTATATCTTCCACACCCACGGCCAAAGAACCAAACTCGGTGAGAATA	1186
QY	301	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320

1187	DB	TATGAATCTCA	TA	TTGGAA	TGAGTAGTCCGGAGCGCTAAAAATTAACTCATACGTTGAATTTT	1244
321	QY	ArgAspGluVal	LeuPro	ArgIle	-LysLysLeuGlyTyrAsnAlaLeuGlnIleMetal	340
1247	DB	AGAGATGAAGTTCTCTCTCGCATAAAAAAGCTGGGTACAATCGCGTGC	CAAAATTA	TATGCG	CAAAATTA	1306
340	QY	alleGlnGluHis	SerTyr	IleAlaSer	PheGlyTyrHisValThrAsnPheAla	350
1307	DB	TATTCAAGACGATCTCTTATTATGCTAGTTTGGTTTATCATGTCACAAATTTT	TTTTCGACC			1366
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1367	DB	AAGCAGCGCTTTGGAA	CGCCGACGACCTTA	AGTCTTTGATGATTA	AAAGCTCATGAGCT	1426
380	QY	uGlyIleValVal	LeuMetAsp	IleValHisSerHisAlaSer	AsnAsnThrLeuAsp	400
1427	DB	AGGAATTTGTTCTCTCATGACATTTGTTACAGCCATGATCAAAATAAT	TA	CTTTAGCT	TTAGATGG	1486
400	QY	YLeuAsnMetPhe	AspCysThrAspSerCysTyrPheHisSer	GlyValaArgGlyTyrHi		420
1487	DB	ACTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCATCTGGAGCTCGTGGT	ATCA			1546
420	QY	sTrpMetTrpAsp	SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLe			440
1547	DB	TTGGATCTGGGATTTCCGCCTCTTTAACTATGAAACCTGGGAGGTACTTAGGTATCTTCT				1606
440	QY	uSerAsnAlaArgTrpTrpLeu	aspAlaPheLysPheAspGlyPheArgPheAspGlyVa			460
1507	DB	CTCAAAATGCCAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTT	CGGTGT			1666
460	QY	lThrSerMetMetTyrIleHisGlyLeuSerValGlyPheThrGlyAsnTyrGluG				480
1667	DB	GACATCAATGATGTGTACTCACCACGGATTA	TCGGTGGGATTCAC	TGGGAACTAC	GAGGA	1726
480	QY	uTyrPheGlyLeuAlaThrAspVal	aspAlaValValTyrLeuMetLeuValAsnAspLe			500
1727	DB	ATACTTTGGACTCGCAACTGATGGGATGCTGTGTGTA	CTGATCTGATGCTGGTCAACGATCT			1786
500	QY	uIleHisGlyLeuPheProAspAlaIleThrIleGlyGluaspValSerGlyMetProth				520
1787	DB	TATTCANGGGCTTTTCCCATGCAATACCATTTGGGAAGAGTTGAGCGGAATGCCGAC				1846
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540	QY	eAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspI				560
1907	DB	TGCTGTATAAAGGATTGAGTTGCTCAAGAACCGGATGAGGATTTGGAGAGTGGGTGATAT				1966
560	QY	eValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHi				580
1967	DB	TGTTTCATACACTGACAAATAGAAGATGGTCCGAAAAAGTGTGTTTTCATACGCTGAAAGTCA				2026
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2027	DB	TGATCAAGCTCTAGTCGGTGATAAAATACTAFAGATTTCTGGCTGATGCACAGGATATGTA				2086
600	QY	rAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHi				620
2087	DB	TGATTTATGGCTCTGGATAGACCGTCAACATCATTTAATAGATCTGGGATGACATTACA				2146
620	QY	sLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetal				640
2147	DB	CAAGATGATTAGGCTTTGTA	CTACTAGGATTTAGGAGGAGAGGGTACCTAAATTTTCATGG			2206
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2207	DB	AAATGAATTCGGCCACCCCTGAGTGAGTTGATTTCCCTAGGCTGACACACACTCTCTG				2266
660	QY	pGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLe				680
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ACCESSION AJ011885
VERSION AJ011885.1 GI:4584502
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
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1 (bases 1 to 2955)
Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M., Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum tuberosum L.) tubers has a major effect on starch structure; cloning and characterisation of multiple forms of SBE II unpublished
JOURNAL 2 (bases 1 to 2955)
AUTHORS Direct Submission
TITLE Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
JOURNAL Location/Qualifiers
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Best Local Similarity: 95.55% Mismatches: 22
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AUTHORS Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher M. and Westcott,R.J.
TITLE IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
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ACCESSION AB071286
VERSION AB071286.1 GI:15553090
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Convolvulaceae; Ipomoea.
1
Kimura,T. and Saito,A.
Ipomoea batatas mRNA for starch branching enzyme II
Unpublished
2 (bases 1 to 3123)
REFERENCE
1 Kimura,T. and Saito,A.
Direct Submission
Submitted (08-SEP-2001) Takashi Kimura, National Agricultural
Research Center for Kyushu Okinawa Region; 2421 Suya, Nishigoshi,
Kumamoto 861-1192, Japan (E-mail:tkimura@affrc.go.jp,
Tel:81-96-242-1150)
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Job time : 5762 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 00:16:41; Search time 469 Seconds
(without alignments)
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Title: US-10-056-454A-15_COPY_49_882

Perfect score: 4465

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Ygapop 10.0, Ygapext 0.5
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4358.5	97.6	2578	17	AAT42631	Class A starch bra
3	4329	97.0	3074	18	AAT69587	Potato starch bra
4	4322	96.8	2576	17	AAT42636	Class A starch bra
5	4274	95.7	2563	23	ABK50301	Potato cDNA encodi
6	4269	95.6	3003	17	AAT42634	Class A starch bra
7	4268.5	95.6	3231	17	AAT42632	Class A starch bra
8	4229	94.7	2531	17	AAT17267	Class A starch bra
9	4218	94.5	2529	17	AAT42635	Class A starch bra
10	4155.5	93.1	2975	17	AAT42637	Class A starch bra
11	3363	75.3	3090	19	AAV38720	Full length cassav
12	3281.5	73.5	2913	19	AAV38719	Full length cassav
13	3269	73.2	2715	21	AAV5939	Arabidopsis thalia
14	3239	72.5	3015	19	AAV5939	Nucleotide sequenc
15	3136	70.2	2726	22	AAH78337	Rice type IV stanc
16	3096	69.3	2919	15	AAQ73750	Rice starch branch
17	3030.5	67.9	2640	19	ABK15494	Wheat starch bran
18	3026.5	67.8	2665	18	AAV70961	DNA encoding maize
19	3026	67.8	2968	22	AAH78342	Plasmid pBE240 ins
20	3021.5	67.7	2725	19	AAV29757	Nucleotide sequenc
21	2676.5	59.9	2087	18	AAV69737	Zea mays starch br
22	2669.5	59.8	2165	18	AAV69736	Corn starch branch
23	2628	58.9	2307	21	AAZ99938	Corn starch branch
24	2628	58.9	2307	21	AAZ99938	DNA encoding part
25	2221.5	49.8	1919	19	AAV38722	cDNA encoding star
26	2165	48.5	3128	16	AAT00774	Potato starch bran
27	2147	48.1	4563	22	AAAF30910	Wheat starch bran
28	2139.5	47.9	2733	15	AAQ62135	Rice starch branch
29	2130.5	47.7	2733	15	AAQ54674	Rice starch branch
30	2107	47.2	2565	18	AAV69752	Corn starch branch
31	2107	47.2	2763	18	AAV29758	Zea mays starch br
32	2104	47.1	2487	18	AAV69747	Corn starch branch
33	2104	47.1	2771	13	AAQ24257	Branching enzyme D
34	2104	47.1	2772	18	AAV69740	Plasmid pB65 inse
35	2100	47.0	2687	20	AAV34646	WSBE I-D4 cDNA seq
36	2098.5	47.0	2909	13	AAQ27778	Potato amylose-amy
37	2058	46.1	2899	22	AAH02926	Human shear stress
38	2058	46.1	2955	24	ABN95650	Gene #2148 used to
39	2052	46.0	3075	24	AAV94880	Human DNA sequence
40	2052	46.0	2713	19	AAV70962	DNA encoding maize
41	1914.5	42.9	3753	23	ABK50305	Red alga DNA encod
42	1899	42.5	2598	23	ABL07067	Drosophila melanog
43	1866	41.8	1452	21	AAV36957	Arabidopsis thalia
44	1828.5	41.0	4147	21	AAV83166	Glycogen branching
45	1805	40.4	6556	23	ABL07066	Drosophila melanog

ALIGNMENTS

RESULT 1

AAT42630

ID AAT42630 standard; DNA; 3033 BP.

XX AAT42630;

XX AAT42630;

DT 25-FEB-1997 (first entry)

XX Class A starch branching enzyme (19con.seq).

DE Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

KW amylose; viscosity; potato; ss.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FT CDS 145..2793

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RESULT 2
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ID AAT42631 standard; DNA; 2578 Bp.
XX
AC AAT42631;
XX
DT 25-FEB-1997 (first entry)
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DE Class A starch branching enzyme (psbe2con.seq - clone psJ90).
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
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FT /*tag= c
XX
PN WO9634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
DR WPI; 1996-506170/50.
DR P-PSDB; AAW06400.
XX
PT New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
FS Claim 32; Page 55-56; 142pp; English.
XX
CC Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
SQ Sequence 2578 Bp; 770 A; 462 C; 616 G; 730 T; 0 other;
XX
```

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Alignment Scores:
Pred. No.: 0 Length: 2578
Score: 4358.50 Matches: 817
Percent Similarity: 98.56% Conservative: 5
Best Local Similarity: 97.96% Mismatches: 11
Query Match: 97.61% Indels: 1
DB: 17 Gaps: 1
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US-10-056-454A-15_COPY_49_882 (1-834) x AAT42631 (1-2578)

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QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaSerGlyLysVal 20
Db 66 GAAAAGTCTTCTTACAAATCCGAATTCGACCTTCTACAGTTCGACGATCGGGGAAGTC 125
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThr 40
Db 126 CTTGTGCCTGGAAACCCAGAGTAGTGTCTCTCATCTCAACAAACCAATTTGATTCAC 185
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
Db 186 GAGACATCTCCAGAAATTTCCCGACGATCAACTGATGTAGATAGTTCAACAATGGGAAC 245
QY 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
Db 246 GCTAGCCAGATTAAACTGAGAACGATGACGTTGAGCCGTCAGTATCTTACAGGAAGT 305
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyLysLeuGluGlu 100
```

306 GTTGAAGAGCTGATTGTTGCTTCATCACTACAACACTACAAGAGGTGGTAACTGGAGGAG 365
101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
366 TCFAAACATTAATAACTCTGAAGAGACAATATTATGATGAATCTGATAGATCAGAGAG 425
121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
426 AGGGGATCCCTCCACCTGGACTTGTCTCAGAGATTTATGAATAGACCCCTTTTGACA 485
141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
486 AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACACAGAACTGAGGGAGGCAATT 545
161 AspLysTyrGluGlyGlyLeuAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
546 GACAAGTATGAGGTGGTGGAGCTTTTCGCGGTGTTATGAATAAAATGGGTTCACCT 605
181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaLeu 200
606 CGTAGTGCTACAGTATCACTTACCGTACGTGGCTCCTGGTGCCTCAGCTGCCTC 665
201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
666 ATTGGAGATTCAACAATTGGAGCGCAATGCTGACATTTATGACTCGGAATGGAATTGGT 725
221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
726 GTCTGGGAGATTTTCTGCCAATAATGTGGATGTTCTCTCGAATTCCTCATGGTCC 785
241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
786 AGAGTGAAGATACGTATGGACACTCCATCAGGTGTTAAGGATTCATTCCTGCTGGATC 845
261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisLysAspProPro 280
846 AACTACTCTTCACAGCTCTCTGATGAATAATCCATATATGGAATATATATATGATCCACC 905
281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
906 GAAGAGGAGAGGTATATCTTCCACACCCACGGCCAAAGAACCAAGTCGCTGAGAATA 965
301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
966 TATGAATCTCATATTTGAATGAGTAGTCCGGAGCCTAAATTAATCTCATAGTGAATTT 1025
321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
1026 AGATGAAGTCTTCTCTCGATATAAAGCTTGGTACAAATGGGTGCAAAATATGAGCT 1085
341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
1086 ATTCAGAGCATCTTATATATGCTAGTTTGGTTATCATGTCACAAATTTTTCACACCA 1145
361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
1146 AGCAGCGCTTTTGAAGCGCCGAGACCTTAAGTCTTTGATGATATAAGCTCATGAGCTA 1205
381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
1206 GGAATTTGTTCTCATGGACATTTTCACAGCCATGATCAATAATATACITTAGATGGA 1265
401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
1266 CTGAACATGTTTGACGGCACCGATAGTTGTTACTTTCACCTCTGGAGCTCGTGGTTATCAT 1325
421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
1326 TGGATGTGGGATTCGCGCTTTTAACTATGCAAACTCGGAGTACTTAGGTATCTTCTC 1385
441 SerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
1386 TCRAATGGAGATGTGGTTGGATGAGTTCAAATTTGATGATTTAGATTTGATGGTGTG 1445

461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
1446 ACATCAATGATGATATCACTCACCGGATTATCGTGGGATTCACTGGGAACCTACAGGAA 1505
481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
1506 TACTTTGGACTCGCACTGATGTGGATGCTGTTGTATCTATCTGATGCTGGTCAACGATCTT 1565
501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
1566 ATTATGGGCTTTTCCAGATGCAATTTACCATGCTGAGATGTTAGCGGAATCCCGACA 1625
521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
1626 TTTTGTATCCCGTTCAAGATGGGTGTTGGCTTTGACTATCGCTGCATATGGCAATT 1685
541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
1686 GCTGATAAATGGATGTAGTTGCTCAAGAAACGGGATGAGGATTGGAGTGGGTGATATT 1745
561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
1746 GTTCATACACTGACAAATAGAGATGGTCGGAAGGTGTGTTTCATACGCTGAAAGTCAT 1805
581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
1806 GATCAAGCTCAGTGGTGTATAAATATAGCATTTCTGGCTGATGGACAGGATATGAT 1865
601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
1866 GATTTTANGGCTCTGGATAGACCGCAACATCATTAATAGATCTGGGATGACATGTCAC 1925
621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly 640
1926 AAGATGATTAGGCTTGTAACTATGGGATTAGGAGAGAGAGGTACCTAAATTTGATGGGA 1985
641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
1986 AATGAATTCGGCCACCTCGAGTGGATTGATTCCTTGGGCTGGAACACACCTCTCTCAT 2045
661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
2046 GACTCAGTAATTCCTGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2105
681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
2106 GGAGATGCAGAAATATTTAAGATACCTCGGTGCAAGAAATTTGACCGGCTATGCAATAT 2165
701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
2166 CTTGAAGATAAATATGACTTTATGACTTACCAACACCACTTCATATCAGAAAGATGAA 2225
721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
2226 GGAGATAGATGATTTGTTATTTGAAAAGAAACCTAGTTTGTCTTAAATTTTCACCTGG 2285
741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
2286 ACARAAAGCTATTCAGACTATCGCATAGCTGCTTCAAGCTGCAAGCTGCAAGCTTGC 2345
761 LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
2346 TTGGACTCAGATGATCCACTTTTGGTGGCTCGGGAATTTGATCAATAATGCCAAATAT 2405
781 PheThrPheGluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
2406 TTCACCTTTGAAGGATGGTATGATGATCGTCTCGTCAATATATGCTATGTCACCTTGT 2465
801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
2466 AGAACAGCAGTGTGCTATGCACTAGTAGACAAA---GAAGAAGAAGAAGAAGAAGAA 2522

Qy	821	GluGluValAlaAlaValGluValValGluGluGlu	834
Db	2523	GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGAAGAAGAA	2564

RESULT 3

AAT69587
 ID AAT69587 standard; cDNA; 3074 BP.

AC AAT69587;

DT 26-AUG-1997 (first entry)

DE Potato starch branching enzyme II gene (beII).

Starch branching enzyme II; bell gene; potato; transgenic plant;
 amylopectin; amylose; starch; ss.

OS *Solanum tuberosum*.

Key	Location/Qualifiers
FH	189..2825
FT	
CDS	

PN WO9720040-A1.

05-JUN-1997.

28-NOV-1996; 96WO-SE01558.

PR 19-APR-1996; 96SE-0001506.

PR 29-NOV-1995; 95SE-0004272.

PA (EKBB/) EK B.

PA (KHOS/) KHOSNOODI J.

PA (LARS/) LARSSON C.

PA (LARS/) LARSSON H.

PA (RASK/) RASK L.

PA (AMYL-) AMYLOGENE HB.

Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;

DR WPI; 1997-310596/28.

DR P-PSDB; AAW19113.

Isolated potato starch branching enzyme II - useful for altering degree of amylopectin branching and amylopectin/amylose ratio in potato starch

PS Claim 4; Page 12-15; 24pp; English.

A cDNA clone (AA169587) codes for potato starch branching enzyme II (BEII) (AA19113). It was isolated from potato tuber cDNA by PCR amplification using primers (AA169588-89) based on tryptic peptides of isolated BEII; the 5' and 3' ends of the sequence were determined by RACE. A vector comprising the whole or a functional active part of the isolated sequence (sense or antisense), plus regulatory sequences active in potato, can be used to produce transgenic potatoes. The starch obtained from such plants will show a changed pattern of amylopectin branching and an altered amylopectin/amylose ratio.

Sequence 3074 BP; 902 A; 560 C; 710 G; 896 T; 6 other; 5Q

Alignment Scores:

Alignment scores:				
Pred. No.:	0	Length:	3074	
Score:	4329.00	Matches:	814	
Percent Similarity:	98.08%	Conservative:	4	
Best Local Similarity:	97.60%	Mismatches:	12	
Query Match:	96.95%	Indels:	4	

DB: 18 Gaps: 1

US-10-056-454A-15_COPY_49_882 (1-834) x AAT69587 (1-3074)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
 |||||
 DB 333 GAAAGAGCTCTTACAATCCGAATCCGACCTTCTACAGTTGCAGCATCGGGAAAGTC 392
 |||||
 QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThr 40
 |||||
 DB 393 CTGTGGCTGGAAACCCAGAGTAGCTCTCATCTCAACAGACCAATTTAGATTCACT 452
 |||||
 QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
 |||||
 DB 453 GAGACATCTCCAGAAAATCCCGACGATCAACTGATGATAGATTCAACAATGGAACAC 512
 |||||
 QY 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerLeuThrGlySer 80
 |||||
 DB 513 GCTAGCCAGAGATTAAACTGAGAAGATGACGTTGAGCCGTCAAGTAGCTATCAGGAAGT 572
 |||||
 QY 81 ValGluGluLeuAspPheAlaSerSerSerLeuGlnLeuGlnGlyLysLeuGluGlu 100
 |||||
 DB 573 GTTGAACAGCTGGATTTGCTTCATCACTACAACACTACAAGAAGTGTAACATGAGGAG 632
 |||||
 QY 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
 |||||
 DB 633 TCTAAAACATTAAATACTTCTGAAGACACAATTTATTGATGAATCTGATAGGATCAGAG 692
 |||||
 QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
 |||||
 DB 693 AGGGCAATCCCTCCACCTGGACTTGGTTCAGAAGATTATGAATAGACCCCTTTTGACA 752
 |||||
 QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGlnAlaIle 160
 |||||
 DB 753 AACTATGCTCAACACCTTGATTACAGGTATTACAGTACAGAAGAACTGAGGAGGCAATT 812
 |||||
 QY 161 AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
 |||||
 DB 813 GACAAGTATCAGGGTGGTTTGGAAAGCTTTTTCGTGGTTATGAAAAAATGGGTTTCACT 872
 |||||
 QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
 |||||
 DB 873 CGTAGTGTACAGGTATCACTTACCGTGAAGTGGGCTCCCTGGTCCCAAGTCAGTGCCTC 932
 |||||
 QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
 |||||
 DB 933 ATTGGAGATTCAACAATTTGGGACGCAATGCTGCACATTATGACTCCGAATCAATTTGGT 992
 |||||
 QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
 |||||
 DB 993 GTCTGGGAGATTTTCTGCCAAATAATGTGGATGGTTCTCTCGCAATTCCTCATGGTCC 1052
 |||||
 QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
 |||||
 DB 1053 AGAGTGAAGATACGTATGACACTCCATCAGGTGTTAAGGATTCATTCTCTGCTTGGATC 1112
 |||||
 QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
 |||||
 DB 1113 AACTACTCTTACAGCTTCTCTGATGAAATCCATATATGGAATATATATTGATGCCACC 1172
 |||||
 QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
 |||||
 DB 1173 GAAGAGGAGAGGTATATCTTCCAACACCCACGCCCAAGAAACAACTCGCTGGAATA 1232
 |||||
 QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
 |||||
 DB 1233 TATGAATCTCATATTGGAATGAGTAGTCCGGAGCCATAAAATAACTCATCATCGTGAATTTT 1292
 |||||
 QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
 |||||
 DB 1293 AGAGATGAAGTTCCTTCCTCGCATAAAAGCTTGGGTCAATGCGGTGCAATTTATGGCT 1352
 |||||
 QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAspPhePheAlaPro 360
 |||||

Db 1353 ATTCAAGAGCAATCTTATTATGCTAGTTTGGTTATCATGCTCAAAATTTTTTGGCACCA 1412
QY
Db 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuLeuLeuLeuLeuLeuLeuLeu 380
Db 1413 AGCAGCGGTTTGGAAACNCCGACGACCTTAAGTCTTTGATGATGAATGAAGCTCATGAGCTA 1472
QY
Db 381 GlyTLeuValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db 1473 GGAATTTGTTCTCATGGACATGTTTCACAGCATGTCATCAAAATAAATCTTTAGATGGA 1532
QY
Db 401 LeuAsnMetPheAspCysThrAspSerCysThrPheHisSerGlyAlaArgGlyTyrHis 420
Db 1533 CTGAACATGTTTGAAGGCACAGATAGTTGTTTACTTTCACCTCTGGAGCTCGTGGTTATCAT 1592
QY
Db 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuLeuArgTyrLeuLeu 440
Db 1593 TGGATGFGGGAATCCCGCCCTCTTAATATGGAACCTGGAGGTACTTAGGTATPCTTCTC 1652
QY
Db 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db 1653 TCAAAATCGAGATGGTGGTGGATGAGTTCAAATTTGATGGATTAGATTGAGGGTGTG 1712
QY
Db 461 ThrSerMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db 1713 ACATCAATGATGATATCTACCCACGGAATATCGGTGGGATTCACCTGGGAACCTACGAGAA 1772
QY
Db 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
Db 1773 TACTTTGGACTCGCAACTGATGGATGCTGTGTGTCATCTGATCGCTGGTCAACGATCTT 1832
QY
Db 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db 1833 ATTCATGGGCTTTCCAGATGCAATTAACCATGSGTGAAGATGTTAGCGGAATCCGACA 1892
QY
Db 521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 1893 TTTTNTATCCCGTCAAGATGGGGGTGTGGCTTTGACTATCGCTGCATATGGCAATT 1952
QY
Db 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db 1953 GCTGATAAATGGATGTAGTGTCTCAAGAAACGGGATGAGGATGGAGATGGGGTGATATT 2012
QY
Db 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db 2013 GTTCATACACGACAAATAGAGATGCTCGAAAGTGTGTTTCATACGCTGAAAGTCAT 2072
QY
Db 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
Db 2073 GATCAAGCTCTAGTCGGTGATAAACTATAGCATTTCTGGCTGATGGACAAGGATATGTAT 2132
QY
Db 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 2133 GATTTTATGGCTCTGGATAGACCCNTCAACATCATTAATAGATCGTGGATAGCATGGAC 2192
QY
Db 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyTyrLeuAsnPheMetGly 640
Db 2193 AAGATGATTAGGCTTGTAACTATGGGATAGGAGGAAGGGTACCTAAATTTTCATGGGA 2252
QY
Db 641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 2253 AATGAATCGGCCACCCCTGAGTGGATGATTTCCTAGGGGTGAACACACCTCTCTCAT 2312
QY
Db 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
Db 2313 GGCTCAGTAATTCGCGGNAACCAATTCAGTTATGNTAATCGACACGGAGATTTGACCTG 2372
QY
Db 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db 2373 GCAGATGCAGAAATATTAAGATACCGTGGGTGCAAGAAATTTGACCGGGCTATGCAGTAT 2432
QY
Db 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
|||||

Db 2433 CTTGAAGATAAATATGATGATTATGACTTCAGAACACCCAGTTCAATACCGAAAGATGAA 2492
QY
Db 721 GlyAspArgMetIleValPheGlyGlyAsnLeuValPheValPheAsnPheHisTrp 740
Db 2493 GGAGATAGGATGATTGTTTGAAGAAGAAACCTAGTTTGTCTTAAATTTTCACTGG 2552
QY
Db 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2553 ACAAAAAGCTATTTCAGACTATCGCATAGGCTGCTGAAGCTGGAAATACAAAGTTGCC 2612
QY
Db 761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2613 TTGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATATGCGCAATAT 2672
QY
Db 781 PheThrPheGluGlyTyrTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2673 TTCACCTTTGAGAGATGGTATCATGATCGTCTCGTTCAATATATGGTGTATGACCTAGT 2732
QY
Db 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
Db 2733 AGAACAGCAGTGGTCTATGCTACTAGTACACAAA-----GAAGAAGAAGAGAA 2780
QY
Db 821 GluGluValAlaAlaValGluGluValValGluGluGlu 834
Db 2781 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAGAA 2822
RESULT 4
AAT42636
ID AAT42636 standard; DNA; 2576 BP.
XX
AC AAT42636;
XX
DT 03-MAR-1997 (first entry)
XX
DE Class A starch branching enzyme (86con.seq) cloned in QE32.
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
PN WO9634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
XX
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX
XX New potato plant starch having high amylose content - also class A
XX starch branching enzyme and corresp. DNA to alter the viscosity of
XX starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 49-51; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
XX potatoes. In class A SBE mols., a flexible N-terminal domain,
XX is found, which is not found in class B mols.
XX
XX Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 0 Length: 2576
Score: 4322.00 Matches: 816
Percent Similarity: 98.44% Conservative: 5

QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
|||||
Db 2164 CTTGAGATAAATATGAGTTTATGACTTCAGAACACCACTTCATATCACGAAAGGATGA 2223
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
|||||
Db 2224 GGAGATAGGATGATTCTATTGAAAAGGAACCTAGTTTCTCTTTAAITTTCACTGG 2283
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
|||||
Db 2284 ACAAAAAGGTATTCAGACTATCGCATAGGCTGAAGCTGGAAGAAATACAAGTTGCC 2343
QY 761 LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
|||||
Db 2344 TTGGACTCAGATCCACTTTTGGCTTCGGGAGAAATTCATCATATATGCCGAATAT 2403
QY 781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
|||||
Db 2404 TTCACCTTTGAAGATGGTATGATGATCGTCTCGTTCAATTATGTTGATGACCTTGT 2463
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGlu 820
|||||
Db 2464 AGAACAGCAGTGTCTATGCTACCTAGTAGACAAA--GAAGAAGAAGAAGAAGAA 2520
QY 821 GluGluValAlaAlaValGluGluValValValValGluGluGlu 834
|||||
Db 2521 GAAGAAGTAGCAGTAGTAGAAGAAGTAGTAGTAGAAGAAGAA 2562

RESULT 5

ABK50301
ID ABK50301 standard; cDNA; 2563 BP.

AC ABK50301;

DT 15-JUL-2002 (first entry)

XX Potato cDNA encoding starch branching enzyme, SBE II.

XX
KW Potato; starch branching enzyme; SBE II; glucan branching enzyme;
KW GBE; ss; gene; plant; transgenic; antisense; food industry;
KW paper industry; chemical industry.

XX Solanum tuberosum.

XX Key Location/Qualifiers

FT CDS 3..2552

FT /*tag= a

FT /product= "SBE II"

FT /partial

FT /note= "No start codon shown"

XX GB2360521-A.

XX 26-SEP-2001.

XX 20-MAR-2000; 2000GB-0006733.

XX 20-MAR-2000; 2000GB-0006733.

XX (DANIT-) DANISCO AS.

XX Poulsen P, Sorensen IS;

XX WPI; 2001-650142/75.

XX P-PSDB; AAU80169.

XX New transformed plants with reduced endogenous starch branching enzyme
PT and heterologous glucan branching enzyme activities, useful for
PT producing starch with improved properties, which is in the food, paper
PT and chemical industries -
XX Example 1; Page 31-35; 61pp; English.

XX

CC The invention relates to a transformed organism, preferably a transformed
CC plant, having a reduced endogenous starch branching enzyme (SBE)
CC activity, and having a heterologous glucan branching enzyme (GBE)
CC activity. The reduced SBE activity is effected via expression of a
CC nucleotide sequence that is antisense to at least part of a SBE exon.
CC Also included are a method of producing starch with altered
CC characteristics comprising (a) providing a plant having reduced
CC endogenous SBE activity, and having heterologous GBE activity
CC from the plant; starch obtainable from the transformed plant; and
CC a nucleic acid construct system capable of directing the expression
CC of all or part of one or more antisense SBE exons and optionally one or
CC more heterologous GBE. The transformed plants are useful for producing
CC starch with modified and improved properties, which is an important raw
CC material and used in the food, paper and chemical industries. The
CC present sequence encodes Potato SBE II, used to make transgenic plants of
CC the invention.

XX Sequence 2563 BP; 749 A; 462 C; 614 G; 738 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 2563
Score: 4274.00 Matches: 802
Percent Similarity: 97.58% Conservative: 6
Best Local Similarity: 96.86% Mismatches: 14
Query Match: 95.72% Indels: 6
DB: 23 Gaps: 1

US-10-056-454A-15_COPY_49_882 (1-834) x ABK50301 (1-2563)

QY 1 GluLysSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
|||||
Db 81 GAAAAGCTCTTCTTACAATTCGGAATCCGACCTTCTACAGTTGAGCATCGGGAAAGTC 140
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
|||||
Db 141 CTTGTGCTGGACCCAGAGTAGCTCTCTCATCTCCACAGACCACTTTCAGTTGACT 200
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
|||||
Db 201 GAGACATCTCCAGAAATTTCCCAAGCATCACTGATGATAGATACTTCAACAATGGAACAC 260
QY 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerSerLeuThrGlySer 80
|||||
Db 261 GCTAGCCAGATTAATAACTGAGACGATGACCTTTCAGCGCTCAGTGTCTTACAGGAAGT 320
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGluGlu 100
|||||
Db 321 GTTGAAGAGCTGGATTTCCTTCATCACTACACTACAGAAAGTGGTAAACTGGAGAG 380
QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
|||||
Db 381 TCTAAACATTAATAACTTTTGAAGAGACAAATTTATGATGAATCTGATAGGATCAGAGAG 440
QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuThr 140
|||||
Db 441 AGGGGCATCCCTCCACCTCGGACTTGGTCAGAAAGATTATGAAATAGACCCCTTTGACA 500
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
|||||
Db 501 AACTATCGTCAACACCTTGATTACAGTATTCACAGTACAGAAACTGAGGAGGCAATT 560
QY 161 AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
|||||
Db 561 GACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAATGGGTTTCACT 620
QY 181 ArgSerAlaThrGlyIleThrTyrArgGluThrPalaLeuGluAlaGlnSerAlaAlaLeu 200
|||||
Db 621 CGTAGTGTACAGGTATCATTACCTGAGTGGGCTCTCTGGTGGCCAGTCAAGCTGCCCTC 680
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
|||||
Db 681 ATTGAGATTTCAACAATTGGACGCAATGCTGACATTTATGACTCGGAATGAATTTGGT 740

QY 221 ValTyrGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
DB 741 GTCTGGGAGATTTTCGCCAAATATGTGATGGTTCTCTCGCAATTCCTCATGGGTCC 800
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTyrIle 260
DB 801 AGAGTGAAGATACGTATGGACACTCCATCAGGTTTAAGGATTCATCTCTGCTGGATC 860
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspPro 280
DB 861 AACTACCTCTTACAGCTTCCTGATGAATTCATATATGGATATATATGATCCACCC 920
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
DB 921 GAAGAGGAGAGGTATATCTTCCACACCCCGCAAGCAAAAGTTCGCTGAGAATA 980
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
DB 981 TATGAATCTCATATTTGAATAGTAGTCCGGAACCTAAATTAACATACGTGAATTT 1040
QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
DB 1041 AGAGTGAAGATTTCTCTCCATATAAAGCTTCGCTGATGCTGCAATTTATGGCT 1100
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
DB 1101 ATTCAGAGCATCTTATTATGCTAGTTTGGTTATCATGTCACAAATTTTTCACCA 1160
QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
DB 1161 AGCAGCGGTTTGGAACTCCGACGACCTTAAGCTTTGATTGATAAAGCTCATGAGCTA 1220
QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
DB 1221 GGAAATTTGTTCTCATGAGCATTTGTTACATTTCAAGCCATGCATCAATATATCTTTAGATGA 1280
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
DB 1281 CTGAACATGTTTGACGGCACAGATAGTTGTTACTTTCACTCTGGAGCTCGGTGTTATCAT 1340
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
DB 1341 TGGATGTGGATTCGCGCTCTTTAACTATGGAACCTGGAGGATCTAGGTATCTTC 1400
QY 441 SerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
DB 1401 TCAATGCCAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGTG 1460
QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
DB 1461 ACATCAATGATGTGTACTCACCGGATTTATCGGTGGATTCCTGGGAACTACGAGGAA 1520
QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
DB 1521 TACTTTGGACTCGCACTGATGCTGGATGCTGTTGTTGATCTGATGCTGCTCAACGATCTT 1580
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
DB 1581 ATTCATGGCTTTTCCAGATGCAATTCATTTGGTGAAGATTTAGATTTGATGGATGCGGACA 1640
QY 521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
DB 1641 TTTTGTATTCCTCCGTTCAAGATGGGTGTGGCTTTGACTATCGCTGCTGATGGCAAT 1700
QY 541 AlaAspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
DB 1701 GCTGATAATGATTTGAGTTGCTGCTCAAGAAACGGGATGAGGATTTGGAGATGAGTGNATTT 1760
QY 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
DB 1761 GTTCATACACTGACAAATAGAGATGGTGGGAAAAGTGTGTTTCATACGCTGAAAGTCAT 1820

QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
DB 1821 GATCAAGCTCTAGTCGGTGATAAACTATACATTCCTGGCTGATGGACAAGATATGAT 1880
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
DB 1881 GATTTTATGGCTCTGGATAGACCTCAACATCATTAATAGATCTGTTGGATAGCATTTGCAC 1940
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly 640
DB 1941 AAGATGATTAGGCTTTGAACATATGGATTAGAGAGAGAGGATACCTTAATTTTCATGGGA 2000
QY 641 AsnGluPheGlyHisProGluTyrIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
DB 2001 AATCAATTCGCCACCCCGAGTGGATTTCCTAGGCTGAAACAACACTCTCTGAT 2060
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
DB 2061 GGCTCAGTAATTCGCCGAAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTG 2120
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyr 700
DB 2121 GGAGATCAGATTTATTAAGATACCGTGGTTGCAAGAAATTTGACCGGGCTATGCCAT 2180
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
DB 2181 CTGGAAGATAAATATGAGTTTATGACTTCAGAACACCATTCATATCATATCAGAAAGATGAA 2240
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
DB 2241 GGAGATAGGATGATTGTTTGAAGAAAGAAACCTAGTTTGTCTTTAATTTTCACTGG 2300
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
DB 2301 ACAAAGACTATTTCAGACTATCGCATAGGCTGCTGAAGCTGGAATAACAAGTTGCC 2360
QY 761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
DB 2361 TTGGACTCGGATATCCACTTTTGTGGTGGCTTTGGGAGAAATTCATCATATATGCCAATAC 2420
QY 781 PheThrPheGluGlyTyrTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
DB 2421 TTTACCTTTTCAGAGATGGATGATGATGATCGCTCGTTCAATATATGGTGTATGCCACCTAGT 2480
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
DB 2481 AGGACAGCAGTGGCTATGCATAGTAGACAAA-----GAAGCAGAA 2522
QY 821 GluGluValAlaAlaValGluGlu 828
DB 2523 GAAGAAGTAGCAGTAGTAGAGAA 2546
RESULT 6
AAT42634
ID AAT42634 standard; DNA; 3003 BP.
XX AAT42634;
AC AAT42634;
DT 03-MAR-1997 (first entry)
XX
XX Class A starch branching enzyme (10con.seq).
XX Starch branching enzyme; SBE; class A; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
XX Solanum tuberosum.
XX
XX WO9634968-A2.
XX
XX 07-NOV-1996.
XX
XX 03-MAY-1996; 96WO-GB01075.
XX

PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
DR
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 38-39; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE moles., a flexible N-terminal domain,
CC is found, which is not found in class B moles.
XX
XX Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 0 Length: 3003
Score: 4269.00 Matches: 804
Percent Similarity: 97.25% Conservative: 8
Best Local Similarity: 96.29% Mismatches: 18
Query Match: 95.61% Indels: 5
DB: 17 Gaps: 1

US-10-056-454a-15_COPY_49_882 (1-834) x AAT42634 (1-3003)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaLaserGlyLysVal 20
DB 287 GAAAGTCCTCTTACAAATCCGAATCCGACCTTACAAATTCAGATCGGGAAATC 346

QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
DB 347 CTTGTGCTGGAAATCCAGAGTGTAGTCTCTCATCTCATCAACAGATCAATTTGAGTTGCT 406

QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
DB 407 GAGACATCTCCAGAAATCCCGACGATCACTGATGATGATGATGATGATGATGATGATGAT 466

QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerSerSerSerThrGlySer 80
DB 467 GCTAGCCAGATTAACACTGAAACGATGACGTTGAGCGCTCAAGTGTATACAGGAAT 526

QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyLysLeuGluGlu 100
DB 527 GTTGAAGAGCTGGATTTGCTTCATCACTACAACCTACAAGAGGTGTAACACTGGAGGAG 586

QY 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
DB 587 TCFAAAACATTAATTAATCTGAGAGACAAATTAATGATGATGATGATGATGATGATGATGAT 646

QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGlnLeuLeuAspProLeuLeuThr 140
DB 647 AGGGGATCCCTCCACCTGGACCTGGTCAGAAAGATTAATGAAATAGACCCCTTTTGACA 706

QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
DB 707 AACTATGTCACACCTTGATTAAGTATTCAGTATTCAGTATTCAGTATTCAGTATTCAGTAT 766

QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
DB 767 GACAAGTATGAGGGTGGTTGGAAAGCTTTTCTCGTGTGTATGAAAGAAATGGGTTTCACT 826

QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
DB 827 CGTAGTCTACAGGTATCACTTACCGTGAGTGGGCTCCTGGTGCCAGTCAGCTGCCCTC 886

QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220

DB 887 ATTGGGATTTCAACAATTTGGGACGCAAAATGCTGACTTTTATGATCGGAATGATTTGGT 946

QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240

DB 947 GCTGAGAGATTTTCTGCCAAATAATGIGATGGTTCCTCTGCAATCTCAAGGTCC 1006

QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260

DB 1007 AGAGTGNAGATACGTATGGACATCCCATCAGGTGTTAAGGATTCATCTCTGCTGGATC 1066

QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280

DB 1067 AACTACTCTTTACAGCTTCTGATGAATTCATATAATGAATATATATGATGATCCACC 1126

QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysProLysSerLeuArgIle 300

DB 1127 GAAGAGGAGAGGTATATCTTCCACACCCAGCCCAAGAAACCAAGTCGGTGAGAATA 1186

QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320

DB 1187 TATGAATCTCATATTTGGAATGAGTAGTCCGGAGCTAAATTAACATCATACGTGAATTTT 1246

QY 321 ArgAspGluValLeuProArgIle-LysLysLeuGlyTyrAsnAlaLeuGlnIleMetAl 340

DB 1247 AGAGATGAAATCTTCTCTCGCATAAAAAGCTTGGGTACATCGGTGCAAAATATAGGC 1306

QY 340 aIleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPr 360

DB 1307 TATCAAGACATCTTATATGCTAGTTTGGTATCATGTCACAAATTTTGTGCACC 1366

QY 360 oSerSerArgPheGlyThrProAspAspLeuLysSerLeuLysAspLysAlaHisGluLe 380

DB 1367 AAGCAGCGGTTTGGAAACGCGGACGACCTTAAGTCTTTGATGATAAGCTCATAGCT 1426

QY 380 uGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnThrLeuAspGl 400

DB 1427 AGGAATTTGTTCTCATGGACATGTTTCACAGCCATGATCAATATATATCTTAGAGG 1486

QY 400 yLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHi 420

DB 1487 ACTGAACATGTTTGACGCGCACAGATAGTTGTTACTTTCTCTGAGCTCGGTATCA 1546

QY 420 sTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLe 440

DB 1547 TTGATGTGGGATTTCCGCCCTTTAACTATGAAACTGGGAGGTACTTAGTATCTTCT 1606

QY 440 uSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVa 460

DB 1607 CTCAAATGCGAGATGGTGGTGGATGAGTTCAAAATTTGATGGATTTAGATTTGATGGT 1666

QY 460 lThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGl 480

DB 1667 GACATCAATGATGTGCTACTACCACGGATTAATCGGTGGATTCATCTGGAACTACGAGGA 1726

QY 480 uTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLe 500

DB 1727 ATACTTTGGACTCCCACTGATGGAGTGTGTGTATCTGATCTGATGCTGGGTCACAGATCT 1786

QY 500 uIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProTh 520

DB 1787 TATTCATGGGCTTTTCCAGATGCAATTTACCATTGGTGAAGATGTTACGGAATCCGAC 1846

QY 520 rPheCysIleProValGlnGluGlyValGlyValGlyPheAspTyrArgLeuHisMetAlaI 540

DB 1847 ATTTTGTCTCCGCTCAAGATGGGGTGTGGCTTTGACTATCGGTGCTCATATGGCAAT 1906

QY 540 eAlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIl 560

DB 1907 TGTGATAAATTTGATTTGATTTGCTCAAGAAACGGGATGAGATTTGGAGAGTGGTATAT 1966

QY 560 eValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHi 580


```
Db 1967 TGTTCATACACTGACAAATAGAGATGGTCGGAAAAAGTGTCTTTCATACGCTGAAAGTCA 2026
Qy 580 sAspGlnAlaLeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTy 600
Db 2027 TGATCAAGCTCTAGTCGGTATGATAAATATAGCAATTCGCTGATGGACAAAGGATATGTA 2086
Qy 600 rAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHi 620
Db 2087 TGAATTTAAGCTCTGATAGACCGTCAACATCATTAATAGATCTGGGATAGCATATACA 2146
Qy 620 sLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetG1 640
Db 2147 CAAGATGATTAGGCTTGAACCTATGGGATAGGAGGAGAGGGTACCTAAATTCATGGG 2206
Qy 640 YAsnGluPheGlyHisProGluThrIleAspPheProArgAlaGluGlnHisLeuSerAs 660
Db 2207 AATGAATTCGGCCACCCTCAGTGGATGATTAATTCCTAGGCTGGAACAACACCTCTCTGA 2266
Qy 660 pGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLe 680
Db 2267 TGGCTCAGTAAATCCCGAGAAACCAATTCAGTTATGATAAATGACAGCGGAGATTGGACCT 2326
Qy 680 uGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTy 700
Db 2327 GGGAGATGCAGATATTTAAGATACCGTGGGTTGCAAGAATTTGACCGGGCTATGCAGTA 2386
Qy 700 rLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspG1 720
Db 2387 TCTTGAAGATAAATATGAGTTTATGACTTCAGAACACCACTTCATATACGAAAGGATGA 2446
Qy 720 uGlyAspArgMetIleValPheGluGlyGlyAsnLeuValPheValPheAsnPheHisTr 740
Db 2447 AGGAGATAGGATGATTGTATTCAAAAAGGAAACCTAGTTTTCCTTTAATTTCACTG 2506
Qy 740 pThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAl 760
Db 2507 GACAAAAGGCTATTCAGACTATCCGATATCGCATAGGCTGCCTGAAGCCCTGGAATAACAAAGGTGC 2566
Qy 760 aLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTy 780
Db 2567 CTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATATATCCCGAATA 2626
Qy 780 rPheThrPheGluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCy 800
Db 2627 TTTTCACCTTTGAAGGATGGTATGATGATGATGCTCTCTCTCAATTAATGGTGTATCCACCTAG 2686
Qy 800 sLysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
Db 2687 TAGAAGCAGGTGGTCTATGCACCTAGTAGACAAA-----GAAGAAGAAGA 2734
Qy 820 uGluGluValAlaAlaValGluGluValValValGluGluGlu 834
Db 2735 AGAAGAAGTAGCAGTAGTAGAGAAGTAGTAGTAGAGAAGA 2777

RESULT 7
AAI42632
ID AAT42632 standard; DNA; 3231 Bp.
XX AC
XX AAT42632;
XX AC
DT 25-FEB-1997 (first entry)
DE Class A starch branching enzyme (psbe2con.seq).
XX
XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
XX Solanum tuberosum.
XX Key Location/Qualifiers
FH misc_RNA 45..3200
FT /tag= a
FT /note= "claim 34"
FT
```

```
FT CDS 228..2855
FT /tag= c
XX
XX W09634968-A2.
XX
XX 07-NOV-1996.
XX
XX 03-MAY-1996; 96WO-GB01075.
XX
XX 10-APR-1996; 96GB-0007409.
XX
XX 05-MAY-1995; 95GB-0009229.
XX
XX (NATI ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
XX Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX
XX New potato plant starch having high amylose content - also class A
XX starch branching enzyme and corresp. DNA to alter the viscosity of
XX starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Claim 31, 34; Page 53-55; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
XX potatoes. In class A SBE mols., a flexible N-terminal domain,
XX is found, which is not found in class B mols.
XX The same sequence is given in Figure 8, however, nucleotides
XX 1-44 omitted.
XX
XX Sequence 3231 Bp; 960 A; 577 C; 739 G; 947 T; 8 other;
```

Alignment Scores:

```
Pred. No.: 0 Length: 3231
Score: 4268.50 Matches: 802
Percent Similarity: 97.12% Conservative: 8
Best Local Similarity: 96.16% Mismatches: 19
Query Match: 95.60% Indels: 5
DB: 17 Gaps: 1
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US-10-056-454a-15_COPY_49_882 (1-834) x AAT42632 (1-3231)

```
Qy 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaLalaSerGlyLysVal 20
Db 372 GAAAGTCTTCTTACGATTCGGAATCCGACCTTCTACAGTTGCAGCATCGGGAAAGTC 431
Qy 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerSerSerSerSerSerSerSer 40
Db 432 CTGTGACCTGGATCCAGAGTGTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 491
Qy 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerSerThrMetGluHis 60
Db 492 GAGACAGCTCCAGAAAATTCCTCCAGCATCAACATGATGTGATGATGATGATGATGATGATG 551
Qy 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerSerSerSerSerSer 80
Db 552 GCTAGCCAGATTAAACTGAGAACGATGACGTTGAGCCGCTCAAGTGTATCTACAGGAAGT 611
Qy 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGlu 100
Db 612 GTTGAAGATGGGATTTTCTTCATCATACTACAACTCAAGAGAGTGGTAAACTGGAGGAG 671
Qy 101 SerLysThrLeuAsnThrSerGluGluThrIleAlaAspGluSerAspArgIleArgGlu 120
Db 672 TCTAAACATTAATACTTCTGAGAGACAAATTAATGATGATGATGATGATGATGATGATGAT 731
Qy 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
Db 732 AGGGGATCCCTCCACCTGGACTTGGTGCAGAGATTTATGAAATAGACCCCTTTTGACA 791
Qy 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGluTyrLysLysLeuArgGluAlaIle 160
```

792 AACATATCGTCAACACCTTGATTACAGGTATTCCACAGTACAGAAATGAGGAGCAATT 851
161 AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
852 GACAAAGTATGAGGGTGTGGAGCTTTTCGTGGTATGAAAAATGGGTTCACCT 911
181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaLeu 200
912 CGTAGTGTACAGGTATACCTACCTGAGTGGCTCCTGGTCCAGTCAGCTGCTC 971
201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
972 ATTGGAGATTTCAACAATTTGGACGCAAAATGCTGACATTTATGACTCGGAATGTTGGT 1031
221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
1032 GTCGGGAGATTTTCGCAAAATGAGTGGATTCCTCGCAATTCCTCAAGGTCC 1091
241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
1092 AGAGTAGAGATAGCATGACACTTCATCAGGTGTTAAGGATTCCTGCTGGATC 1151
261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
1152 AACTACTCTTTACAGCTTCTCGTGAATTTCCATATATGGAATATATTATGATCCACCC 1211
281 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
1212 GAGAGAGAGGATGCTTCCANACCCAGGCCCAAGAAACCAAGTCGCTGAGAAAT 1271
301 TyrGluSerHisIleGlyMetSerProGluProLysIleAsnSerTyrValAsnPhe 320
1272 TATGAATTCATATTGGAATGAGTAGTCGGAGCCCTAAATTAACATACGTGAATTTT 1331
321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
1332 AGAGATGAAGTCTCTCTCGCATAAAAACCTTGGGTACAAATCGGTGCAAAATATGGCT 1391
341 IleGlnGluHisSerTyrTrpAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
1392 ATTCAGAGCATTTCTATTATGCTAGTTTGGTATCATGTCACAAATTTTTCACCA 1451
361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
1452 AGCAGCCGTTTGGAGCCGCGACGACCTTAAGTCTTTGATGATAAAGCTCATGAGCTA 1511
381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
1512 GGAATGCTGCTCATGGACATGTTTCAGCCATGCTACAGCCATGCATCAATAATCTTTAGATGGA 1571
401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
1572 CTGAACATGTTTCAGCGCACAGATAGTTGTTACTTTCACICTGGAGCTCGTGTATCAT 1631
421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
1632 TGGATGGGATTCGCGCTCTTTAACTATGGAACCTGGGAGGTACTTAGGTATCTCTC 1691
441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
1692 TCAAAATCGAGATGGTGGTGGATGAGTGCAAAATTTGRTGGATTTAGATTGATGGTGTG 1751
461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
1752 ACATCAATGATGATATCACTACCGGATTTATCGTGGGATTCAGTGGAACTACGAGGAA 1811
481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
1812 TACTTTGGATCGCAACTGATGTGATGCTGCCGTGATCTGATCTGCGCAACGATCTTT 1871
501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
1872 ATTCATGGGCTTTTCCAGATGCAATTTACCAITGGTGAAGATGTTACGGGAATGCCACA 1931

521 PheCysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
1932 TTTTGTATTTCCCGTTCAAGATGGGGTGTGGCTTTCACTATCGGTGCATATGGCAATT 1991
541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
1992 GCTGATAAATGGATTTGAGTTGCTCAAGAAACGGGATGAGGATTTGGAGATGGGTGATTT 2051
561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
2052 GTTCATACACTGACAAATAGAGATGGTCGAAAAAGTGTGTTTCATACGCTGAAAGTCAT 2111
581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheThrPheLeuMetAspLysAspMetTyr 600
2112 GATCAAGCTCTAGTCGGTGATAAACTATAGCATTTCTGCTGATGGACAAGGATATGATAT 2171
601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
2172 GATTTTATGGCTTTGGATAGACGCTCAACATCATTAATAGATCGTGGGATAGCATTCGAC 2231
621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
2232 AAGATGATAGGCTTGTAATATGGGATTAGGAGGAGAGGATACCTTAATTTTCATGGGA 2291
641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
2292 AATGAATTCGCCACCCCTGAGTGGATGATTTCCCTAGGGCTGAACAACACCTCTCTGAT 2351
661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
2352 GGCTCAGTAAATCCCGAAACCAATTCAGTATGATAAATGCAGCCGAGATTTGACCTG 2411
681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgPrometGluTyr 700
2412 GGAGATGCAAAATATTAAGTACCTGGGTGCAAGAAATTTGACCGGCTATGACGATAT 2471
701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
2472 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCATTCATATCAGAAAGGATGAA 2531
721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
2532 GGAGATGAGGATGATGTTATTTGAAAAAGGAAACCTAGTTTGTCTTTAATTTTCACCTGG 2591
741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
2592 ACAAAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCCTGAAAAATACAGGTTGCC 2651
761 LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
2652 TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATTAATGCCGAATGT 2711
781 PheThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCys 800
2712 TTCACCTTTGAAGGATGATGATGATGATGCTGCTGCTCAATATATGGGTATGACCTAGT 2771
801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
2772 AGACAGCAGCTGCTATGCACTAGTAGACAAA-----GAAGAAGAGAA 2816
821 GluGluValAlaAlaValGluGluValValValValGluGluGlu 834
2817 GAAGAAGTAGCAGTAGTAGTAGAAGAAGTAGTAGTAGAAGAGAA 2858

RESULT 8
AAT17267 standard; DNA; 2531 BP.
XX AAT17267;
XX AC
XX DT 03-MAR-1997 (first entry)
XX

Class A starch branching enzyme (direct sequencing).

Starch branching enzyme; SBE; class A; class B; Solanum tuberosum; amylose; viscosity; potato; ss.

Solanum tuberosum.

WO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R; Sidebottom CM, Westcott RJ;

WPI: 1996-506170/50.

P-PSDB; AAR93804.

New potato plant starch having high amylose content - also class A starch branching enzyme and corresp. DNA to alter the viscosity of starch; for use in food, biodegradable products, adhesives, etc.

Example 1; Fig 9; 142pp; English.

Class A starch branching enzyme (SBE) has been obtained from potatoes. In class A SBE mols., a flexible N-terminal domain, is found, which is not found in class B mols.

This sequence was obtained by direct sequencing of PCR fragments amplified from first strand cDNA. Nucleotides which could not be unambiguously assigned are indicated using standard IUPAC notation.

Sequence 2531 BP; 735 A; 458 C; 599 G; 723 T; 16 other;

Alignment Scores:

Pred. No.: 0 Length: 2531
Score: 4229.00 Matches: 793
Percent Similarity: 96.96% Conservative: 4
Best Local Similarity: 96.47% Mismatches: 25
Query Match: 94.71% Indels: 0
DB: 17 Gaps: 0

US-10-056-454A-15_COPY_49_882 (1-834) x AAT17267 (1-2531)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
DB 59 GAAAGTCCTTACAAATCCGAAATCCGACCTTACAGTTCCAGATCGGGGAAAGTC 118
QY 21 LeuValProGlyThrGlnSerAspSerSerSerThrAspGlnPheGluPheThr 40
DB 119 CTGTGCTGGAAAYCCAGAGTAGTACTCTCATCTCTCAACACCAATTTGATTCAC 178
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
DB 179 GAGACATCTCCAGAAATTTCCCGACATCAACTGATGATAGTATGATTCACAAATGGAAC 238
QY 61 AlaSerGlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySer 80
DB 239 GCTAGCCAGATTAATACTGAGACGATGAGTTGAGCCGCTCAAGTGATCTTACAGGA 298
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGlnGlu 100
DB 299 GTTGAAGAGCTGGATTTTGCTTCATCCTACATACACATACAGAGAGTGGTAACTGGAG 358
QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
DB 359 TCTAAACATTAATACTTCTGAAGAGACAATTAATGATGAATCTCTAGGATCAGAG 1418

QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
DB 419 AGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAATAGACCCCTTTTGACA 478
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAla 160
DB 479 AACTATCGTCAACACCTTGATACAGGTATTCACAGTACAGAAACTGAGGAGCAATT 538
QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
DB 539 GACAAGTATGAGGGTGGTTCGAGCTTTTCTCGTGTATGAAAAATGGGTTCAC 598
QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
DB 599 CGTAGTCTACAGCTATCACITACGTCAGTGGCTCTCTGTCGCCAGTCAGTCGCCCTC 658
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
DB 659 AITGGAGATTTCAACAATTTGGGAGCAATGCTGACATTATGACTCGGAATGAATTTGGT 718
QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
DB 719 GTCTGGGAGATTTTTCGCAAAATATGATGATGCTCTCTGCAATTCCTCATGGGTCC 778
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
DB 779 AGAGTGAAGATACGATGGACATCCATCAGGTGTAAGGATTCATTCCTGCTGGATC 838
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
DB 839 AACTACTCTTTACAGCTCTCTGATGAAATTCATATATATGGAATATATATGATCCACCC 898
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
DB 899 GAGAGGAGAGGTATRTCTTCCACACCCAGCGCCAAAGAACCAAGTCCCTGAGATA 958
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysLysLeuAsnSerTyrValAsnPhe 320
DB 959 TATGAATCTCATATTTGGAATGAGTAGTCCGAGCTAAATTAATCACTCATGCTGAATTT 1018
QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
DB 1019 AGAGATGAAGTCTCTCTCGCATAAATAAAGCTTGGGTACATGCGGTGCAATTTATGGCT 1078
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro 360
DB 1079 ATTCAAGAGCATCTTATTTATGCTAGTTTGGTTATCATGTCACAAATTTTTTGCACCA 1138
QY 361 SerSerArgPheGlyThrProAspLeuLysSerLeuLeuAspLysAlaHisGluLeu 380
DB 1139 AGCAGCGGTTTGAGACGCGCGAGCTTAAGTCTTTGATTGATAAAGCTCATGAGCTA 1198
QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
DB 1199 GGAATGTGTTCTCATGGACATTTGTCAGAGCATCATCAATAATATCTTTAGATGGA 1258
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
DB 1259 CTGAACATGTTTGACGCGCAGATAGTTGTTACTTTTCTTCCATCTGGAGCTCGGTATCAT 1318
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
DB 1319 TGGATGTGGATTCGCGCTCTTTAACTATGAAACTGGGAGGTACTTAGGTATCTTCTC 1378
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
DB 1379 TCAATTCGAGATGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1438
QY 461 ThrSerMetMetTyrIleHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
DB 1439 ACATCANTGATGATTAATCTCACCACGAGTATTCGCTGGGATTCCTGGGAACCTACGAG 1498

481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
 1499 TACTTTGGACTCCCACTCATGTGGATGCTGTGTGTATCTGATGCTGGTCAACGATCTT 1558
 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
 1559 AUTCACGGGCTTTCCACAGATGCAATACCATTTGGTGAAGATGTTAGCGGAATGCCGACA 1618
 521 PheCysIleProValGlnGlyValGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
 1619 TTTTGTATTCCCGGTTCAAGATGGGGTGTGGCTTTGACTATCGCTGCATATGGCAATT 1678
 541 AlaAspLysArgIleGlyLeuLeuLysLysArgAspGluAspTyrArgValGlyAspIle 560
 1679 GCTGATAAATGGATTGCTCAAGAACGGGATGAGGATTGGAGAGTGGTGATATT 1738
 561 ValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHis 580
 1739 GTTCATACACTGACAAATAGAGATGGTCGGAAGAGTGTGTTTCATMCGCTGAAGTCAAT 1798
 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyr 600
 1799 GATCAAGCTCTAGTCGGTGATAAACTATAGCATCTGGCTGATGGCAAGGATATGTAT 1858
 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
 1859 GATTTATGSCCTGGATAGACCGTCAACATCATTAATAGATCGTGGATAGCATTCAC 1918
 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyTyrLeuAsnPheMetGly 640
 1919 AAGATGATTAGGCTTGTAACTATCGGATTAGGAGAGAGGATACCTAAATTCATGGGA 1978
 641 AsnGluPheGlyHisProGluTyrIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
 1979 AATGAATCGCCACCTGAGTGGATGTATTCCTAGGCTGACAAACCTCTCTGAT 2038
 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
 2039 GGCTCAGTAATCCCGGAACCAATTCAGTTATGATAAATGCAGACGGAGATTGACCTG 2098
 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyr 700
 2099 GGAGATGCAGAAATTTAAGATACCATGGTTCGCAAGAATTCACCGGGCTATGCAGTAT 2158
 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
 2159 CTTGAGATAAATATGAGTTTATGACTTCAGAACACCCAGTTCATATCAGGAAGATGAA 2218
 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTyr 740
 2219 GGAGATAGGATGATTGTTTGAARAGGAACCTAGTTTGTGCTTTAATTTTCACTGG 2278
 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
 2279 ACAAAATAGCTATTACAGATATCGCATAGGCTGCTGAAAGCTGGAATAACAGGTTGGC 2338
 761 LeuAspSerAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
 2339 TTGACTCAGATATCCACTTTTGGTGGCTTCGGGAGATTTGATATATGCCGAATAT 2398
 781 PheThrPheGluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCys 800
 2399 TTCACCTCTGAAGATCGTATGATGATCGTCCTCGYCAATTTATGGTGTATGCCACCTAGT 2458
 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGlu 820
 2459 AGAACACAGCTGGTCTATGCTACTAGTAGACAAATAGTAAGNAGGAAGAAGAAAGAACCC 2518
 821 GluGlu 822
 2519 GNNGAA 2524

RESULT 9

AAT42637
 ID AAT42637 standard; DNA; 2529 BP.
 XX
 AC AAT42637;
 XX
 DT 03-MAR-1997 (first entry)
 XX
 DE Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.
 XX
 KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 KW amylose; viscosity; potato; ss.
 XX
 OS Solanum tuberosum.
 XX
 PN WO9634968-A2.
 XX
 PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96WO-GB01075.
 XX
 PR 10-APR-1996; 96GB-0007409.
 PR 05-MAY-1995; 95GB-0009229.
 XX
 PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
 PI Sidebottom CM, Westcott RJ;
 XX
 DR WPI; 1996-506170/50.
 XX
 PT New potato plant starch having high amylose content - also class A
 PT starch branching enzyme and corresp. DNA to alter the viscosity of
 PT starch; for use in food, biodegradable products, adhesives, etc.
 XX
 PS Example 1; Page 51-53; 142pp; English.
 XX
 CC Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.
 XX
 SQ Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;
 Alignment Scores:
 Pred. NO.: 0 Length: 2529
 Score: 4218.00 Matches: 790
 Percent Similarity: 96.72% Conservative: 5
 Best Local Similarity: 96.11% Mismatches: 27
 Query Match: 94.47% Indels: 0
 DB: 17 Gaps: 0
 US-10-056-454A-15_COPY_49_882 (1-834) x AAT42637 (1-2529)
 QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysVal 20
 Db 59 GAAAGATCTCTTCAATTCGAAATCCGACCTTCTACAGTTGAGCATCGGGANAGTC 118
 QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
 Db 119 CTTGTGCTGGAAYCCAGAGTAGTCTCTCATCTCAACAGACCAATTTGAGTTCAT 178
 QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis 60
 Db 179 GAGACATCTCCAGAAAATTCGCCAGCATCAACTGATGATAGTAGTTCAACATGGAACAC 238
 QY 61 AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer 80
 Db 239 GCTAGCCAGATTAAACCTGAGACGATGACGCTTGGAGCTCAAGTATCTTACAGGAGT 298
 QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyGlyLysLeuGluGlu 100
 Db 299 GTTGAAGAGCTGGATTTTGTCTCATCACTACAACTACAAAGAGGTGGTAAACTGGAGAG 358
 QY 101 SerLysThrLeuAsnThrSerGluThrIleIleAspGluSerAspArgIleArgGlu 120

Db 359 TCTAAACATTAATACTCTGAAGAGACAAATTAATGATGAATCTGATAGGATCACAGAG 418
QY 121 ArgGlyLeuProProGlyLeuGlyGlnLysIleTyrGluLeuAspProLeuLeuThr 140
Db 419 AGGGGATCCCTCCACCTGACCTGGTGTGTCAGAAATTTATGAAATAGACCCCTTTTGACA 478
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
Db 479 AACTATCGTCAACACCTTGATACAGGTATTCAGGTACAAGAACTGAGGGAGGCAAT 538
QY 161 AspLysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
Db 539 GACAACTATGAGGCTGTTTCAAGCTTTTCTCGTGGTATGAAAAATGGGTTTCACT 598
QY 181 ArgSerAlaThrGlyLeuThrTyrArgGluThrAlaLeuGlyAlaGlnSerAlaLeu 200
Db 599 CGTAGTGTACAGGTATCACTACCTGAGTGGCTCCCTGGTCCCGCAGTCAGCTGCCCTC 658
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
Db 659 ATTGGAGATTTCAACAATTTGGACCGCAATGCTGACATTAATGACTCGGAATGAATTTGGT 718
QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
Db 719 GTCTGGGAGATTTTCTGCCAAATAATGTGGATGTTCTCTCGCAATTCCTCATGGGTCC 778
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
Db 779 AGAGTGAAGATACGATGAGACACTCCATCAGGTGTTAAGGATTTCCATTCCTGTTGGATC 838
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
Db 839 AACTACTCTTTACAGCTTCTGATGAAATTCATATAATGGAATATTAATGATCCACC 898
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
Db 899 GAAGAGGAGAGGTATCTCTCCAAACACCACCCAGCCCAAGAAACCAAGGCTGCTGACAA 958
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
Db 959 TATGAATCTCATTTGGAATGAGTAGTCCGAGCCCTAAAATTAACATCACTACGTGAATTT 1018
QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
Db 1019 AGAGATGAAGTTCTTCCTCGCATAAAAASCTTGGGTACAAATGGGTGCAAAATTAAGCT 1078
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
Db 1079 APTCAAGAGCATTTTATATGCTAGTTTGGTTTATCATGTCCACAAATTTTTCACCA 1138
QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db 1139 AGCACCGTTTGGAAAGCCCGACGACCTTAGTCTTTGATTGATAAAGCTCATGAGCTA 1198
QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
Db 1199 GGAATTTGTTCTCATGGACATTTGTCACACCATGATCAATAATTAATTAATTAAGATGA 1258
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
Db 1259 CTGAACATGTTTGGAGGACACATAGTTGTTACTTTCACTCTGGAGCTCGTGGTTATCAT 1318
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
Db 1319 TGGATGTGGGATTCGCCGCTCTTTAACTATGAAACTGGGAGGTACTTAGGTATCTTCTC 1378
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
Db 1379 TCAATGCGAGATGCTGTTGATGAGTTCAAATTTGATGGAATTTAGATTTGATGGTGTG 1438
QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
|||||

Db 1439 ACATCAATGATGTATACTACCAGGGATTAATCGGTGGGATTAATCTGCGAACTACGAGAA 1498
QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValTyrLeuMetLeuValAsnAspLeu 500
Db 1499 TACTTTGGACTCGCAACTGAIGTGAIGCTGTTGTGTATCTGATGCTGGTCAACGATCTT 1558
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db 1559 ATTCACGGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATGTTAGCGAATGCCGACA 1618
QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 1619 TTTTGTATTCCTGTTCAAGATGGGGTGTGGCTTTGACTATCGGTGCATATGGCAATT 1678
QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db 1679 GCTGATAAATGGATTGAGTTGCTCAAGAAACGGATGAGGATGGAGAGTGGGTATATT 1738
QY 561 ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db 1739 GTTCATACACTGACAAATAGAGATGGTCGGAAGAGTGTGTTTCATMCGCTGAAAGTCAT 1798
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
Db 1799 GATCAGCCTAGTCGGTGATAAACTATAGCATYCTGGCGTGAAGGACAGGATATGTAT 1858
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 1859 GATTTATGGCTCTGGATAGACCGYCAACAYCATTAATAGATGCTGGGATAGCATTCAC 1918
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640
Db 1919 AAGATGATTAGGCTTTGAACTATGGGATTAGGAGGAGGAGGTTACCTAAATTTTCATGGGA 1978
QY 641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 1979 AATGAATTCGGCCACCTCGATGGATTGATTTCCCTAGGCTGACAAACCTCTCTGAT 2038
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
Db 2039 GGCTCAGTAATTCGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTG 2098
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyr 700
Db 2099 GGAGATGCAAGATATTAAAGATACCATGGGTTGCAAGAAATTTGACCGGCTATGCAAGTAT 2158
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db 2159 CTTGAAGATAAATATGAGTTTATGACTTCAGAACACCATGTCATATCAGCAAGAGATGAA 2218
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
Db 2219 GGAGATGAGTATGATTGATTGAAAARAGAAACCTAGTTTGTCTTTAATTTTCACTGG 2278
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2279 ACAATAGTATTTACAGACTATCGATAGCTGCTGAAAGCTGGAAGCTGGAAGGTGGC 2338
QY 761 LeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2339 TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATTAATGCCGAAAT 2398
QY 781 PheThrPheGluGlyTyrTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2399 TTCACCTCTGAAGGATCGTATGATGCTCCTCGTTCATTAATATGGTGTATGCACCTAGT 2458
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
Db 2459 AGAACAGCAGTGTCTATGCTAGTACAAATAAGAGNAGAGAGAGAGAGAGAGAGAGAGAG 2518
QY 821 GluGlu 822
|||
Db 2519 GNNGAA 2524

RESULT 10

AA42635

ID AA42635 standard; DNA; 2975 BP.

XX AA42635;

XX DT 03-MAR-1997 (first entry)

XX Class A starch branching enzyme (11con.seq).

XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX Solanum tuberosum.

XX WO9634968-A2.

XX PD 07-NOV-1996.

XX PF 03-MAY-1996; 96WO-GB01075.

XX PR 10-APR-1996; 96GB-0007409.

XX PR 05-MAY-1995; 95GB-0009229.

XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

XX Sidebottom CM, Westcott RJ;

XX WPI; 1996-506170/50.

XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX Example 1; Page 40-41; 142pp; English.

XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX Sequence 2975 BP; 871 A; 548 C; 693 G; 863 T; 0 other;

Alignment Scores:

Pred. No.: 0 Length: 2975
Score: 4155.50 Matches: 791
Percent Similarity: 95.79% Conservative: 6
Best Local Similarity: 95.07% Mismatches: 26
Query Match: 93.07% Indels: 11
DB: 17 Gaps: 1

US-10-056-454a-15_COPY_49_882 (1-834) x AA42635 (1-2975)

QY 1 GluLysSerSerTyrAsnSerGluPheArgProSerThrValAlaLaserGlyLysVal 20
DB 289 GAAAGTCTCTTACAAATCCGAATTCGACCTCTACAGTTGCAGCATCGGGGAAGTC 348
QY 21 LeuValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGluPheThr 40
DB 349 CTTGTGCCCTGGAAACCCAGAGTGATAGCTCTCATCTCAACAGACCAATTGAGTTCACT 408
QY 41 GluThrSerProGluAsnSerProAlaSerThrAspValaspSerSerThrMetGluHis 60
DB 409 GAGACATCTCCAGAAAATCCCCAGCATCAACTGATGATAGATTCAACAATGGAACAC 468
QY 61 AlaSerGluLeuLysThrGluAsnAspValGluProSerSerSerSerSerThrGlySer 80
DB 469 GCTAGCCAGATTAAAACTGAGAACGATGAGCTTGAGCCGCTCAAGTCACTTACAGGAAGT 528
QY 81 ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyGlyLysLeuGluGlu 100
DB 529 GTTGAAGAGCTGGATTTCCTTCATCACTACAACTACAGAGGTGGTAAACTGGAGGAG 588

QY 101 SerLysThrLeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGlu 120
DB 589 TCTAAACATTAATAACTTCTGAAGACAAATATTGATGAATCTGATAGATCAGAGAG 648
QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
DB 649 AGGGCATCCCTCCACCTGGACWTGGTCAGAACATTTATGAAATAGACCCCTTTTGACA 708
QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
DB 709 AACTATCGTCACACCTTGATTACAGGTATTCACAGTACAGAACAACTGAGGAGGCAATT 768
QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
DB 769 GACAAGTATGAGGGTGGTTTGAAGC-TTTTCTCTGGTTATGAAAAAATGGGTTTCAC 827
QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
DB 828 CGTAGTGCTACAGGTATCACTTACCGTGAAGGGCTCTGGTCCAGTCCAGTCCGCTC 887
QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
DB 888 ATTGGAGATTCAACAATTGGGACGCAATGCTGACATTAIGACTCGGAATGAATTGGT 947
QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
DB 948 GTCGGGAGATTTTCTGCCAAATAATGTGGATGGTTCTCTCTCAATTCCTCATGGTCC 1007
QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
DB 1008 AGAGTGAAGATACGTATGGACATCCACTCAGGTGTTAAGGATTCATCTCTGCTGGATC 1067
QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280
DB 1068 AACTACTCTTACAGCTTCTCGATGAATTCATATAATGAATATATTATGATCCACCC 1127
QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
DB 1128 GAAGAGGAGAGGTATATCTTCCACACCCAGCCGCAAGAAACAAAGTCGCTGAGAATA 1187
QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysLysIleAsnSerTyrValAsnPhe 320
DB 1188 TATCAATCTCATATTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1247
QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
DB 1248 AGAGATGAATCTTCTCTCGCAATAAAAGCTTGGGTACAAATGCGCTGCGAATTTATG 1307
QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
DB 1308 ATTCAAGAGCATTCCTTATTATGCTAGTTTGGTTATCATCATCAAAATTTTTCACCA 1367
QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuLysAlaHisGluLeu 380
DB 1368 AGCAGCGTTTGGAGCGCCGAGACCTTAAGTCTTCGATTGATAAGCTCAAGACTA 1427
QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
DB 1428 GGAATGTGTTCTCTCATGGACATCGTTTCACAGCCATGCATCAAAATATACTTTAGAT 1487
QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis 420
DB 1488 CTGAACATGTTTGACGSCACCGATAGTTTACTTTCACCTCTGAGCTCGTGGTTATCAT 1547
QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuAspTyrLeuLeu 440
DB 1548 TGAATGGGATTC-CGCCCTCTTTAACTATGGAACAGGGAGGTACTTAGTATCTTC 1606
QY 441 SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
DB 1607 TCAAAATGCGAGATGGTGGTGGATGAGTTTCAAAATTTGATGATTTAGATTGATGGTGTG 1666


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QY 461 ThrSerMetMetTyrIleHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
Db 1667 ACATCAATGATGATATCACTCAACCGGATTCGGTGGGATTCACCTGGGAACCTACGAGAA 1726
QY 481 TyrPheGlyLeuAlaThrAspValAlaValValTyrLeuMetLeuValAsnAspLeu 500
Db 1727 TACTTTGGACTCGCACTGATGATGATGCTGTGTGTATCTGTGATGCTGGTCAACGATCTT 1786
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db 1787 ATTCAATAGGCTTTCCACAGATCAATTACCATTTGGTGAAGATGTTAGCGGAATGCCGACA 1846
QY 521 PheCysIleProValGluGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 1847 TTTTGTATCCCGTTCCAGATGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1906
QY 541 AlaAspLysArgIleGluLeuLysLysArgAspGluAspTyrArgValGlyAspIle 560
Db 1907 GCTGATAAATGGATTCAGTGTCTCAAGAAACGGGATGAGATGGAGAGTGGGTGATATT 1966
QY 561 ValHisThrLeuThrAsnArgArgTyrPheSerGluLysCysValSerTyrAlaGluSerHis 580
Db 1967 GTTCATACACTGCAATAGAGATGGTCCGGAAGTGTGTTCTATAGCTGGAAGTCAT 2026
QY 581 AspGluAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAspLysAspMetTyr 600
Db 2027 GATCAAGCTCTAGTGGTGTATAAATATAGCATTTCTGGCTGATGGACAGGATATGTAT 2086
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 2087 GATTTATGCTCTGATAGACCGCCACATCAATTAATAGATCGTGGATGATGATGCAC 2146
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGluGlyTyrLeuAsnPheMetGly 640
Db 2147 AAGATGATTAGGCTTCTAATATGGGATTAGGAGAGAGAGGTACCTAAATTTTCAGGGA 2206
QY 641 AsnGluPheGlyHisProGluTyrPheAspPheProArgAlaGluGluHisLeuSerAsp 660
Db 2207 AATGAATGGCCACCTCAGTGGATGATTTCCCTAGGCTGAGCCACACCTTCTGAT 2266
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
Db 2267 GGTCTAGTAATTCCTGGGAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTG 2326
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGluGluPheAspArgProMetGlnTyr 700
Db 2327 GGAGATGCAGAAATTAAGATACCATGGTTTACAGAATTTGACTGGGCTATGCAATAT 2386
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db 2387 CTGAGATAAATCAGTTTATGACTTCAGAACACCACTTCATATACGAAAGATGAA 2446
QY 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTyr 740
Db 2447 GGAGATAGGATGATTTATTTTGAAGAGGAACCTAGTTTTCGTCCTTTAAATTTTCACTGG 2506
QY 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2507 ACAATAGCTATTACAGATATCCGATAGCTGCCGAGAGCCCTGGAAATACAAAGTTGTC 2566
QY 761 LeuAspSerAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2567 TTGGACTCAGATGATCCACTTTTGTGGCTTCGGGAGAAATTCATCAATATGCCGAATAT 2626
QY 781 PheThrPheGluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2627 TTCACCTCTGAAGATGATGATGATGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2686
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
Db 2687 AGAACACGACGTGGTCTGACCTAGTAGACAAA----- 2719
QY 821 GluGluValAlaAlaValGluGluValValGlu 832
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Db 2720 CTAGAAGTAGCAGTAGTAGAAGAACCACCTAGTGAGAA 2755
RESULT 11
AAV38720
ID AAV38720 standard; DNA; 3090 BP.
XX AAV38720;
AC AAV38720;
DT 21-SEP-1998 (first entry)
XX Full length cassava tuber cDNA in pSJ146.
XX Starch branching enzyme; SBE; cassava; ss.
XX Manihot esculenta.
XX Key Location/Qualifiers
FT misc_feature 35..2760
FT /*tag= a
FT /*note= "these nycleotides are SBE II sequence, the
FT remainder are derived from the plamsid"
FT CDS 131..2677
FT /*tag= b
FT /*product= SBE II
XX W09820145-A2.
XX 14-MAY-1998.
XX 04-NOV-1997; 97WO-CB03032.
XX 05-NOV-1996; 96GB-0023095.
XX (NATT ) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX Jobling SA, Safford R;
XX WPI: 1998-286958/25.
XX P-PSDB; AAM62800.
XX Starch branching gene from cassava - useful for producing altered
XX plants giving modified starch
XX Claim 2; Fig 13; 67pp; English.
XX The present sequence encodes starch branching enzyme (SBE) II. It
XX was isolated from cassava tubers. The products can be used for
XX producing plants having altered starch quantities and qualities.
XX They can also be used for producing altered plants such as cassava,
XX banana, potato, pea, tomato, maize, wheat, barley, oat, sweet potato
XX and rice plants.
XX Sequence 3090 BP; 877 A; 578 C; 721 G; 914 T; 0 other;
Alignment Scores:
Pred. No.: 3,27e-315 Length: 3090
Score: 3363.00 Matches: 618
Percent Similarity: 84.20% Conservative: 75
Best Local Similarity: 75.09% Mismatches: 98
Query Match: 75.32% Indels: 32
DB: 19 Gaps: 4
US-10-056-454a-15_COPY_49_882 (1-834) x AAV38720 (1-3090)
QY 2 LysSerSerTyrAsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeu 21
Db 284 AAGTCTCTTATGAATCTGACTCTCTCAAAATTAATCTCTCTGATCTGAGAAGTCTT 343
QY 22 ValProGlyThrGlnSerAspSerSerSerSerThrAspGlnPheGluPheThrGlu 41
Db 344 GTTCTCGATGATCAGATGATGGCTCTCTCTTCTTCAACATATCAATTAGAACCTGGC 403
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QY 42 ThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAla 61
DB 404 ACAGTGGGAGGAAATCCAGGTTCTGTGGATGCGAGAGAGTCTTGATGGAGAGATGAT 463
QY 62 SerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySerVal 81
DB 464 AAGATGTT-----GAGGAGGATGAAGTAAAA-----490
QY 82 GluGluLeuAspPheAlaSerSerLeuGlnGluGlnGlyLysLeuGluGluSer 101
DB 491 -----AAGAGTCGGTTCCATTCAGATGACAGACA 517
QY 102 LysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGluArg 121
DB 518 ATTAGCAATGGAAGAGTGAATCT-----AAACCAAGG 550
QY 122 GlyIleProProGlyLeuGlyGlnLysIleTyrGlnIleAspProLeuLeuThrAsn 141
DB 551 TCCATTCTCCACCTGGCAGTGGGAGAGATATATGACATAGATCCAGCTTGGCAGGT 610
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
DB 611 TTCGGTCAGCATCTGACTACCGATATTCAGATACAAAAGCTCGGTGAGGAATTCAC 670
QY 162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
DB 671 AAGTATGAAGTGGTTGGATGCATCTCTCGTGGATTGAAAGTTTGGTTCTCTACGC 730
QY 182 SerAlaThrGlyIleThrTyrArgGluThrAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
DB 731 AGTGAACAGGAATAACTTATAGGGAATGGGACCTGGAGTACGTGGGGCTGCACATTAT 790
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
DB 791 GGAGATTTCACAAATTTGAATCCTAATGCAGATGTCTATGCTCGGAATGAGTTGGTGT 850
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
DB 851 TGGGAGATTTTTTGGCAATAACCGAGATGGTTCCACCACCAATTCCTCATGGTCTTCGA 910
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaIleTrpIleAsn 261
DB 911 GTAAAGATACGATGGATATCCATCTGGCATCAAGATTCAAATTCCTGCTTGGATCAAG 970
QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
DB 971 TTCATGTTTTCAGGCACCTGGTGAATCCCATACAAATGCCATATATGATCCACCAAG 1030
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
DB 1031 GAGGAGAAGTATGTGTTCAACATCCCTCAGCCAAAGACCAAAATCATCTAGGATTTAT 1090
QY 302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
DB 1091 GAATCTCATGTTGGATGAGTAGTATGAGCCAAATATTAACACATATGCCAACTTTAGA 1150
QY 322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
DB 1151 GATGATATGCTTCCTCGCATCAAAAAGCTTGGCTCAATGCTGTGTCAGATCATGGCTAT 1210
QY 342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSer 361
DB 1211 CAAGACATTCCTATATATGCTAGTTTGGTACCATGTCACAACTTTTTCACCTAGC 1270
QY 362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
DB 1271 AGCCGATTTGGAACTCTCTGATGATTTGAAGTCTTTAATAGATAAAGCTCATGAGTAGGG 1330
QY 382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
DB 1331 CTGCTTGTCTCATGGATATTTGTCATAGCCATCGCTCAAAATATACGTGGATGGCTG 1390
QY 402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
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DB 1391 AACATGTTTATGGTACGGATAGTACTACTTCCATCCCGATACACGGGTCAATCATGG 1450
QY 422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
DB 1451 TTGGGGACCTCGCCCTTCAACTATGGAAGCTGGGAGGTGCTAAAGATTCTTCTTCA 1510
QY 442 AsnAlaArgTrpTrpLeuAspAlaPheIysPheAspGlyPheArgPheAspGlyValThr 461
DB 1511 AATCAAGATGGTGGTTGGAAGACAGTACAGGTTTATGAGTTTATGATTGATGGGTGACT 1570
QY 462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
DB 1571 TCCATGATGATACCTCCCATCGGTGTCAGTACGCTTTTACTGGCACTACATAGAGTAC 1630
QY 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
DB 1631 TTGGATATGCAACTGATGATGCTGTGATTTATTTGATGCTTGTGAATGATGAT 1690
QY 502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
DB 1691 CACGGTCTTTTCCCTGAGGCTGTTACCATGTGTGAGATGTTAGCGAAAGCAACATTT 1750
QY 522 CysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
DB 1751 TGCATTCCACTGGAAGATGGTGTGTGGATTGATTACCGTCTCCACATGGCCATGGC 1810
QY 542 AspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
DB 1811 GATAAATGGATTGAGATCTTAAAGAGAGATGAGGACTGGAAATGGGTGACATGGT 1870
QY 562 HisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
DB 1871 CATACACTCCACCAACAGAGTGGTGGAAAAATGTGTGCTTATGTGAAGTCATGAC 1930
QY 582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
DB 1931 CAAGCTCTTGTGTGTGACAAAACATATTGCTATTTGGCTGTGATGGACAAAGGACATG 1990
QY 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
DB 1991 TTCATGGCTCGTCAGACACCATCTACTCCCTCTTATAGATCGTGGATAGCATTCACAAA 2050
QY 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
DB 2051 ATGATCAGGCTTATTACCATCGGCTTAGCGGAGAGAGATATTGAAATTTATGGGAAAT 2110
QY 642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
DB 2111 GAAATTTGGACATCTCTGAGTGGATTGATTTTCCAGAGGGGATCGACATCTGCCCAATGGT 2170
QY 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGly 681
DB 2171 AAAGTAATTTCCAGGAAACACACACATGATGATAAATGCCGTCGTAGATTGATCTAGT 2230
QY 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
DB 2231 GATGCAGACTATCTAAGATATCATGATGATGCAAGAGCTTTGATCAGCAATGCAACATCT 2290
QY 702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
DB 2291 GAAGAAGCCTATGCTTTCATGACTTCTGAGCACCATGATATATACCGAGGATGAAGGA 2350
QY 722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
DB 2351 GATCGGATCAITGCTTTGAGAGGGGNAACCTGTTTGTATTCACTTCACTTGGACT 2410
QY 742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
DB 2411 AACAGCTATTTCAGATTACCGAGTGGCTGCTTCAAGTCAGCAAGTACAGATTGTTTG 2470
QY 762 AspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
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1146	ACCGGATTTGGAACCTCCTGATGATTTAAAGTCTCTAATACATAAAGCTCACGAGTTAGGT	1205	742	LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrIleValAlaLeu	761
382	IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu	401	2286	ACGAGCTATTTCGGATTTACCGAGTTGGCTGCTTAAAGCCAGGAAAGTACAAGATAGTCTTG	2345
1206	CTTCTCTGTCATCGGATATTTTCATPAGCATGCATCAACTAATAGTTGGATGGGCTG	1265	762	AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe	781
402	AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTyr	421	2346	GATTCAGATGATCCTTTGTTGGAGGCTTTGGCAGGCTTAGTCATGATCGAGAGCACTTC	2405
1266	AATATGTTGATGTGATGGATGGGATGGTCACTACTTTCACCTCTGCACACGGGGTCATCA	1325	782	ThrPheGluGlyTyrPyrAspAspArgProArgSerIleMetValTyrAlaProCysLys	801
422	MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer	441	2406	AGCTTTCAAGGGTGGTACGATACACCGGCCCTCGATCCTTCATGCTGTACACACCATGTAGA	2465
1326	ATGTTGGGACTCTCGCTTTTCAACTATGGGAGCTGGGAGGTCTTAAGGTTCTCTTCA	1385	802	ThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu	821
442	AsnAlaArgTyrTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr	461	2466	ACACAGTGGTCTATGCTTTAGTG-----GAGGATCAAGTGGAGAAATGATGGAA	2516
1386	AAATGCAAGTGTGTTGGATGAGTACAGTACAGTGAAGTTGATGGTTTCAGATTTGATGGGTGACT	1445	822	GluValAla 824	
462	SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr	481	2517	CCTGTGCGCC 2525	
1446	TCAATGATGATACACCAATCATGGATGTCAGGTAGATTTTACCGGCAACTACAAATGAATAC	1505	RESULT 13		
482	PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle	501	ID AAC45939	standard; DNA; 2715 BP.	
1506	TTTGGATATGCAACTGATGATGATGCTGTGGTTTATTTGATGCTGTGAATGATATGAT	1565	XX AAC45939;		
502	HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe	521	AC AAC45939;		
1566	CATGTGCTCTTCCACAGGCTGTCACCATTTGGTGAAGATCTTAGTGAATGCCACAGTT	1625	XX 18-OCT-2000 (first entry)		
522	CysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla	541	DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.		
1626	TGCATTCGGTGAAGATGGTGGTGTGGTTGATTTATCGTCTCCACATGGCTGTGCT	1685	KW Hybridisation assay; genetic mapping; gene expression control;		
542	AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal	561	KW protein identification; signal transduction pathway;		
1686	GATAAAATGGGTTGAGATTAATTCAGAGAGAGATGGAAGATGGGAATGGGTGACATGTA	1745	KW metabolic pathway; promoter; termination sequence; ss.		
562	HisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHisAsp	581	XX Arabidopsis thaliana.		
1746	CATATGCTGACCAACAGCGCGTGGTTGGAAGATGTTCTTATGCTGAAAGTCATGAC	1805	XX EP1033405-A2.		
582	GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp	601	XX 06-SEP-2000.		
1806	CAGCCCTTGTGTGTGACAAAATATTCATTTGGCTGATGGACAAAGATATGATGAC	1865	XX 25-FEB-2000; 2000EP-0301439.		
602	PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys	621	XX 9905-0121825.		
1866	TTTCATGGCTCTGACAGACCATTCACCTCTCATAGATCTGGAGTAGCATTCACAAA	1925	XX 05-MAR-1999;		
622	MetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGlyAsn	641	XX 09-MAR-1999;		
1926	ATGATCAGGCTTATACCATGGGATAGCGGAGAGGATATTTGAAATTTTATGGGAAAT	1985	XX 23-MAR-1999;		
642	GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly	661	XX 25-MAR-1999;		
1986	GAAATTTGACACCCCGAGTGGATGATTTTCCAGAGGTGATCTACATCTTCCCGAGTGGT	2045	XX 09-MAR-1999;		
662	SerValIleProGlyAsnGluPheSerTyrAspLysCysArgArgPheAspLeuGly	681	XX 23-MAR-1999;		
2046	AAATTTGTTCTCTGGGAAATTCATAGTTATGATTAATTCGCGCGGTAGTTTATCTAGGC	2105	XX 28-APR-1999;		
682	AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu	701	XX 30-APR-1999;		
2106	AAATCAAGCATCTGAGATATCATGGAATGCAAGAGTTTGATCAAGCAATTCAGCATCTT	2165	XX 04-MAY-1999;		
702	GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly	721	XX 06-MAY-1999;		
2166	GAAGAAGCCTATGGTTTTCATGACTTCTGACGCCATATCATCAGGAAGATGAAGG	2225	XX 07-MAY-1999;		
722	AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr	741	XX 11-MAY-1999;		
2226	GATCGGATCATGCTCTCCAGAGGGGAACCTCGCTTTTGTATTCTCAATTTTCATTGGACT	2285	XX 14-MAY-1999;		

PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
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PR 27-AUG-1999; 99US-0151086.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
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PR 07-SEP-1999; 99US-0151930.
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PR 29-SEP-1999; 99US-0156596.
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PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.

PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:		
Pred. No.:	3.44e-306	2715
Score:	3269.00	Matches:
Percent Similarity:	83.1%	Conservative:
Best Local Similarity:	72.3%	Mismatches:
Query Match:	73.21%	Indels:
DR:	21	Gaps:

US-10-056-454A-15 COPY 49 882 (1-834) X AAC45939 (1-2715)

QY	2	LyS	Ser	Tyr	Asn	Ser	Glu	Phe	Arg	Pro	Ser	Thr	Val	Ala	Ala	Ser	Gly	Val	Leu	21
DB	160	AAG	CCAT	CGT	ATG	ATT	CT	GAT	-----	TCG	TC	TCC	TAG	CAC	CTG	CAT	CTG	AAG	213	
QY	22	Val	Pro	Gly	Thr	Gln	Ser	Asp	Ser	Ser	Ser	Thr	Asp	Gln	Phe	Glu	Phe	Thr	Glu	41
DB	214	CTC	CGT	GGC	ATC	CAG	TAG	TCT	CTC	TCT	CTC	GCT	GAT	CAG	TAC	AAAT	CTC	GGG	AT	273
QY	42	Thr	Ser	Pro	Glu	Asn	Ser	Pro	Ala	Ser	Thr	Asp	Val	Asp	Ser	Ser	Thr	Met	Glu	61
DB	274	ACT	GTC	TCT	CGC	GAT	CTC	AGG	TCT	CGG	CAAT	TAG	CAG	CTT	CAG	AAA	CTG	AAG	ACC	333
QY	62	Ser	Gln	Leu	Leu	Thr	Glu	Asn	Asp	Val	Glu	Pro	Ser	Ser	Asp	Leu	Thr	Gly	Ser	81
DB	334	CAG	GAA	-----	AC	A	G	A	G	A	C	A	C	T	A	C	T	C	T	387
QY	82	Glu	-----	Glu	Leu	Asp	Phe	Ala	Ser	Ser	Leu	Gln	Gln	Glu	Gly	Gly	Leu	Glu	Glu	100
DB	388	AGT	TAT	AAA	GAA	GAT	TTT	TGCA	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	420
QY	101	Ser	Leu	Thr	Leu	Asn	Thr	Ser	Glu	Glu	Thr	Leu	Leu	Leu	Ser	Asp	Arg	Leu	Glu	120
DB	421	TCT	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	444
QY	121	Arg	Gly	Leu	Pro	Pro	Gly	Leu	Gly	Gln	Leu	Ser	Leu	Leu	Leu	Leu	Leu	Leu	Thr	140
DB	445	AGG	AAT	TTCC	ACCT	CTC	TGG	GAG	ATG	GGA	GAA	GAT	TAT	GAC	ATT	GAT	TCT	ATG	TGA	504
QY	141	Asn	Tyr	Arg	Gln	His	Leu	Asp	Tyr	Arg	Tyr	Ser	Gln	Tyr	Leu	Ser	Leu	Arg	Leu	160
DB	505	AGT	CAT	CGT	AAAT	CAT	CTG	ATT	ACG	GAT	ATG	GCG	AGT	CAC	GAA	AAA	CTC	CGT	CAG	564
QY	161	Asp	Leu	Tyr	Glu	Gly	Leu	Glu	Ala	Phe	Ser	Arg	Gly	Tyr	Glu	Leu	Ser	Met	Gly	180
DB	565	GAC	AA	GA	TGA	AGG	TGG	TGG	AGG	CA	TTT	CTC	G	TG	G	T	TAT	GAA	AT	624
QY	181	Arg	Ser	Ala	Thr	Gly	Leu	Thr	Tyr	Arg	Glu	Tyr	Ala	Leu	Gly	Ala	Gln	Ser	Ala	200
DB	625	CGA	AGC	CC	CACT	TGG	TAT	CACT	TAC	CGG	GAAT	GGG	CAC	CGG	AGT	CAT	AAG	CAG	CAT	684
QY	201	Ile	Gly	Asp	Phe	Asn	Asn	Trp	Asp	Ala	Asn	Ala	Asp	Ile	Met	Thr	Arg	Asn	Glu	220
DB	685	ATC	GG	AGAT	TTT	AAT	AACT	CGGA	ATG	GCA	AAAT	CTG	ATG	TAT	GCT	CGG	AAC	GAC	ATT	744
QY	221	Val	Trp	Glu	Leu	Phe	Leu	Pro	Asn	Asn	Val	Asp	Gly	Ser	Pro	Ala	Leu	Pro	His	240
DB	745	G	TG	TGG	GAAT	AT	TTCT	G	CAAA	TAAT	GC	TGAT	GGCT	CA	CCAG	CAAT	CCCC	ATG	CTCC	804
QY	241	Arg	Val	Leu	Ser	Ile	Arg	Met	Asp	Thr	Pro	Ser	Gly	Val	Leu	Asp	Ser	Ile	Pro	260
DB	805	CGT	GTG	AAG	AT	CCCAT	TGG	ATAC	CCCC	ATC	TGG	TAT	TAAG	AC	TCCAT	TC	CAG	CTT	GGATC	864
QY	261	Asn	Tyr	Ser	Leu	Gln	Leu	Pro	Asp	Glu	Leu	Pro	Tyr	Asn	Gly	Ile	His	Tyr	Asp	280
DB	865	AAG	TAT	TTCT	G	TCC	AGCC	AC	CTG	GGC	GAG	AT	CCCA	TAT	AT	TAAT	GG	AGT	TAT	924
QY	281	Glu	Glu	Glu	Arg	Tyr	Ile	Phe	C	His	Pro	Arg	Pro	Leu	Ser	Pro	Leu	Arg	Ile	

Db	925	GAGAGAGATAAATATGCGTCCAAACATCCTCGTCCAAAGAAACCCACACATCGCTGGGTATA	984
Qy	301	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320
Db	985	TATGAATCACATGTTGGAAATGAGTAGTAGCGGAACCAAGATAAATACATATGCCACACTT	1044
Qy	321	ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnLeuMetAla	340
Db	1045	AGAGAAGATGACTTCCCGCGTATAAARAAGCTAGGCTATAATGCTGTGCAGATAAATGGCC	1104
Qy	341	IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro	360
Db	1105	ATTCAAGAGCATGCGCTACTATGCCAGCTTTGGGTATCATGTGCACAAATTTTTCGCACCT	1164
Qy	361	SerSerArgPheGlyThrProAspLeuLysSerLeuIleAspLysAlaHisGluLeu	380
Db	1165	AGCAGCGCGTTGGAAACACCTGATGACCTTAATCTTTGATACACAAAGCTCATGAGCTA	1224
Qy	381	GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly	400
Db	1225	GGTCTGGTGTCTGATGATATGTCACAGCATGCATCAAAAACACACCTGGATGGC	1284
Qy	401	LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis	420
Db	1285	CTGGACATGTTGATGGTACTGATGGTCAATATTTCCACCTCGGATCGCGGTATCAT	1344
Qy	421	TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu	440
Db	1345	TGGATGTGGGATCTCGTCTTTCAATTCAGGAAGCTGGGAAGTCTAGGTATCTCTT	1404
Qy	441	SerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal	460
Db	1405	TCCAACGCGAGATGGTGGCTGGGAAGAATAAAGTTTGTATGGTTCACATTTGATGGTGTG	1464
Qy	461	ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu	480
Db	1465	ACTTCCATGATGATACACTCATCGACTCAGGTCGAAATTTACTGGCAATTACAATGAG	1524
Qy	481	TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu	500
Db	1525	TACTTTGGATATCTACTGATGTTGACGCTGTGCTATCAATGCTGGTGAACGATTGT	1584
Qy	501	IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr	520
Db	1585	ATTTCATGGCTATACCCGAGGCTATGTTGTCGGCGAAGATGTAGCGGGATGCCAGCT	1644
Qy	521	PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle	540
Db	1645	TTTTGCGTTCCTGCGAAGACGGTGGTGTGGTGTGTTGACTACCGCTACACAAGCGAGT	1704
Qy	541	AlaAspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIle	560
Db	1705	GCAGATAAATGGATGAGCTTCTTAAGAAGAGAGACGAGGACTGGCAGTTGGTGATATA	1764
Qy	561	ValHisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHis	580
Db	1765	ACTTTCACGCTTACCACAGGAGGTGGGAGAGAAAATGTGCTCTATGCAGAGATCAT	1824
Qy	581	AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetMetAspLysAspMetTyr	600
Db	1825	GATCAAGCCCTGTTGGACACAAAAGATAGCTTTCTGGCTAATGGATATAGGACATGAT	1884
Qy	601	AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis	620
Db	1885	GATTTTCATGGCGTTGATACAGAGCCACTCCGCGGTAGACCGGTGGGATGCTTTTACAC	1944
Qy	621	LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly	640
Db	1945	AAAATGATCCGCTCATTTACGATGGGATTTGGTGGGAAGGATACCTCAATTTTCATGGGA	2004
Qy	641	AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGlnHisLeuSerAsp	660
Db	2005	AACGAATTTGGACACCCAGAAATGATCGACTTCCCAAGGACCGACGACCTTCCCTGAT	2064

PT wheat and barley -

PS Example 1; Fig 1; 103pp; English.

XX

CC The present sequence encodes wheat starch branching enzyme 9,
 CC designated BE1a. The specification describes BE1b. BE1b is a
 CC type II starch branching enzyme (SBE). The BE1b nucleic acids may
 CC be used to genetically transform cereal plants such as wheat or
 CC barley and for altering their nutritional content by modulating
 CC the starch biosynthetic pathway to vary levels of amylopectin and/or
 CC amylose produced in the plant.

SQ Sequence 2726 BP; 726 A; 564 C; 701 G; 735 T; 0 other;

Alignment Scores:

Pred. No.:	2.62e-293	Length:	2726
Score:	3136.00	Matches:	577
Percent Similarity:	81.95%	Conservative:	86
Best Local Similarity:	71.32%	Mismatches:	98
Query Match:	70.24%	Indels:	48
DB:	22	Gaps:	6

US-10-056-454A-15_COPY_49_882 (1-834) x AAH78337 (1-2726)

QY 12 SerThrValAlaAlaSerGlyLysValLeuValProGlyThrGlnSerSerSer 31
 DB 127 GCGAGCTTCGGGTGTCGGCGGACCCCTC-----GGTGTGGCGCGCGCGCGGCG 180
 QY 32 SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr 51
 DB 181 GCGCAACCTGAGAAATACAGATACCTGAA----- 210
 QY 52 AspValAspSerSerThrMetGluHisAlaSerGlnLeuLysThrGluAsnAspVal 71
 DB 211 GACATCGAGGAGCAAAACGGCTGAA----- 234
 QY 72 GluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerLeuGln 91
 DB 235 -----GTAACATGACGGGGGCGACTGCAGAA----- 261
 QY 92 LeuGlnGluGlyGlyLysLeuGluSerLysThrLeuAsnThrSerGluGluThrIle 111
 DB 262 -----AACTTGAATCTTCAGAACCGACTCAAGCGCAATTGTGGAACAATC 306
 QY 112 IleAspGluSerAspArg---IleArgGlu-----ArgGlyIle 123
 DB 307 ACTGATGTGTAAACCAAGAGCTTAAGGAACCTAGTCGTGGGAGAAACCGCGAGTTGTC 366
 QY 124 ProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg 143
 DB 367 CCAAACACGAGAGATGGCAGAAAATATACGAGATGACCCACGCTGAAAGATTTCGG 426
 QY 144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLeuArgGluAlaIleAspLysTyr 163
 DB 427 AGCCATCTTGACTACCGATACAGCAATACAGGAAATTCGTGCTGCTATTGACCAACAT 486
 QY 164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
 DB 487 GAAGGTGGATGGAGCAATTTCTCGTGTATGAAGAGCTTGAATTCACCGCAGTGTCT 546
 QY 184 ThrGlyIleThrTyrArgGluThrAlaLeuGlyAlaGlnSerAlaLeuIleGlyAsp 203
 DB 547 GAAGGTATCACTTACCGAGAAATGGCTCTGGAGCGCAATTCGAGCAATTAGTAGTGAC 606
 QY 204 PheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 223
 DB 607 TTCACAAATGGAAATCCGATGACAGATACATGACAGAGATGATTGTTGGGAG 666
 QY 224 IlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgVallys 243
 DB 667 ATTTCTCTCCCTAACAAATGCTGATGGATCCCGACTATTCTCTGATGCTCAGGTGAAG 726
 QY 244 IleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSer 263

DB 727 ATACGGATGGATCTCACTCTGGTGAAGGATCAATTCTCTGGATCAAGTCTCT 786
 QY 264 LeuGlnLeuProAspGluLeuProTyrAsnGlyIleHisTyrAspProGluGluGlu 283
 DB 787 GTGCGAGCTCCAGGTGAATACCATTCATGCGCATATATATGATCCACCTGAAGAGG 846
 QY 284 ArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSer 303
 DB 847 AAGTATGCTTCCACATCTCAACCTAAACAGCAGACACTGAGGATTTATGAATCA 906
 QY 304 HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu 323
 DB 907 CACATTGGAATGAGCAGCCCAAGAGATTAATCAATGCTTAATTTAGGATGAG 966
 QY 324 ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 343
 DB 967 GTGCTGCCAAGAATTAAGGCTTGATACAATGCAATGCAATGCAATGCAATGCAATG 1026
 QY 344 HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArg 363
 DB 1027 CATTCATCTATGCGAGCTTTGGGTACCATGTTACTAATTTTTCACCAAGTAGCCGT 1086
 QY 364 PheGlyThrProAspAspLeuLysSerLeuLysAlaHisGluLeuGlyIleVal 383
 DB 1087 TTTGGAACCTCCAGAGGACTTAAATCCCTGATCATAGACACATGAGCTTGGTTGGCTT 1146
 QY 384 ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 403
 DB 1147 GTTCTTATGGATATGTTTCATAGTCAATCAATAATATACCTTGAGCGCTTGATGGT 1206
 QY 404 PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrp 423
 DB 1207 TCGATGCGACTGATACACATTTCTCCAGGCTCCACGTCGATCATGATGATGATGG 1266
 QY 424 AspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuSerAsnAla 443
 DB 1267 GATTCGTCTATTCAACTATGGAGTGGAGATTTGAGATTCCTTACTGTCAACGCG 1326
 QY 444 ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet 463
 DB 1327 AGATGGTGGCTTGAAGAATATAAGTTTGTGATGGATTTGATGGGGTACCTCATG 1386
 QY 464 MetTyrIleHisHisGlyLeuSerValGlyPheThrClyAsnTyrGluGluTyrPheGly 483
 DB 1387 ATGTATATCACCATGGATTACAAATGACATTTACTGGGAATATGCGGAGTATTTGGA 1446
 QY 484 LeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGly 503
 DB 1447 TTTGCTACTGATGTTGATGGGTAGTTTACTTGTATGCTGTGTCAACGATCTAATCAAGA 1506
 QY 504 LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle 523
 DB 1507 CTTATCTCCGATGCTGATCCCATGTTGAGAGATGTCAGTGAATGCCACATTTGCATC 1566
 QY 524 ProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys 543
 DB 1567 CCGTGTCCAGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1626
 QY 544 ArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
 DB 1627 TGGATTGAACCTCTCAAGCAAAAGTCAACCAATCTTGGAAAAATGGGTGATATTGTGCACACC 1686
 QY 564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
 DB 1687 CTAACAAATAGAAGGTGGCTTGAAGATGCTGAATATGCAAGAAAGTCATGATCAACA 1746
 QY 584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
 DB 1747 CTACTTGGTGACAGACTATTGCAATCTGGTTGATGATGATGATGATGATGATGATGAT 1806
 QY 604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623

Mon Jul 7 12:40:56 2003

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Db      1807 GCTCTGGATAGGCTTCAACTCTCGCATTTGATCGGTGGCATAGCATTAATAAATGATC 1866
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QY      684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp 703
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QY      704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db      2107 AATATATGGGTTTATGACATCTGACACCAAGAGTATGTTTTCAGTTCACACTCCACTGGAGCAATAG 2166
QY      724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db      2167 GTGATCACTTCGAAGAGAGAGATTGGTATTTGTTTCACTTCCACTGGAGCAATAG 2226
QY      744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrIlyValAlaLeuAspSer 763
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QY      764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
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QY      784 GluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCysLysThrAla 803
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Db      2407 GTCGTGTATGCCCTTACAGAGTAAGAA 2433

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Search completed: July 6, 2003, 03:15:45
Job time : 646 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: July 6, 2003, 02:55:51 ; Search time 100 seconds
(without alignments)

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Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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- 6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4320	96.8	3074	4	US-09-087-277-1	Sequence 1, Appli
2	4320	96.8	3074	4	US-09-658-499-1	Sequence 1, Appli
3	3026.5	67.8	2665	4	US-09-257-894-1	Sequence 1, Appli
4	3021.5	67.7	2725	3	US-08-941-445A-14	Sequence 14, Appli
5	2676.5	59.9	2087	4	US-09-257-894-9	Sequence 9, Appli
6	2669.5	59.8	2165	4	US-09-257-894-8	Sequence 8, Appli
7	2462	55.1	1393	4	US-09-087-277-3	Sequence 3, Appli
8	2462	55.1	1393	4	US-09-658-499-3	Sequence 3, Appli
9	2165	48.5	3128	3	US-08-716-449-1	Sequence 1, Appli
10	2107	47.2	2565	3	US-09-257-894-24	Sequence 24, Appli
11	2107	47.2	2763	3	US-08-941-445A-16	Sequence 16, Appli
12	2104	47.1	2487	4	US-09-257-894-19	Sequence 19, Appli

13	2104	47.1	2772	4	US-09-257-894-12	Sequence 12, Appli
14	2098.5	47.0	2909	4	US-08-104-158-1	Sequence 1, Appli
15	1699.5	38.1	1809	4	US-09-257-894-25	Sequence 25, Appli
16	1696.5	38.0	1855	4	US-09-257-894-20	Sequence 20, Appli
17	1524.5	34.1	11478	3	US-08-981-803-29	Sequence 29, Appli
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19	1514.5	33.9	5402	4	US-09-221-017B-194	Sequence 194, Appli
20	522.5	11.7	2426	4	US-08-528-0260-3	Sequence 3, Appli
21	516.5	11.6	4411529	4	US-09-103-840A-1	Sequence 1, Appli
22	507.5	11.4	4403765	4	US-09-103-840A-2	Sequence 2, Appli
23	455.5	10.2	11384	4	US-08-961-527-45	Sequence 45, Appli
24	261.5	5.9	1680	4	US-09-242-690A-14	Sequence 14, Appli
25	261.5	5.9	2691	4	US-09-298-924-5	Sequence 5, Appli
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29	233	5.2	1791	1	US-08-607-321-3	Sequence 3, Appli
30	233	5.2	1791	2	US-08-961-240-3	Sequence 3, Appli
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35	233	5.2	2056	2	US-08-605-501-13	Sequence 13, Appli
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ALIGNMENTS

RESULT 1

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; Sequence 1, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: beII gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
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; LOCATION: (333)..(2825)
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
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QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLeuArgGluAlaIle 160
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QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
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QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysProLysSerLeuArgIle 300
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; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
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; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
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; ORGANISM: Unknown
; FEATURE:
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; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
; US-09-658-499-1
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Alignment Scores:

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Best Local Similarity:	97.36%	Mismatches:	13
Query Match:	96.75%	Indels:	4
DB:	4	Gaps:	1

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Db	393	CTTGTGCTGGAAACCCAGAGTAGCTCCTCATCTCAACAGACCAATTTGAGTTCACT	452
QY	41	GluThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHis	60
Db	453	GAGACATCTCCAGAAATATCCCGACGATCAACTGATGATAGATTCAACAATGGAACAC	512

QY	61	AlaSerGlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySer	80	QY	421	TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu	440
DB	513	GCTAGGCAGATTAAACTGAGAACGATGACGTTGAGCGCTCAAGTGATCTTACAGGAAGT	572	DB	1593	TGGATGTGGGATTCGGGCTCTTAACTATGSAAACTGGAGGTACTTAGGTATCTTCTC	1652
QY	81	ValGluGluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyGlyLysLeuGluGlu	100	QY	441	SerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal	460
DB	573	GTTGAAGAGCTGGGATTTTGCTTCATCACTACAACTACAAAGAGTGGTAAACTGGAGGAG	632	DB	1653	TCAATGGCAGATGGTGGTGGATGAGTTCAAATTTGATGGATTTAGATTTGATGGTGG	1712
QY	101	SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu	120	QY	461	ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu	480
DB	633	TCTRAACATTAATACTTCGAAGAGACAATATTGATCAATCTGATAGGATCAGAGAG	692	DB	1713	ACATCAATGATGATPACTCACACCGATATCGTGGGATTCACCTGGGAACCTACGAGAA	1772
QY	121	ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr	140	QY	481	TyrPheGlyLeuAlaThrAspValAspAlaValTyrLeuMetLeuValAsnAspLeu	500
DB	693	AGGGCATCCCTCCACCTGGGCTTGGTCAGAGATTTATGAATAAGACCCCTTTTGACA	752	DB	1773	TACTTTGGACTCGCAACTCATGTCGATGCTGTGTGTATCTGATGCTGTGTCACCACTCT	1832
QY	141	AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle	160	QY	501	IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr	520
DB	753	AACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAGAACTCAGGGAGGCAATT	812	DB	1833	ATTCATGGGCTTTTCCAGATGCAATACCATTTGGTGAAGATTTAGCGGAATGCCGACA	1892
QY	161	AspTyrGlyGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr	180	QY	521	PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle	540
DB	813	GACAAGTATGAGGGTGTGGAGCTTTTCTCGTGGTTATGAATAATGGGTTTCACT	872	DB	1893	TTTTNTATTCGGCTTCAAGATGGGCTGTGGCTTTGACTATCGGCTGCATATGGCAATT	1952
QY	181	ArgSerAlaThrGlyIleThrTyrArgGluThrPalaLeuGlyAlaGlnSerAlaLeu	200	QY	541	AlaAspLysArgIleGluLeuLeuLysLysLysArgAspGluAspTyrArgValGlyAspIle	560
DB	873	CGTAGTGTACAGGTATCACCTTACCGTGAGTGGGCTCCGTGGCCACGTCACGTCGCCCTC	932	DB	1953	GCTGATAAATGGATTGAGTTGCTCAAGAACCGGATGAGGATGGAGAGTGGGTATATT	2012
QY	201	IleGlyAspPheAsnAspTyrAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly	220	QY	561	ValHisThrLeuThrAsnArgTyrTrpSerGluLysCysValSerTyrArgLysHis	580
DB	933	ATTGGAGATTTCACAAATTGGACGCAATGCTGACATTTATGACTCGGAATGAATTTGGT	992	DB	2013	GTTTCATACACTGACAATAGAGATGGTCGGAAGAGTGTTCATACGCTGAAAGTCAT	2072
QY	221	ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer	240	QY	581	AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr	600
DB	993	GTCGGGAGATTTTCTGCCAAATAATGTGGATGTTCTCTCCATTCCTCATGGGCTCC	1052	DB	2073	GATCAAGCTCTAGTCGGTGATAAACTATAGCATTTCTGGCTGATGGAGAAGGATATGAT	2132
QY	241	ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle	260	QY	601	AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis	620
DB	1053	AGAGTGAAGATACGATGACACTCCATCAGGTGGTAAAGATTCCATTCCTCGTGGATC	1112	DB	2133	GATTTATGGCTCTGATAGACCTCAACATCATTAATAGATCGTGGATAGCATTTGCCAC	2192
QY	261	AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro	280	QY	621	LysMetIleArgLeuValThrMetGlyLeuGlyGlyGlyTyrLeuAsnPheMetGly	640
DB	1113	AACTACTCTTTACAGCTTCTGATGAATTCATATAATGGAATATATTATGATCCACCC	1172	DB	2193	AAAGATGATAGGCTTGTAACATGTTGGATTAGGAGGAGAAGGATACCTAAATTTTCATGGGA	2252
QY	281	GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle	300	QY	641	AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp	660
DB	1173	GAAAGAGAGGTATATCTTCCAAACACCCAGCCCAAGAAACCAAGTCGCTGAGAATA	1232	DB	2253	AATGAATTCGGCCACCTCGAGTGGATTGATTTCCCTAGGGCTGAACACACCTCTCTCAT	2312
QY	301	TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe	320	QY	661	GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu	680
DB	1233	TATGAATCATATTTGGAAGAGTATGTCGGAGCCCTAAATTAACCTCATACGTGAATTTT	1292	DB	2313	GGCTCAGTAATTCGGGAAACCAATTCAGTTATGATAAATGACACGAGGATTTGACCTG	2372
QY	321	ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla	340	QY	681	GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgPrometGlnTyr	700
DB	1293	AGAGATGAGTTCTTCTCGCATAAAAAGCTTGGGTACAAATGCGGTGCAAAATATGGCT	1352	DB	2373	GGAGATCGCAGAAATATTAAGATACCGTGGGTTCAGAAATTTGACCGGCTATGACGAT	2432
QY	341	IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaPro	360	QY	701	LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu	720
DB	1353	ATTCAAGAGCATTTCTTATTATGCTAGTTTGGTTATCATGCTCAAAATTTTNGCACCA	1412	DB	2433	CTTCAAGATAAATATGATTTTATGACTTCAGAACACCATGTTTCATATCAGAAAGAGTAA	2492
QY	361	SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu	380	QY	721	GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp	740
DB	1413	AGCAGCGCTTTTGGAAACCCCGACGACCTTAAGTCTTGTGATGATAAAGCTCATGAGCTA	1472	DB	2493	GGAGATAGGATGATGTATTGAAAAAGGAAACCTAGTTTGTGCTTTAATTTTCACTGG	2552
QY	381	GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly	400	QY	741	ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla	760
DB	1473	GGAATTTCTTCTCATGGACATTTGTTACAGCCATGCATCAAAATAATACTTTAGATGGA	1532	DB	2553	ACAAAAGCTATTTCAGACTATCGCATAGGCTGCCTGAAGCTGGAATAACAGGTTGCC	2612
QY	401	LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHis	420	QY	761	LeuAspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGlnTyr	780
DB	1533	CTGAACATGTTTGACGGCACAGATGTTGTTACTTTCACCTGAGCTCGTGGTTATCAT	1592	DB	2613	TTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGATCATTAATCCCGAATAT	2672
DB				DB	781	PheThrPheGluGlyTyrTyrAspArgProArgSerIleMetValTyrAlaProCys	800

Db 2673 TTCACCTTGAAGGATGGTATGATGATCGTCTGCTCAATTATGCTGATGACCTAGT 2732
QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
Db 2733 AGACACAGTGGTCTAGTACCTAGTACAAA-----GAAGAAGAAGAA 2780

QY 821 GluGluValAlaAlaValGluGluValValValValValValValValVal 834
Db 2781 GAAGAAGTACAGTACGTAGTAGAGAGTAGTAGTAGAGAGAA 2822

RESULT 3

US-09-257-894-1
; Sequence 1, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Version 7.0a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/257,894

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/091,052

FILING DATE: JUNE 10, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Majarian, William R.

REGISTRATION NUMBER: 41,173

REFERENCE/DOCKET NUMBER: BB-1066-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-992-4926

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2665 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 79..2476

US-09-257-894-1

Alignment Scores:
Pred. No.: 0 Length: 2665
Score: 3026.50 Matches: 553
Percent Similarity: 83.85% Conservative: 75
Best Local Similarity: 73.83% Mismatches: 100
Query Match: 67.78% Indels: 21
DB: 4 Gaps: 3

US-10-056-454a-15_COPY_49_882 (1-834) x US-09-257-894-1 (1-2665)

QY

67 GluAsnAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86

Db 277 GAGATGATGCGCTCGCATCAAGGGCTGAC----- 306
QY 87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db 307 -----TCGGCTCAATTCCAGTCG-----GATGAACCTGGAGGTACACGACATT 348
QY 107 SerGluGluThr-----IleLeuAspGluSerAspArgIleArgGluArg 121
Db 349 TCTGAAGAGACACAGCTGCGGTGCTGGTCTGCTCAAGCTTCAAGCTTCAAGAGTTCGA 408
QY 122 GlyLeuProProGlyLeuGlyGlnLysIleTyrGluLeuAspProLeuLeuThrAsn 141
Db 409 GTGTCCTCCCAAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 468
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaLeuAsp 161
Db 469 TATAAGTACCATCTTGAGTATCGGTACAGCTCTATAGAAGATCCGTTTCAGACATTGAT 528
QY 162 LysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 529 GAACATGAAGGAGGCTTGAAGCCTCTCCCGTAGTTATGAGAACTTTGGATTAAAGCC 589
QY 182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaLeuLeu 201
Db 589 AGCGCGGAAGGTATCATCATATCGAAGATGGCTCTCGAGCATTTTCTCGAGCATTTGGT 648
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 649 GGTGACTTCAACAACTGGGATCCAAATGAGATCGTATGAGCAAAATGAGTTGGTGT 708
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 709 TGGGAAATTTTCTGCTAACTAATGAGATGGTACATCACTATCTCTCATGATCTCGT 768
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db 769 GTAAAGTGAGATGGATCTCCATCAGGATTAAGGATTCATATCCAGCTGGATCAAG 828
QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db 829 TACTCAGTCAGGCCCCAGGAGAAATACCATATGATGGGATTTATTATGATCTCTCTGAA 888
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db 889 GAGGTAAAGTATGTGTTCAGGATCGCAACCTTAAACGACCAAAATCATTCGCGATATAT 948
QY 302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db 949 GAACACATGTCGGAATGAGTAGCCCGGAACCGAAGATAAGACATATGTAACCTTAGG 1008
QY 322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db 1009 GATGAAGTCTCCCAAGATAAAATAAATGATGATCAATGCGATGCAAAATAATGCAATC 1068
QY 342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSer 361
Db 1069 CAAGAGCACTCATATTATGGAAGCTTTGGATACCATGTAACATAATTTTTCGCGCACT 1128
QY 362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db 1129 AGTCCTTTTGGTACCCAGAGATTTGAAGTCTTTGATTGATAGACATGAGCATGAGCTTGT 1188
QY 382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db 1189 TTGCTAGTTTCATGATGTTGGTTCATAGTATGATGATGATGATGATGATGATGATGAT 1248
QY 402 AsnMetPheAspCysThrAspSerCystTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db 1249 AATGGTTTGTGATGGTACAGATACACATTACITTCACAGTGGTCCAGTGGCATCCTGG 1308
QY 422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441

Db 1309 ATGTGGGATTCCTCCCTATTTAACTATGCGGAAGTTTAAAGATTCTTCCTCC 1368
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Db 1369 AATGCTAGATGGTGGCTGAGGAATATAAGTTTGTATGGTTTCCGTTTGTATGGTGGTACC 1428
Qy 462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db 1429 TCCATGATGATACACTCCACCGGATTAACAATACATTTACGGGAAGCTTCAATGAGTAT 1488
Qy 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db 1489 TTTGGCTTGGCCACCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1548
Qy 502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db 1549 CATGGACTTATCTCGAGGCTTAACCATTTGGTGAAGATGTAGTGAATGCTACATTT 1608
Qy 522 CysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db 1609 GCCCTTCCTGTTCACGATGGTGGGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1668
Qy 542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
Db 1669 GACAATGGATGACCTTCTCAAGCAAGTGTGAAGTGTGAAGTGTGAAGTGTGAAGTGT 1728
Qy 562 HisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db 1729 CACACACTGACAAATAGGAGTGGTGTAGAGAGTGTGTAACTTATGCTGAAGTGTATGAT 1788
Qy 582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db 1789 CAAGCATTAGTGGCGACAGACTATTCGCTTTGGTGTGTGTGTGTGTGTGTGTGTGTGT 1848
Qy 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db 1849 TTTATGGCCCTCGATAGACTTCAACTCTACCATTTGATCGTGGGATGATACATAAG 1908
Qy 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 641
Db 1909 ATGATTAGACTTATCAATGGGTTTGGAGGAGGAGGCTTCTTAACTTTCATGCGAAT 1968
Qy 642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db 1969 GAGTTGGACATCTCGATGATAGATTTTCCAAAGAGTCCGCAAGACTTCCAAAGTGT 2028
Qy 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db 2029 AAGTTTATCCAGGAATAACAACAGTTATGACAAATGCTGCAAGATTTGACCTGGGT 2088
Qy 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db 2089 GATGACAGACTATCTTAGTATCATGTTGATGCAAGAGTTTGTATGAGCAATGCAACATCT 2148
Qy 702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
Db 2149 GAGCAAAATATGAATCATGACATCTGATCACCAGTATATTTCCCGGAAACATGAGGAG 2208
Qy 722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
Db 2209 GATAAGGTGATTGTGTGCAAAAGGAGATTTGGTATTTGTGTTCACCTTCCACTGCAAC 2268
Qy 742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeu 761
Db 2269 AACAGCTATTTGACATACCTGATTTGGTTGCGAAAGCCGTGGGTGTATAGGTGGTCTTG 2328
Qy 762 AspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
Db 2329 GACTCCGACGCTGGACTATTTGGTGGATTTAGCAGGATCCATCCGACGCGGACACTTC 2388
Qy 782 ThrPheGluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLys 801
Db 2389 ACCGCGGACTGTTCGCAATGATAATAGGCCATATTCCTCCGTTTATACCAACGACAGA

Qy 802 ThrAlaValValTyrAlaLeuValAsp 810
Db 2449 ACATGTGCTGCTATGCTCCAGTGAG 2475
RESULT 4
US-08-941-445A-14
; Sequence 14, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/941,445A
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P.
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2725 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 91..264
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 265..2487
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 91..2490
; US-08-941-445A-14
Alignment Scores:
Pred. No.: 0
Score: 3021.50
Percent Similarity: 83.71%
Best Local Similarity: 73.70%
Query Match: 67.67%
DB: 3
Length: 2725
Matches: 552
Conservative: 75
Mismatches: 101
Indels: 21
Gaps: 3
US-10-056-454A-15_COPY_49_882 (1-834) x US-08-941-445A-14 (1-2725)
Qy 67 GluAsnAspValGluProSerSerAspLeuThrGlySerValGluLeuAspPhe 86
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Db 289 GAGATGATGGCTCGCATCAAGGGCTGAC----- 318
QY 87 AlaSerSerLeuGlnLeuGlnGluGlyGlyLysLeuGluSerLysThrLeuAsnThr 106
Db 319 -----TCGGCTCAATTCAGTGC-----GATGAATGGAGGTACCAGACATT 360
QY 107 SerGluGluThr-----IleIleAspGluSerAspArgIleArgGluArg 121
Db 361 TCTGAAGAGACACAGCTGGGTGCTGGTGGCTGATGCTCAAGCCCTTGAACAGAGTCTGA 420
QY 122 GlyIleProProGluGlyLeuGlyGlnLysIleTyrgluLeuAspProLeuLeuThrAsn 141
Db 421 GTGGTCCCCCAACCAAGCATGACAAATAATTCAGATTGACCCCATGTTGCAAGGC 480
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 481 TATAAGTACCATTCTTGAGTATCGGTACAGCCCTATAGAAATCCGTTTCAGACATTGAT 540
QY 162 LysTyrGluGlyGlyLeuAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 541 GAACATGAAGAGGGCTTGAAGCCTTCTCCCGTAGTTATGAGAAGTTTGGATTAAATGCC 600
QY 182 SerAlaThrGlyIleThrTyrArgGluTyrAlaLeuGlyAlaSerAlaLeuIle 201
Db 601 AGCGGGAAGGTATCACATATCGAATGCGGCTCTGGAGCATTTTCTGCACCATTTGGTG 660
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 661 GGTGACGTCAACAAGTGGATCCAAATGCAGATCGTATCAGCAAAATGAGTTGGTGT 720
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 721 TGGGAATTTTCTGCCTAACATGCAGATGCATGATCATCACTATTCTCATGGATCTCGT 780
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
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QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db 841 TACTCAGTGCAGGCCCCAGGAGAAATACCATATGATGGATTATATGATCCTCTGTAA 900
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerIleArgIleTyr 301
Db 901 GAGGTAAAGTATGTCTTCAGGCATCGCAACCTAAACGACCAAAATCATCTCGGATAT 960
QY 302 GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db 961 GAACACATGTCGGNATGAGTAGCCCGAACCGAAGATAACACATATGTAACCTTTAGG 1020
QY 322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGluIleMetAlaIle 341
Db 1021 GATGAAGTCTCCCAAGAAATAAAAAAATCGATACATGCGATGCAATATGCGCAATC 1080
QY 342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSer 361
Db 1081 CAAGAGCATTATATGGAAGCTTTGGATACCAATGTAATATTTTGGGCCAAGT 1140
QY 362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db 1141 AGTCGTTTTGTACCCAGAGATTGAAGTCTTTGATGATAGACACATCAGCTTGGT 1200
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Db 1201 TTGTAGTTCTCATGGATGTGTTATGATCAATGCTCAAGTAAATACTCTCGATGGGTG 1260
QY 402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
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Db 1321 ATGTGGGATCTCGCCATTAACTATGGGAACCTGGGAAGTTTTTAAAGATTTCTCTCTCC 1380

QY 442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db 1381 AATGCTAGATGGTGGCTCGAGGAATATAAGTTTCATGGTTCCGTTTGTATGGTGTGACC 1440
QY 462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db 1441 TCCATGATGATACATCCACCGGATTACAAGTAACTATTACGGGGAACTTCAATGAGTAT 1500
QY 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db 1501 TTTGGCTTTGCCACCGATGATAGTCAGTGGTTTACTTGTATGCTGGTAAATGATCTAAT 1560
QY 502 HisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db 1561 CATGGACTTATCTCCTAGGCTGTAACCATTTGGTGAAGATGTTAGTGAATGCCATACATT 1620
QY 522 CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db 1621 GCCCTTCTCTCAGATGGTGGGTAGGTTTGTACTATCGATCGATGATGGTGTGGCT 1680
QY 542 AspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal 561
Db 1681 GACAAATGGATTGACCTTCTCAAGCAAGTGTGAACCTTGGAGATGGGTGATATGTG 1740
QY 562 HisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db 1741 CACACTGACAAATAGGAGGTGGTTAGCAAGTGTAACTTATGCTGAAAGTCATGAT 1800
QY 582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db 1801 CAAGCATTAGTTCGGCAGCAAGACTATTGGCTTTTGGTTGATGACAAGATATGTATGAT 1860
QY 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db 1861 TTCATGGCCCTCGATAGACTTCAACTCTACCATTGATCGGGGATAGCATTTACATAG 1920
QY 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn 641
Db 1921 ATGATTTAGACTTATCACAAATGGTTTATGAGGAGAGGGCTATCTTAATTTATGGGAAT 1980
QY 642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db 1981 GAGTTTGGACATCCCTGAATGGATAGATTTTCAAGAGAGTCCGCAAGACTTCCAAGTGT 2040
QY 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGly 681
Db 2041 AAGTTTATCCAGGGAATAACAACAGATTATGACAAATGTCGTCGAAGATTTGACCTGGGT 2100
QY 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrIleu 701
Db 2101 GATGAGACTATCTTTAGGTATCATGATGCAAGAGTTTGTATGATGCAAGTCAACATCTT 2160
QY 702 GluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGly 721
Db 2161 GAGCAAAATATGATTCATGACATCTGATCACCAGTATTTCCCGGAAACATCAGGAG 2220
QY 722 AspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThr 741
Db 2221 GATAAGGTGATTGTCTCGAAAAGGAGATTTGGTATTTTGTCTCACTTCCACGCGAAC 2280
QY 742 LysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysValAlaLeu 761
Db 2281 AACAGCTATTTTGACTACCGTATTGGTTGTCGAAAGCCCTGGGTCTATAAGGTGGTCTTG 2340
QY 762 AspSerAspAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyrPhe 781
Db 2341 GACTCCGAGCGTGGACATTTTGGTGGATTTAGCAGGATCCATCAGCGAGCGGACATTC 2400
QY 782 ThrPheGluGlyTyrTrpTyrAspArgProArgSerIleMetValTyrAlaProCysLys 801
Db 2401 ACCGCCGACTCTCTCGCATGATAATAGGCATATTCATCTCTCGGTTTATACCAAGCAGA 2460

QY 802 ThrAlaValValTyrAlaLeuValAsp 810
Db 2461 ACATGTGCTGCTATGCTCCAGTGGAG 2487

RESULT 5

US-09-257-894-9
Sequence 9, Application US/09257894

Patent No. 6376749

GENERAL INFORMATION:

APPLICANT: Broglie, Karen E.

APPLICANT: Klein, Theodore M.

APPLICANT: Hubbard, Natalie L.

APPLICANT: Lightner, Jonathan E.

TITLE OF INVENTION: No. 6376749el Starches via Modification of

TITLE OF INVENTION: Expression of Starch Biosynthesis

TITLE OF INVENTION: Enzyme Genes

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. du Pont de Nemours and Company

STREET: 1007 Market Street

CITY: Wilmington

STATE: Delaware

COUNTRY: USA

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Microsoft Windows 95

SOFTWARE: Version 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/257,894

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/091,052

FILING DATE: JUNE 10, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Majarian, William R.

REGISTRATION NUMBER: 41,173

REFERENCE/DOCKET NUMBER: BB-1066-A

TELEPHONE: 302-992-4926

TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 2087 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

MOLECULE TYPE: DNA (genomic)

US-09-257-894-9

Alignment Scores:

Pred. No.: 2087

Score: 2676.50

Percent Similarity: 85.12%

Best Local Similarity: 75.19%

Query Match: 59.94%

DB: 4

Length: 2087

Matches: 485

Conservative: 64

Mismatches: 75

Indels: 21

Gaps: 3

US-10-056-454a-15_COPY_49_882 (1-834) x US-09-257-894-9 (1-2087)

QY 67 GluAsnAspValGluProSerAspLeuThrGlySerValGluLeuAspPhe 86

Db 199 GAGAAAGATGGCTCCATCAGGGGTGAC----- 228

QY 87 AlaSerSerLeuGlnLeuGlnGlyLysLeuGluSerLysThrLeuAsnThr 106

Db 229 -----TCGGCTCAATTCAGTCG-----GATGAAGTGGAGGTACCAGACATT 270

QY 107 SerGluGluThr-----IleIleAspGluSerAspArgIleArgGluArg 121

Db 271 TCTGAAGAGACAAACGTCGGTGTGCTGATGCTCAAGCCTTGACAGAGTTCGA 330

QY 122 GlyIleProProGlyLeuGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db 331 GTGTCCCCCAACCAAGCGATGGACAAAATAATCCAGATTGACCCCATGTTCAGGCG 390
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 391 TATAAGTACCATCTGTAGTATCGGTACAGCCTCTATAGAGAATCCGTTCAGACATGAT 450
QY 162 LysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 451 GAACATGAAGGAGGCTTGGAAAGCCCTCTCCCGTAGTTATGAGAAAGTTTGGATTATGCC 510
QY 182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 201
Db 511 AGCGCGGAAGGTATCACATATCGAGAATGGCTCTCGGAGCATTTCTTCAGCATTTGGTG 570
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 571 GGTCACTTCAACACTGGGATCCAAATCGATCATGATGAGAAAATGAGTTTGTGT 630
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 631 TGGGAAATTTTCTGCCTAACANTCCAGATGTATCATCACCTATTCTCATGATCTGT 690
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpLeu 261
Db 691 GTAAAGGTGAGATGATCTCCATCAGGATAAAGGATTCATTCACGCTGATCAAG 750
QY 262 TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGlu 281
Db 751 TACTCAGTCAGGCCCCAGGAAATACCATATGATGGGATTTATATGATCTCTGAA 810
QY 282 GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr 301
Db 811 GAGTAAAGTATGTGTTCAGCATCGCAACCTAAACGACCAAAATCATTCGGATAT 870
QY 302 GluSerHisIleGlyMetSerProGluProLysIleAsnSerTyrValAsnPheArg 321
Db 871 GAAACACATGTGGATGAGTACGCGGAACCGAAGATAACACATATATAACTTTTGG 930
QY 322 AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle 341
Db 931 GATGAGTCTCCCAAGAAATAAATACTTGATACATGATGATGATGATGATGATGATG 990
QY 342 GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSer 361
Db 991 CAAGACACTCATATATGGAAGCTTTGGATACCATGTAACATAATTTTTTGGCCAA 1050
QY 362 SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly 381
Db 1051 AGTCGTTTGGTACCCACCAAGATTTTGAAGTCTTTGATTGATGATGATGATGATGAT 1110
QY 382 IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu 401
Db 1111 TTGCTAGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1170
QY 402 AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp 421
Db 1171 AATGGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1230
QY 422 MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer 441
Db 1231 ATCTGGGATTTCTGCCTATTTAACTATGGGAATGGGAAGTTTATAGATTCTTCTCC 1290
QY 442 AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr 461
Db 1291 AATGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1350
QY 462 SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr 481
Db 1351 TCCATGATGTACACTCACCACGGATTACAAGTAAACATTTACGGGGAACCTTCAATG 1410


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QY 482 PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle 501
Db 1411 TTTGGCTTTGCCACCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1470
QY 502 HisGlyLeuProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe 521
Db 1471 CATGGACTTATCTCCCTGAGGCTGATGATGATGATGATGATGATGATGATGATGAT 1530
QY 522 CysIleProValGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla 541
Db 1531 GCCCTCTCTGTCAGATGGTGGGTAGGTTTGGTATCTGATGATGATGATGATGATG 1590
QY 542 AspLysArgIleGluLeuLeuLysLysArgAspGluAspTyrArgValGlyAspIleVal 561
Db 1591 GACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1650
QY 562 HisThrLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAsp 581
Db 1651 CACACACTGACAAATAGGAGGTGGTGTAGAGAACTGTAACTATGCTGAAAGTCATGAT 1710
QY 582 GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp 601
Db 1711 CAAGCATAGTCGGCGCAAGACTATGCTGTTTGGTGTGATGCAAGGATGATGATGAT 1770
QY 602 PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLys 621
Db 1771 TTCATGGCCCTCGATAGACCTTCAACTCTCATCATGATGATGATGATGATGATGATG 1830
QY 622 MetIleArgLeuValThrMetGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 641
Db 1831 ATGATTAGACTATACAAATGGGTTTAGAGAGAGGCTATCTTAATTTTCATGGAAAT 1890
QY 642 GluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db 1891 GAGTTTGACATCTCGAATGATGATGATGATGATGATGATGATGATGATGATGATG 1950
QY 662 SerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGly 681
Db 1951 AAGTTTATCCAGGGAATAACAACAGTTATGACAAATGCTGTCGAAGATTGACCTGG 2010
QY 682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspProMetGlnTyrLeu 701
Db 2011 GATCGACACTATCTAGTATCATGATGATGATGATGATGATGATGATGATGATGATG 2070
QY 702 GluAspLysTyrGlu 706
Db 2071 GAGCAAAAATGAA 2085
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RESULT 6

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US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-257-894-8
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Alignment Scores:

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Pred. No.: 1,81e-288 Length: 2165
Score: 2669.50 Matches: 484
Percent Similarity: 84.96% Conservative: 64
Best Local Similarity: 75.04% Mismatches: 76
Query Match: 59.79% Indels: 21
DB: 4 Gaps: 3
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US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-8 (1-2165)

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QY 67 GluAsnAspAspValClnProSerSerAspLeuThrGlySerValGluGluLeuAspPhe 86
Db 1889 GAGATGATGGCTCCATCCATCAAGGGCTGAC-----1860
QY 87 AlaSerSerLeuGlnLeuGlnGluGlyLysLeuGluGluSerLysThrLeuAsnThr 106
Db 1859 -----TCGGCTCAATTCAGTCG-----GATGAACCTGAGGTACCAGACATT 1818
QY 107 SerGluGluThr-----11eIleAspGluSerAspArgIleArgGluArg 121
Db 1817 TCTGAAGACACAACTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1758
QY 122 GlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsn 141
Db 1757 GTGGTCCCCCAACCAAGCATGACAAATAATATCCAGATTGACCCCATGTTGCAAGC 1698
QY 142 TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAsp 161
Db 1697 TATAAGTACCATCTTGAGTATCGTACAGCCCTATAGAGAATAATCGTTTCAGACATTGAT 1638
QY 162 LysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg 181
Db 1637 GAACAATGAGGAGGCTTCGAGCCCTTCGCCGTAGTTATGAGAAGTTTGGATTATATGCC 1578
QY 182 SerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIle 201
Db 1577 AGCGGGAAGGTATCATATCGAATGGGCTCTCGGAGCATTTTCTGCAGCATTTGGTG 1518
QY 202 GlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyVal 221
Db 1517 GGTGACGTCAACACTGGGATCCAAATCGATATCGATATGAGCAAAATGAGTTTGGTGT 1458
QY 222 TrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg 241
Db 1457 TGGAAATTTTCTGCCTAAACATGACATGATGATGATGATGATGATGATGATGATG 1398
QY 242 ValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsn 261
Db 1397 GTAAAGGTGAAATGGATATCCATCAGGGATAAAGGATTCATTCAGCCTGGATCAAG 1338
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Qy	262	TyrSerLeuGlnIeuProAspGluIleProTyrAsnGlyIleHisTyrAspProProGlu	261
Db	1337	TACTCAATGCGCCAGGAGAAATACCATATGATGGGATTTATTAATGATCTCCTGAA	1278
Qy	282	GluGluArgTyrIlePheGlnHisProArgProLysProLysSerLeuArgIleTyr	301
Db	1277	GAGTAAGAATGTGTTTCAGCATGCCCACTTAACGCCACCAAAATCATTTCCGGATATAT	1218
Qy	302	GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg	321
Db	1217	GAACAACATGTCGAATGAGTACCGCGGAACCGAAGATAAACACATATGTAAACTTTAGG	1158
Qy	322	AspGluValIeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIle	341
Db	1157	GATGAAGTCCTCCCAAGATAAAAAAACTTTGGATACAACTCAGTGGCAAAATAATGGCAATC	1098
Qy	342	GlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSer	361
Db	1097	CAAGAGCACATCATATTAATGAAGCTTTGGGATACCATTAACCTAAATTTTTTTGGCCCAAGT	1038
Qy	362	SerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGly	381
Db	1037	AGTCGTTTTTGGTACCCAGGAAGATTGAAGTCTTTTGATTGATAGAGCACATGAGCTTGGT	978
Qy	382	IleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeu	401
Db	977	TTGCTAGTTCTCATGGATGGTTCATAGTCATGCGGTCAAGTAATACCTCTGGATGGGTTG	918
Qy	402	AsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrp	421
Db	917	AATGGTTTTTGGTGTACAGATACACATTAATTTTCACAGTGTCCAGTGGCCCACTCATGG	858
Qy	422	MetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSer	441
Db	857	ATGNGGATTTCTCGCCTATTAACTATGGGAAGTGGGAAGTTTAAAGATTCTCTCTCC	798
Qy	442	AsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThr	461
Db	797	AATGCTAGATGGTGGCTCGAGGAATATAAGTTTGATGTTTCCGTTTGTATGTTGTGACCC	738
Qy	462	SerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyr	481
Db	737	TCCATGATGTCACCTCACACGGATACAGTAACATTTACGGGGAACTTCAATGAGTAT	678
Qy	482	PheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIle	501
Db	677	TTTGGCTTTGCCACCGATGTAGATGCAGTGGTTTACTGTATGCTGGTAAATGATCTAATT	618
Qy	502	HisGlyIeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPhe	521
Db	617	CATGGACTTATCTGTAGGCTGTAAACATTGGTGAAGATGTTAGTGAATGCCCTACATTT	558
Qy	522	CysIleProValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAla	541
Db	557	GCCCTTCTCTGTACGATGTGGGGTAGGTTTGACTATCGGATGCATATGGCTGTGGCT	498
Qy	542	AspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleVal	561
Db	497	GACAAATGGATGACCTTCTCAAGCAAAAGTATGAACTTTGGAGATGGGTGATATGTG	438
Qy	562	HisThrLeuThrAsnArgTyrTrpSerGluLysCysValSerTyrAlaGluSerHisAsp	581
Db	437	CACACACTGACAAATAGAGGTGGTTAGAGAAAGTGTACTTATGCTGAAGATCATGAT	378
Qy	582	GlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAsp	601
Db	377	CAAGCATATAGTCGGCGCAAGACATATTCGGTTTTTGGTTGATGGACAAAGGATATGTATCAT	318
Qy	602	PheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaIleuHisLys	621
Db	317	TTCAATGCCCTCGATAGACCTTCAACTCCCTACCACTTCCTACCATGATCGTGGGATAGCATATACAAAG	258
Qy	622	MetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsn	641

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Db      257 ATGATTAGACTTATPACAAATGGGTTTAGGAGGAGGGCTATCTTAATTCATGGGAAT 198
Qy      642 GluPheGlyHisProGluTyrIleAspPheProArgAlaGluGlnHisLeuSerAspGly 661
Db      197 GAGTTTGGACATCCTGAATGATAGATTTCCTCCAGAGGTCGCGAAAGACATCCCAAGTGGT 138
Qy      662 ServallieProGlyAsnGlnPheSerTyrAspIysCysArgArgPheAspLeuGly 681
Db      137 AAGTTTATCCAGGGAATAACAACAGTTATGACAAATGCTGTCGAAGATTGACCTGGGT 78
Qy      682 AspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeu 701
Db      77 GATGACAGATCTCTAGGTATCATGGTATGCAAGAGTTTGATCAGGCAATGCCACATCTT 18
Qy      702 GluAspLysTyrGlu 706
Db      17 GAGCAAAAATATGAA 3

RESULT 7
US-09-087-277-3
; Sequence 3, Application US/09087277B
; Patent No. 6169226
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
; US-09-087-277-3

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Pred. No.: 1,44e-265 Length: 1393
Score: 2462.00 Matches: 454
Percent Similarity: 98.49% Conservative: 3
Best Local Similarity: 97.84% Mismatches: 7
Query Match: 55.14% Indels: 0
DB: 4 Gaps: 0

US-10-056-454a-15_COPY_49_882 (1-834) x US-09-087-277-3 (1-1393)

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DB 2 CWCACAAATAATGTGGATGCTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACGT 61
QY 246 MetAspThrProSerGlyValIysAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
DB 62 ATGGACATCCATCAGGTGTTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACAG 121
QY 266 LeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGluArgTyr 285
DB 122 CTTCTGTAGAAATCCATATATGAATATATATGATCCACCCGAGAGAGATAT 181
QY 286 IlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIle 305
DB 182 ATCTTCCACACCCCGGCAAGAAACCAAAAGTCGCTGAGATATATGAATCTCATATT 241
QY 306 GlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeu 325
DB 242 GGAATGAGTAGTCCCGAGGCTAAATTAATCTCATAGCTGAATTTTAGAGATGAAGTCTT 301
QY 326 ProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSer 345
DB 302 CCTCGCATAAAAAGCTTGGGTACAAATGGGTGCAAAATTTATGCTATTTCAAGAGCATTC 361
QY 346 TyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGly 365
DB 362 TATTTAGTGTAGTTTGGTTATCATGCTCAAAATTTTTCGACCAAGCAGCGGTTTGAA 421
QY 366 ThrProAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeu 385
DB 422 ACNCCCGAGCCTTAAGTCTTTGATGTATAAGCTCATGAGTAGGAATTTGTGTCTC 481
QY 386 MetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp 405
DB 482 ATGGACATTTTCACAGCCATCATCAATAATACCTTAGATGGAGTGAACATGTTGAC 541
QY 406 CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSer 425
DB 542 GCACAGATAGTGTACTTCTCCTGAGCTCGTGGTTATCATTTGGATGTGGGATTC 601
QY 426 ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrTyrLeuSerAsnAlaArgTrp 445
DB 602 CGCCTCTTTAATATGGAACCTGGAGGTACTTAGGTATCTTCTCAATGGAGATGG 661
QY 446 TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 465
DB 662 TGGTTGGATGATTTCAAAATTTGATGATTTAGATTTGATGGTGTGACATCAATGATGAT 721
QY 466 IleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla 485
DB 722 ACTCACCGGATATCGGTGGATTCATCTGGAACTACGAGGAATACCTTTGGACTCGCA 781
QY 486 ThrAspValAspAlaValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe 505
DB 782 ACTGATGTGATGCTGTGTATCTGATGCTGGTCAAGCATCTTATTCATGGGCTTTTC 841
QY 506 ProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 525
DB 842 CCAGATGCAATTAACCATTTGGTGAAGATGTTACGGGAATGCCGACATTTTNTATTCGGT 901
QY 526 GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspArgIle 545
DB 902 CAAGATGGGGGTGTGGCTTTGACTATCGCTGCATGCGCATATGCGCAATTCCTGATAAATGAT 961
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QY 546 GluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThr 565
DB 962 GAGTTGCTCAAGAAACGGGATGAGGATTTGGAGATGGGTGATATTTGTTCATACACTGACA 1021
QY 566 AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal 585
DB 1022 AATAGAGATGGTGGGAAAGTGTGTTTCATACGCTGAAAGTCAITCAAGCTCTAGTC 1081
QY 586 GlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeu 605
DB 1082 GGTGATAAACTATAGCAITTCCTGGCTGATGGACAGGATATGATGATTTTATGGCTCTG 1141
QY 606 AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeu 625
DB 1142 GATGACACCTCAACATCAITTAATAGATCGTGGGATGACATTCGACAGATGATAGGCTT 1201
QY 626 ValThrMetGlyLeuGlyGlyGluTyrLeuAsnPheMetGlyAsnGluPheGlyHis 645
DB 1202 GTAACCTATGGGATTAGAGAGAGAGGATCTAAATTTCAATGGAATGAAATTCGGCCAC 1261
QY 646 ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIlePro 665
DB 1262 CCTGAGTGGATTCATTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAGTAATTC 1321
QY 666 GlyAsnGluPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyr 685
DB 1322 GGAACCAATTCAGTTATGATAAATGCAGCGGAGATTTGACCTGGGAGATGAGAAATAT 1381
QY 686 LeuArgTyrArg 689
DB 1382 TTAAGATACCGT 1393
RESULT 8
US-09-658-499-3
: Sequence 3, Application US/09658499
: Patent No. 6469231
: GENERAL INFORMATION:
: APPLICANT: EK, Bo
: APPLICANT: KHOSMOODI, Jamshid
: APPLICANT: LARSSON, Clas-Tomas
: APPLICANT: LARSSON, Hakan
: APPLICANT: RASK, Lars
: TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
: FILE REFERENCE: 003300-486
: CURRENT APPLICATION NUMBER: US/09/658,499
: PRIOR FILING DATE: 2000-09-08
: PRIOR APPLICATION NUMBER: 09/087,277
: PRIOR FILING DATE: 1998-05-29
: PRIOR APPLICATION NUMBER: PCT/SE96/01558
: PRIOR FILING DATE: 1996-11-28
: PRIOR APPLICATION NUMBER: SE 9504272-7
: PRIOR FILING DATE: 1995-11-29
: PRIOR APPLICATION NUMBER: SE 9601506-0
: PRIOR FILING DATE: 1996-04-19
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 1393
: TYPE: DNA
: ORGANISM: Unknown
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: beII gene fragment
: OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
: OTHER INFORMATION: (potato)
: NAME/KEY: CDS
: LOCATION: (2)..(1393)
: NAME/KEY: misc.feature
: LOCATION: (424)..(1150)
: OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
: OTHER INFORMATION: C, G or T.
: NAME/KEY: misc.feature
: LOCATION: (422)..(424)
: OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
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NAME/KEY: misc.feature
LOCATION: (890)..(892)
OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
OTHER INFORMATION: or Phe.
NAME/KEY: misc.feature
LOCATION: (1148)..(1150)
OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-658-499-3

Alignment Scores:
Pred. No.: 1.44e-265 Length: 1393
Score: 2462.00 Matches: 454
Percent Similarity: 98.49% Conservative: 3
Best Local Similarity: 97.84% Mismatches: 7
Query Match: 55.14% Indels: 0
DB: 4 Gaps: 0

US-10-056-454a-15_copy_49_882 (1-834) x US-09-658-499-3 (1-1393)

QY 226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
DB 2 CTGCCAATAATGTGATGGTCTCTCTGCAATTCCTCATCTGGTCCAGAGTGAAGATCGT 61
QY 246 MetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGln 265
DB 62 ATGGACACTCCATCAGGTGTTAAGGATTCCTCTCTGCTGGATCAACTACTCTTTACAG 121
QY 266 LeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGluGluArgTyr 285
DB 122 CTCTCTGATGAATTCATATATGAATATATATATGATCCACCGAGAGAGAGTAT 181
QY 286 IlePheGlnHisProArgProLysProLysSerLeuArgIleTyrGluSerHisIle 305
DB 182 ATCTTCCAAACCCACGCGCAAGAAACCAAGTCTGCTGAGATATATGATCTATAT 241
QY 306 GlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeu 325
DB 242 GGATGAGTACTCGGAGCGCTAAATTAACATCATAGTGAATTTAGAGATGAAGTCTT 301
QY 326 ProArgIleLysLysLeuGlyTyrAsnAlaIleGlnIleMetAlaIleGlnHisSer 345
DB 302 CCTGCATATAAAAGCTGGGACAACTGCGGTGCAATATATGCTATCAAGAGCATTC 361
QY 346 TyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGly 365
DB 362 TATTATGCTACTTTTGGTTATCATGTCACAAATTTTTTNGCCACCAAGCAGCGTTTGA 421
QY 366 ThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeu 385
DB 422 ACNCCGACGACCTTAAGTCTTTGATTGATTAAGCTCATGAGCTAGGAATTTGTTCTC 481
QY 386 MetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAsp 405
DB 482 ATGGACATGTCACAGCGATGATCAATAATATCTTTAGTGGACTGAACATGTTGAC 541
QY 406 CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTyrMetTrpAspSer 425
DB 542 GGCACAGATAGTTGTTACTTTTCACTCTGGAGCTCGGTTATCATTTGGATGTTGGATTC 601
QY 426 ArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrp 445
DB 602 CGCTCTTTACTATGGAACATGGGAGTACTTAGGTATCTTCTCTCAATCGGAGATGG 661
QY 446 TrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMetTyr 465
DB 662 TGGTGGATGAGTTCAATTTGATGATTTAGATTTGATGGTGCACATCATGATGAT 721
QY 466 IleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAla 485
DB 722 ACTCACCGAGATATCGGTGGGATTCCTAGGAACTACGAGGAATATCTTTGAGCTCGCA 781
QY 486 ThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPhe 505

DB 782 ACTGATGTGGATGCTGTTCTGTATCTGTATCTGTGCTGGTCAAGCATCTTATTATCATGGCTTTTC 841
QY 506 ProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIleProVal 525
DB 842 CCAGATGCAATTAACCAATGTGTGAAGATGTAGCGAATGCCGACATTTTATTCCTCCGT 901
QY 526 GlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArgIle 545
DB 902 CAAGATGGGGTGTGGCTTTCATCATCGCTGCATATGCAATTCCTGATTAATGAT 961
QY 546 GluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThrLeuThr 565
DB 962 GAGTTGCTCAAGAAACGGATGAGGATTCGAGAGTGGTGCATATTTTCATACACATGACA 1021
QY 566 AsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAlaLeuVal 585
DB 1022 AATGAAGATGTGCGAAAGTGTGTTTCATCGCTGGAAGTCATGATCAAGCTCAGTTC 1081
QY 586 GlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeu 605
DB 1082 GGTGATAAACTATAGCATTCCTGGCTGATGGACAGGATATGATGATTTATGGCTCTG 1141
QY 606 AspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysKetIleArgLeu 625
DB 1142 GATAGACCTCAACATCATTAATAGATCGTGGGATAGCATTCGACAGATGATAGCTT 1201
QY 626 ValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPheGlyHis 645
DB 1202 GTRACTAUGGATAGGAGAGAGAGGTACCTTAATTTTCATGGGAATCAATTCGGCCAC 1261
QY 646 ProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerValIlePro 665
DB 1262 CCTGAGTGGATGATTCCTCCTAGGCGTGAACAACACCTCTCTGATGGCTCAGTAATCC 1321
QY 666 GlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyr 685
DB 1322 GAAACCAATTCAGTTATGATTAATGACAGCGAGATTTGACCTGGGAGATCGAATAT 1381
QY 686 LeuArgTyrArg 689
DB 1382 TTAAGATACCGT 1393

RESULT 9
US-08-716-449-1
Sequence 1, Application US/08716449
Patent No. 6103893
GENERAL INFORMATION:
APPLICANT: National Starch and Chemical Investment
APPLICANT: Holding Corporation
TITLE OF INVENTION: Method for Producing Altered Starch
TITLE OF INVENTION: from Potato Plants
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott & Aylen
STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower
CITY: Toronto
STATE: Canada M5K 1H6
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM 1.44 MB High Density Diskette
COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible)
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: Word 7.0 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/716.449
FILING DATE: FILED CONCURRENTLY HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00634
FILING DATE: 22.03.95
ATTORNEY/AGENT INFORMATION:
NAME: Anita E. Nador
REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 1552

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 368-2400

TELEFAX: (416) 363-7246

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3128 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE:

DESCRIPTION: cDNA encoding starch branching enzyme

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE:

ORIGINAL SOURCE: clone 1.2.1 and E2

ORGANISM: Solanum tuberosum

STRAIN: cv desiree

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE: mature tuber

HAPLOTYPE:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

IMMEDIATE SOURCE:

LIBRARY: lambda Zap tuber cDNA

CLONE: 1.2.1 and E2

POSITION IN GENOME:

CHROMOSOME/SEGMENT:

MAP POSITION:

UNITS:

FEATURE: open reading frame

NAME/KEY: starch branching enzyme

LOCATION: 44-2788

IDENTIFICATION METHOD: lone ORF with homology to other starch

IDENTIFICATION METHOD: branching enzymes

OTHER INFORMATION: complements KV832 E. coli glycogen

OTHER INFORMATION: branching enzyme mutant

US-08-716-449-1

Alignment Scores:

Pred. No.: 9,74e-232 Length: 3128
Score: 2165.00 Matches: 423
Percent Similarity: 64.73% Conservative: 124
Best Local Similarity: 50.06% Mismatches: 218
Query Match: 48.49% Indels: 80
DB: 3 Gaps: 12

US-10-056-454A-15_COPY_49_882 (1-834) x US-08-716-449-1 (1-3128)

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QY 6 AsnSerGluPheArgProSerThrValAlaAlaSerGlyLysValLeuValProGlyThr 25
DB 95 TCCTCCTCACTAAAGTTCTTCAGGGGCTTCTAGAAATAAGATATGTTTCCTCTCAA 154
QY 26 GlnSerAspSerSerSerSerThrAspGlnPheGluPheThrGluThrSerProGlu 45
DB 155 CATAGTACTGACTCAAGTTTGGATCTCAGAACGGTCTTGGGATATTTCTCCACCCA 214
QY 46 AsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGlnIleLys 65
DB 215 AAATCAAGAGTAGAAAAGAT-----GAAAGAGTAGAACACAGTTCAGCTATT-- 262
QY 66 ThrGluAsnAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAsp 85
DB 263 -----TCCGCTGTTTGGACCGAT-----GAC 283
QY 86 PheAlaSerSerLeuGlnGluGlyLysLeuGluGluSerLysThrLeuAsn 105
DB 284 AATTCGACAATGGCACCCCTAGAGGAAGATGCAAGACTGAATATTGACCTCCTAAAT 343
QY 106 ThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGluArgGlyPro 125
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DB 343 ----- 343
QY 126 ProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHis 145
DB 344 -----TTGGATCCAACCTTGGAACTTATCTAGATCAC 376
QY 146 LeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGly 165
DB 377 TTCAGACACAGAAATGAAGATATGTGGATCAGAAATGCTCATTTGAAATATAGGGA 436
QY 166 GlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGly 185
DB 437 CCCCTTGAGGAATTGCTCAAGTTATTAAATTTGGATTCAACAGGAAGATGCTTGC 496
QY 186 IleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsn 205
DB 497 ATAGTCTATCGTGAATGGCTCTGCTGCTCAGGAAGCAGAAAGTTATTGGCATTTCAAT 556
QY 206 AsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePhe 225
DB 557 GGATGGACGGTTCTTAACACATGATGGAGAGGACCACTTTGGTGTGGAGTATTAGA 616
QY 226 LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg 245
DB 617 ATTCTCT---GATGTTGACAGTAGCAGTCATCCACAACTCCAGAGTTAGTTCTGT 673
QY 246 MetAspThrProSerGlyVal---LysAspSerIleProAlaTrpIleAsnTyrSerLeu 264
DB 674 TTCAAACATGTTAATGGAGCTGTGGTAGATCCTATCCCTGCTGGGATAAAGTATGCCACT 733
QY 265 GlnLeuProAspGluIle-----ProTyrAsnGlyIleHisTyrAspProProGluGlu 282
DB 734 GCAGACGCCACAAAGTTTCAGCACCATATGATGTGTCTACTGGGACCCACCACTTCA 793
QY 283 GluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGlu 302
DB 794 GAAAGTACCCTTCAAAATACCCTCCCTCCCAAAACCCGAGCCCAAGATCTACGAA 853
QY 303 SerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAsp 322
DB 854 GCACATGTGGCATGAGCAGCTCTGAGCCACGTGTAATTCGTATCGTGTGAGTTCGAGAT 913
QY 323 GluLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGln 342
DB 914 GATGTTTACCTCGGATTAAGCAATAACTATACTATCTCCAGTGTGCGCATGAGGCAATG 973
QY 343 GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSer 362
DB 974 GAACATTCCTACTATGATCATTTGGATATCATGTTACAAACTTTTTCCTGTGAGCAAT 1033
QY 363 ArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIle 382
DB 1034 AGATATGGAACCCGAGGAGCCTAAAGTATCTAGATATAAGACATAGTCTGGGTGTTA 1093
QY 383 ValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsn 402
DB 1094 CAGGTTCTGGTGGATAGTGTTCACAGTCAIGCAAGCAATATGTCACCTAGTGGCTTCAAT 1153
QY 403 MetPheAspCys-----ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyr 419
DB 1154 GCTTTGATATTGGCCCAAGTTCTCAGAAATCCTACTTTTCATGCTGGAGCGAGGTAC 1213
QY 420 HisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeu 439
DB 1214 CATAAGTTTGGGATAGCAGGCTGTTCAACTATGCCAATTTGGGAGGTTCTTCGTTTCCTT 1273
QY 440 LeuSerAsnAlaArgTrpIleAspAlaPheLysPheAspGlyPheArgPheAspGly 459
DB 1274 CTTTCCAACTGAGGTGGTGGCTAGAGAGTAACTTTGACGGATTTTCGATTTGATGGA 1333
QY 460 ValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGlu 479
DB 1334 ATAACCTCTGCTGTATGTTTCATCATGGAATCAATATGGGATTTACAGGAACATATAAT 1393
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QY 480 GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAsp 499
    |||||
Db 1394 GAGTATTTCAGGAGCTACAGATGTTGATGCTGGTCTATTTAATGTTGCCATATAT 1453
    |||||
QY 500 LeuLeHisGlyLeuPheProAspAlaThrIleGlyGluAspValSerGlyMetPro 519
    |||||
Db 1454 CTGATTCACAAGATTTCCAGACGCAACTGTTAATGCCGAAGATGTTTCTGATGCCG 1513
    |||||
QY 520 ThrPheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAla 539
    |||||
Db 1514 GGCCTTACCCGCCCTGTTCTGAGGAGGAATGTTTGAATACCGCTGCCATGGCA 1573
    |||||
QY 540 IleAlaAspLysArgIleGluLeuLeuLys---LysArgAspGluAspTyrArgValGly 558
    |||||
Db 1574 ATCCAGATAGTGGATAGATATTAAAGATAAGATGATGAAGATGGTCCCAAGAG 1633
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QY 559 AspIleValHisThrLeuThrAsnArgTyrPheSerGluLysCysValSerTyrAlaGlu 578
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Db 1634 GAACTTAACATCGAGTTTGACAAATAGAGATATACAGAAAGTGTATAGCATATCGGAG 1693
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QY 579 SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrPheMetAspLysasp 598
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Db 1694 AGCCATGATCAGTATGTCGTGACAGACCATGCTTCTCTTAAGACCAAGAG 1753
    |||||
QY 599 MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla 618
    |||||
Db 1754 ATGTATTCTGGCATCTCTGCTTGACAGATGCTTCTCTGTTGTTGATCGAGGAATGG 1813
    |||||
QY 619 LeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPhe 638
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Db 1814 CTTCACAGATGATCCATTTTTCACAAATGGCCTTGGGAGGAGAGGGTACCTCAATTTC 1873
    |||||
QY 639 MetGlyAsnGluPheGlyHisProGluTyrPheAspPheProArgAlaGluGlnHisLeu 658
    |||||
Db 1874 ATGGGTACAGATTGGCCATCCGAGTGGATGATGACTTCCCTCAGAG----- 1918
    |||||
QY 659 SerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPhe 678
    |||||
Db 1919 -----GAGGGCAATAATTGGAGTATGACAAATGATAGACGCCAGTGG 1960
    |||||
QY 679 AspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMet 698
    |||||
Db 1961 AACCTCGCAGATGACGACACTTGAGATACAGATTATCAATGCAATTTGATAGACTAG 2020
    |||||
QY 699 GlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLys 718
    |||||
Db 2021 AATTCGCTCGAAGAAAGTTCTCATCTCGCATCAGGAACACATAGTAGAAGCAGATG 2080
    |||||
QY 719 AspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPhe 738
    |||||
Db 2081 GATGATGATAATAAGGTGTGTGTTGAACGTGTGACCTGCTGTTATTTGATTCACATTC 2140
    |||||
QY 739 HisTyrThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLys 758
    |||||
Db 2141 CACCAATAACACATACAGAGAGGGTATAAAGTTGGATGACTTCCAGGGAAGTACAGA 2200
    |||||
QY 759 ValAlaLeuAspSerAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAla 778
    |||||
Db 2201 GTTGACATGGGCAGTGATGCTTGGGAATTTGGTGGCCATGGAAGAGCTGCTCATGATGT 2260
    |||||
QY 779 GluTyrPheThrPhe-----GluGlyTyrPyrAspAspArg 790
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Db 2261 GACCAATTTCACATCACAGAGGAATACTGAGTTCAGAGAACAAATTTCAATGGTGTG 2320
    |||||
QY 791 ProArgSerIleMetValTyrAlaProCysLysThrAlaValAlaTyrAlaLeuValasp 810
    |||||
Db 2321 CCAAAATCTTCAAAAGTGTCTCTCTCGCGGAACATGTGTGGCTTATTACAGAGTTGAT 2380
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QY 811 LysGluGluGluGluGluGluGluGluGluVal----- 823
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Db 2381 GAACGCATGTGAGAAACTGAAGATTACAGACAGACATTTGTAGTGAGCTACTACCAACA 2440
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QY 824 AlaAlaValGluGlu 828
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Db 2441 GCCAATATCGAGAA 2455
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RESULT 10
US-09-257-894-24
; Sequence 24, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-257-894-24
Alignment Scores:
Pred. No.: 2,16e-225 Length: 2565
Score: 2107.00 Matches: 404
Percent Similarity: 66.33% Conservative: 124
Best Local Similarity: 50.75% Mismatches: 206
Query Match: 47.19% Indels: 62
DB: 4 Gaps: 10
US-10-056-454a-15_COPY_49_882 (1-834) x US-09-257-894-24 (1-2565)
QY 43 SerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSer 62
    |||||
Db 16 TCGCCCTCTCTCCGCCGACTCCGCTTCCGCCGCCGCCGCGCTCTGCTCGCATGCT--- 72
    |||||
QY 63 GlnIleLysThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGlu 82
    |||||
Db 73 -----GATCGGGCGGCAACCGCGGGGATCCCGGGTGGCGGCAATGTG 114
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QY 83 GluLeuAspPheAlaSer-----Ser 89
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Db 115 CGCCCTGAGTGTGTGTTCTCTCCAGTCAGAGGTCGCCGCTCAGGGGTGGCGAAGTCAAG 174
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Db 1082 CAAGCACCACCAAGAGTCCTATTTTCATCGGAGATAGAGGTATCATAAACTTTGGGAT 1141
QY 425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuSerAsnAlaArg 444
Db 1142 AGTCGGCTGTTCAACTATGCTAACTGGGAGGTATTAAGGTTTCTTCTTAACCTGAGA 1201
QY 445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
Db 1202 TAITGGTGGAGAAATTCATGTTTTCATGGCTTCCGATTTGATGGAGTTACATCAATGCTG 1261
QY 465 TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluTrpPheGlyLeu 484
Db 1262 TATCATCACCATTGATCAATGAGGTTTACTGGAACACTACAGAAATATTTACGTTTG 1321
QY 485 AlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLeu 504
Db 1322 GACACAGCTGTGGATGCGAGTTGTTTACATGATGCTTGCAAAACCAATTAATGACAAACTC 1381
QY 505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
Db 1382 TTGCCAGAGCAACTGTTGTTGCTGAAGATGTTTCAGGCATGCCGCTCCTTTCGCCGCCA 1441
QY 525 ValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
Db 1442 GTTGATGAAGTGGGTTGGGTTGACATATCGCTGGCAATGGCTATCCCTGATAGATG 1501
QY 545 IleGluLeuLeuLysLysArgAspGlu---AspTrpArgValGlyAspIleValHisThr 563
Db 1502 ATTGACTACCTGAAGAATAAAGATGACTCTGAGTGTGCTGAGTGGTGAATAGCGCATACT 1561
QY 564 LeuThrAsnArgTyrTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
Db 1562 TTGACTACAGAGATATCTGAAAATGCAATGATGCTATGCTGAGAGCATGATCAGTCT 1621
QY 584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db 1622 ATTGTGGCGCAAAACTATTGCAATTTCTCTGTGAGACAGGAATGTACACTGGCATG 1681
QY 604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db 1682 TCAGACTTGGACGCTGCTACCTACCAATATGTCAGGGATGTCACATCAAAAGATGATT 1741
QY 624 ArgLeuValThrMetGlyLeuGlyGlyGluTyrLeuAsnPheMetGlyAsnGluPhe 643
Db 1742 CACTTCATCACAAATGGCCCTTGGAGGTGATGCTACTTGAATTTATGGGAATAGATT 1801
QY 644 GlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVal 663
Db 1802 GGTCAACCCAGATGATGACTTTCACAAGA----- 1831
QY 664 IleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAla 683
Db 1832 ---GAAGGGAACACTGGAGCTATGATAAATGCACAGACACAGTGGAGCCTTGTGACACT 1888
QY 684 GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGluTyrLeuGluAsp 703
Db 1889 GATCATTGCGGTACAACTATGATGATGCGTTTGACCAAGCGATGAATGCCCTCGATGAG 1948
QY 704 LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg 723
Db 1949 AGATTTTCTCTCCCTTCCTGCTCAAAAGCAGATCGTCAGCGACATGAACGATGAGGAAAG 2008
QY 724 MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer 743
Db 2009 GTTATGTCTTTGAACGTGGAGATTTAGTTTGTGTTTTCATATTTCCATCCCAAGAAACT 2068
QY 744 TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer 763
Db 2069 TACGAGGCTACAAAGTGGGATGGATTGCTGGGAATACAGATGAGCCCTGGACACT 2128
QY 764 AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe 783
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Db 2129 GATGCTCTGGTCTTCGTGGACATGGAAGAGTTGGCCACGACGTGGATCACTTCACGTG 2188
QY 784 -----GluGlyTyrTyrAspArgProArgSerIleMet 795
Db 2189 CCGTGAAGGGTGCAGGGGTGCCGGAACGAACTTCAACACACGGCGGAACTGTTCAAA 2248
QY 796 ValTyrAlaProCysLysThrAlaValValTyrAlaLeuValAspLys 811
Db 2249 GTCCCTTCTCCGCGCCGACCTGTGTGGCTTATTACCGTGTAGACGAA 2296

RESULT 12
US-09-257-894-19/c
; Sequence 19, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. du Pont de Nemours and Company
; STREET: 1007 Market Street
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2487 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-257-894-19

Alignment Scores:
Pred. No.: 4,45e-225 Length: 2487
Score: 2104.00 Matches: 393
Percent Similarity: 70.60% Conservative: 121
Best Local Similarity: 53.98% Mismatches: 172
Query Match: 47.12% Indels: 42
DB: 4 Gaps: 8

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QY 98 LeuGluSerLysThrLeuAsnThrSerGluGluThrIleAspGluSerAspArg 117
Db 2178 GTGCAAGAAGATAAACTATGCAACTGCCAAAGCGATGTC-----GACCAT 2131
QY 118 IleArgGluArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspPro 137
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Patent No. 6376749
GENERAL INFORMATION:
APPLICANT: Broglie, Karen E.
APPLICANT: Klein, Theodore M.
APPLICANT: Hubbard, Natalie L.
APPLICANT: Lightner, Jonathan E.
TITLE OF INVENTION: No. 6376749el Starches via Modification of
TITLE OF INVENTION: Expression of Starch Biosynthesis
TITLE OF INVENTION: Enzyme Genes
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. du Pont de Nemours and Company
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Microsoft Windows 95
SOFTWARE: Version 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/257,894
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/091,052
FILING DATE: JUNE 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R.
REGISTRATION NUMBER: 41,173
REFERENCE/DOCKET NUMBER: BB-1066-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 49...2580
US-09-257-894-12

Alignment Scores:
Pred. No.: 5,34e-225 Length: 2772
Score: 2104.00 Matches: 393
Percent Similarity: 70.60% Conservative: 121
Best Local Similarity: 53.98% Mismatches: 172
Query Match: 47.12% Indels: 42
DB: 4 Gaps: 8

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-257-894-12 (1-2772)

QY 98 LeuGluSerLysThrLeuAsnThrSerGluGluThrIleLeuAspSerAspArg 117
Db 310 GTGCAAGAAAGATAAAACATATGGCAACTGCTCAAGAGCGCATGTC-----GACCAT 357
QY 118 IleArgGluArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspPro 137
Db 358 CTC-----CCCATATAGCAGCTGGACCCC 381
QY 138 LeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArg 157
Db 382 AAGCTGGAGATATTCAGAGGACCATTCAGGTACCGGATGAAAGATTCCTAGAGCAGAAA 441
QY 158 GluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMet 177
Db 442 GGATCAATTAAGAAAAATGAGGGAAGTCTTGAATCTTTTCTAAAGGCTATTTCGAATTT 501

QY 178 GlyPheThrArgSerAlaThrGlyIleThrTyrArgGluThrAlaLeuGlyAlaGlnSer 197
Db 502 GGGATTAAATACAAATGAGGATGAACTGTATTCGTGAATGGSCACCTCTGCGCAGAG 561
QY 198 AlaAlaLeuIleGlyAspPheAsnThrPheAspAlaAsnAlaAspIleMetThrArgAsn 217
Db 562 GCAGAGCTTATTGGTGAATGCTCAATGCTGAAATGCTGCAAAACATAAGATGAGAGGAT 621
QY 218 GluPheGlyValTyrGluIlePheLeuProAsnAsnValAspGlySerProAlaIlePro 237
Db 622 AAATTTGGTGTGGTTCGATCAAAATTT---GACCATGTCAAGAGGAAACCTGCCATCCCT 678
QY 238 HisGlySerArgValLysIleArgMetAspThrProSerGlyValLysAspSerIlePro 257
Db 679 CACAATTCGAAGTTAAATTTCCCTTTTCATCATGTGGAGTATGGGTTCATGCTATTCGA 738
QY 258 AlaTyrPheAsnTyrSerLeuGlnLeuProAspGluIle-----ProTyrAsnGlyIle 275
Db 739 GCATTTGATTCGTATGCGACTGTTGATGCTCTAAATTTGGAGCTCCCTATGATGCTGT 798
QY 276 HisTyrAspProGluGluGluTyrIlePheGlnHisProArgProLysLysPro 295
Db 799 CATGGGATCCCTCTCTCTGAAAGGTACACATTTAAGCATCTCGGCTTCAAGCCT 858
QY 296 LysSerLeuArgIleTyrGluSerHisIleGlyMetSerSerProGluProLysIleAsn 315
Db 859 GCTGCTCCAGCTATCTATGAAGCCCATGTAGTATGATGAGTGTGAAAGCCAGCAGTAAGC 918
QY 316 SerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAla 335
Db 919 ACATATAGGGAATTTGCAGACAAATGTGTGCACGCATACGAGCAAAATACTACACACA 978
QY 336 LeuGlnIleMetAlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisValThr 355
Db 979 GTTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCTTTCGGGTACCATGTGACA 1038
QY 356 AsnPhePheAlaProSerSerArgPheGlyThrProAspAspLysLysSerLeuLeuAsp 375
Db 1039 AATTTCTTTGGCGTTAGCAGCAGATCAGCAGCACACAGGAGACCTCAAAATATCTTTGAT 1098
QY 376 LysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsn 395
Db 1099 AAGCACACAGTTTGGGTTCGGAGTTCTGTATGATGATGTTCATAGCCATGCAAGTAAAT 1158
QY 396 AsnThrLeuAspGlyLeuAsnMetPheAsp-----CysThrAspSerCysTyrPhe 412
Db 1159 AATGTCACAGATGGTTTAAATGGCTATGATGTTGGCAAAAGCACCCACAGCTCTATTTT 1218
QY 413 HisSerGlyAlaArgGlyTyrHisThrPheMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
Db 1219 CATCGGGAGATAGAGGTTATCATAAACTTTTGGGATAGTCGGCTGCTTCAACTATGCTAAC 1278
QY 433 TrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTyrTrpLeuAspAlaPheLysPhe 452
Db 1279 TGGGAGCTATTAAGGTTCTTCTTCAACCTGAGATATGTTGGTGGATGAATTCATGTTT 1338
QY 453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
Db 1339 GATGCTTCCTCCATTTGATGGAGTTACATCAATGCTGATCATCACCATGGATCAATCATG 1398
QY 473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
Db 1399 GGGTTTACTGGAACACTACCGAATATTTTCATGTTGGACACACAGCTGTGGATGCACTGTT 1458
QY 493 TyrLeuMetLeuValAsnAspIleHisGlyLeuPhePheProAspAlaIleThrIleGly 512
Db 1459 TACATGATGCTTGCACCAACCATTTAATGCACAAACCTTTGGCAGAGCAACTGTTGTTCT 1518
QY 513 GluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyValGlyValGlyPhe 532
Db 1519 GAAGATGTTTCAGCATGCCCGTCTCTTTGCCGCCAGTCATGTATGAGGTGGGGTGGGTTT 1578

QY	533	AspTyrArgLeuHisMetAlaIleAlaAspLysArgIlecluLeuLeuLysLysArgAsp	552
Db	1579	GACTATCGCGTGGCAATGCTCTCCCTGATAGATGAATTCACCTACTCTGAAGATAAAGAT	1638
QY	553	Glu---AspTirArgValGlyAspIleValHisThrLeuThrAsnArgArgTirpSerGlu	571
Db	1639	GACTCTGAGTGGTCGATGGTGAAATAGCGCATACCTTTGACTAACAGGAGATATACTGAA	1698
QY	572	LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValcilyAspLysThrIleAla	591
Db	1699	AAATGATCGCATATGCTCAGAGCCATGATCAGTCATTTGTTGGCAGCAAAACATATGCA	1758
QY	592	PheTirLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer	611
Db	1759	TTTCTCCTGAAGCAGGAAGATGTACTGGCATGTCCAGCTGCAGCTGCTGTCCACCT	1818
QY	612	LeuIleAspArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly	631
Db	1819	ACAAATGTATCGAGGATTCGACTCCAAAAGATGATTCACCTTCATCAACAATGGCCCTTGG	1878
QY	632	GlyGluGlyTyrIleuAsnPheMetGlyAsnGluPheGlyHisProGluIrrpIleAspPhe	651
Db	1879	GGTGATGGCTACTTGAAATTTATGGGAATGAGTTTGGTCACCCGAATGGATGTACTTT	1938
QY	652	ProArgAlaGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyr	671
Db	1939	CCAAGA-----GAAGGGACAACTGGAGCTAT	1965
QY	672	AspLysCysArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeu	691
Db	1966	GATAAATGACAGCAGCAGTGGAGCCCTTGTGGACACTGATCACTTGGCGGTACAAAGTACATG	2025
QY	692	GlnGluPheAspArgProMetGlnTyrLeuGluAspLysTyrGluPheMetThrSerGlu	711
Db	2026	ATGCGCTTGACCAACCGATGAATGCGCTCGATGAGAGATTTTCCTTCCTTCGTGCTCA	2085
QY	712	HisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPheGluLysGlyAsn	731
Db	2086	AAGCAGATCGTCAGCCACATGAACGATGAGGAAAGGTTATTGCTCTTGAACGTGGAGAT	2145
QY	732	LeuValPheValPheAsnPheHisTirpThrLysSerTyrSerAspTyrArgIleAlaCys	751
Db	2146	TTAGTTTTGTTTTCAATTTCCATCCCAAGAAACTTACGAGGCTACAAAGTGGGATGC	2205
QY	752	LeuLysProGlyLysTyrLysValAlaLeuAspSerAspProLeuPheGlyGlyPhe	771
Db	2206	GATTTCCCTGGGAAATACAGAGTAGCCCTGGACTCTGATGCTCTGGTCTCTGGTGGACAT	2265
QY	772	GlyArgIleAspHisAsnAlaGluTyrPheThrPhe-----	793
Db	2266	GGAAAGAGTGGCCACGACCGTGGATCACTTCACGTCGCCCTGAAGGGGTGCGAGGGGTGCC	2325
QY	784	GluGlyTirpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla	803
Db	2326	GAACCAACTTCAACAAACGGCCGAACCTGTTCAAGAGTCTTTCTCCGCCCCGACCTGT	2385
QY	804	ValValTyrAlaLeuValAspLys	811
Db	2386	GTGGCTTATTACCGTGTAGACGAA	2409

RESULT 14

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US-08-104-158-1
; Sequence 1, Application US/08104158
; Patent No. 6215042
; GENERAL INFORMATION:
; APPLICANT: Willmitzer, Lothar
; APPLICANT: Sonnewald, Uwe
; APPLICANT: Kossmann, Jens
; APPLICANT: Mueller-Roeber, Bernd
; APPLICANT: Vissler, Richard Gerardus Franciscus
; APPLICANT: Jacobsen, Evert
; TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE TITRE OF INVENTION: CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
QY      Db      QY
66.00%   50.74%   66.00%
Best Local Similarity: 47.00%
Query Match:         4
DB:                  12
Gaps:                12
Indels:              78
Mismatches:         196
Conservative:       123
Accumulated Gaps: 123
Score: 66.00%
US-10-056-454A-15_COPY_49_882 (1-834) x US-08-104-158-1 (1-2909)
QY      46 AsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGlnIleLys 65
:::||||| |||| |::::|::::| |
26 TCCACCCCNAATCAAGAGTTAGAAGATGAAGAGGTGAAGCAGTTCAGCTATT --- 82
Db
QY      66 ThrGluAsnAspAspValGluProSerSerAspLeuThrGlySerValGluGluLeuAsp 85

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Db	83	-----TCGCTGTTTGCAC-----	1034	CATAAGTTGGGATAGCAGGCTGTTCAACTATGCCAATTGGGGAGGTTCTTCGTTTCCTT	1093
QY	86		440	LeuSerAsnAlaArgTrrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGly	459
Db	98	-----GATGACAAATCGACAATGGCA	1094	CTTTCCAACTTGAGGTGGTGGCTAGAAAGACTATAAATTTGACCGATTTCGATTTCATGGA	1153
QY	106		460	ValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAspTyrGlu	479
Db	119	-----ATTGGC-----	1154	ATAACTTCTATGCTGATGTTTCATCATGGAATCAATATGGGATTTACAGGAACATAAAT	1213
QY	126	ProGlyLeuGlyGlnLysIleArgGluLeuThrAsnTyrArgGlnHis	480	GluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsp	499
Db	149	-----ATTGGC-----	1214	GAGTATTTACGACGAGGCTACAGATGTTGCTGCTGCTATTTAATGTTGGCCAAATAAT	1273
QY	146	LeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGly	500	LeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetPro	519
Db	197	TTACAGACACAGATGAAGATATGTTGGATCAGAAATGCTATTGAAAATATAGAGGA	1274	CTGATTACAAAGATTTTCCACGACGCAACTGTTATTGCCGAAGATGTTTGGTATGCCG	1333
QY	166	GlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGly	520	ThrPheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAla	539
Db	257	CCCTTGAGGAATTGCTCAGAGTTATTAAATTTGGATTCAACAGGGAAGATGGTGC	1334	GGCCTTAGCCGGCCTGTTTCTGAGGGGAATTTGGTTTGTATTACCGCTGGCAATGGCA	1393
QY	186	IleThrTyrArgGlnTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsn	540	IleAlaAspLysArgIleGluLeuLysLysLysArgAspGluAspTyrArgValGly	558
Db	317	ATAGTCTATCGTGAATGGCTCTGCTCAGGAAGCAGAGATTTATGGCGATTTCAT	1394	ATCCAGATAAGTGGATAGATTATTAAAGAAATAAGAAATGATGAAGATTTGGTCCAGAG	1453
QY	206	AsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePhe	559	AspIleValHisThrLeuThrAsnArgArgTrrpSerGluLysCysValSerTyrAlaGlu	578
Db	377	GGTAGACGGTCTTAACCATATGATGGAGAGACCACTTTGGTGTGGAGTATTAGA	1454	GAAGTAACATCGAGTTTGACAAATAGGAGATATACAGAGAAGTGTATAGCATATGCGAG	1513
QY	226	LeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLysIleArg	579	SerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAsp	598
Db	437	ATTCTCT--GATGTTGACAGTAGCCAGTCATCCACAACTCCAGAGTTAAGTTTCGT	1514	AGCCATGATCAGTCTATTTGTCGGTGACAAAGACCATTTCCATTTCTCTTAATGAACAAAG	1573
QY	246	MetAspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeu	599	MetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAla	618
Db	494	TTCAAACTATGTAATGAGTGTGGTAGATCGTATCCCTGCTTGGATAAAGTATGCCACT	1574	ATGATATCGGCATGCTCTGCTGACAGATGCTCTCTCTGTTGTTGATGACAGAAATTCG	1633
QY	265	GlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGlu	619	LeuHisLysMetIleArg-LeuValThrMetGlyLeuGlyGlyGlyGlyTyrLeuAsnPh	638
Db	554	GCAGAGCCCAAAAGTTTCACACACCATATGATGTTGTTCTACTGGACCCACACCTTCA	1634	CTTGACAAGATGATCCATTTTTCACAAATGGCTTGGGAGGAGAGGGTACCTCAATTT	1693
QY	283	GluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGlu	638	eMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLe	658
Db	614	GAAGGTACCACTTCAAAATACCTCGCCTCCCAAAACCCGACCCCAAGATCAGAA	1694	CATGGGTACAGATTGGCCATCTCGATGGATGATGATCTCCCTAGT-----	1739
QY	303	SerHisIleGlyMetSerProGluProLysIleAsnSerTyrValAsnPheArgAsp	658	uSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPh	678
Db	674	GCACATGTCGGCATGAGCAGCTCTGAGCCACGTTGTAATTCGTATCGTATTCAGAT	1740	-----GAGGCAATAATTGGAGTTATGACAAATGTAGACCCAGTG	1780
QY	323	GluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGln	678	eAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMe	698
Db	734	GATGTTTACCTCGGATTAAGCAATAACTATAACTGTCAGTTGATGGCCAAATG	1781	GAACCTCGCAGATAGCAACACTTGATACAAAGTTTATGATGATGATGATGATGAT	1840
QY	343	GluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaProSerSer	698	tGlnTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLy	718
Db	794	GAACATCTTACTATGATCAATTGGATATCATGTTACAACTTTTTCCTGTGACCAAT	1841	GAATTCCTCGATGAAAGTTCTCATCTCCGATCAGGAAACACATAGTAGCAGCAT	1900
QY	363	ArgPheGlyThrProAspAspLeuLysSerIleAspLysAlaHisGluLeuGlyIle	718	sAspGluGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPh	738
Db	854	AGATATGGAACCCGAGGACCTAAAGTATCTGTAGATAAAGCACAATAGCTTGGTTTA	1901	GGATGATGATAATAAGTTTGTGTTTGAACGTTGTTGACCTGGTGGTATTTGATTCAACT	1960
QY	383	ValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsn	738	eHisTrpThrLysSerTyrArgIleAlaCysLeuLysProGlyLysTyrLy	758
Db	914	CAGGTTCTGGTGGATGTAGTTACACATCATGCAAGCAATAATGCTACTGATGGCTCAAT	1961	CCACCCAAATACACATACAGAGGTATAAAGTTTGGATGATGATGATGATGATGATGAT	2020
QY	403	MetPheAspCys-----ThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyr	758	sValAlaLeuAspSerAspAspProLeuPheGlyGlyPheGlyArgIleAspHisAla	778
Db	974	GCCTTGATATGGCCAGGTTCTCAAGAACTCTTTCATGCTGGAGGAGGGGTAC	2021	AGTTCACCTGGACAGTATGCTTGGGAATTTGGTGGCCATGGAAGAGCTGCTCATGATCT	2080
QY	420	HisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeu	778	aGluTyrPheThrPhe-----GluGlyTyrTyrAspAspArg	790
			2081	TGACCATTCATCATCACCAGGAAGTAATACCTGGAGTTCCAGAAACAAATTTCAATGGTGC	2140


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QY 406 ---CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
Db 1084 CAAAGCACCACAGAGTCCTATTCTATGCGGAGATAGAGGTATCATAACTTTGGGAT 1143
QY 425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArg 444
Db 1144 AGTCGGCTGTTCAACTATGCTAACTGGGAGGATTAAAGTTCTTCTTCTAACCTGAGA 1203
QY 445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
Db 1204 TATTGGTTGGATGAATTGATTGATGCTTCCGATTTCGAGTTACATCAATGCTG 1263
QY 465 TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeu 484
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Db 1324 GACACAGCTGTGCATGCAGTCTTACATGATGCTTGCAACCATTTAATGCACAACTC 1383
QY 505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
Db 1384 TTGCCAGAGCTGTGCATGCAGTCTTGTGCTGAAGAATGTTTCAGGCATGCCGCTCTTCCGCGCA 1443
QY 525 ValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
Db 1444 GTTGATGAGGTGGGTTGGGTTTACTATCCCTGGCAATGGCTATCCCTGATAGATGG 1503
QY 545 IleGluLeuLeuLysLysArgAspGlu---AspTrpArgValGlyAspIleValHisThr 563
Db 1504 APTGACTACCTCAAGAATAAAGATGACTCTGAGTGGTCGATGGTGAAATAGCGCATACT 1563
QY 564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
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QY 584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet 603
Db 1624 ATTGTTGGGACAAACTATTTCATTTCTCTGTGGACAGGAAATGTACACTGGCATG 1683
QY 604 AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle 623
Db 1684 TCAGACTTGCAGCCTGCTTACCTACATTTGATCGAGGATGCTCCAAAGATGATT 1743
QY 624 ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe 643
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QY 644 GlyHis 645
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Job time : 269 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 03:05:21 ; Search time 337 Seconds

(without alignments)
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Perfect score: 4465

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4320	96.8	3074	9	US-10-254-534-1
2	3309.5	74.1	2418	9	US-09-938-842A-872
3	3266	73.1	2577	9	US-09-938-842A-337
4	3037	68.0	3039	10	US-09-792-127-3
					Sequence 1, Appli
					Sequence 872, App
					Sequence 337, App
					Sequence 3, Appli

5	2997	67.1	2559	10	US-09-792-127-1	Sequence 1, Appli
6	2462	55.1	1393	9	US-10-254-534-3	Sequence 3, Appli
7	2058	46.1	2955	9	US-09-918-624B-30	Sequence 30, Appl
8	2058	46.1	2955	10	US-09-880-107-2148	Sequence 2148, Ap
9	2058	46.1	2994	9	US-10-084-817-92	Sequence 92, Appl
c 10	627	14.0	602	10	US-09-770-149-955	Sequence 955, App
11	530.5	11.9	1830121	9	US-10-329-960-1	Sequence 1, Appli
12	513.5	11.5	2193	9	US-09-738-626-1354	Sequence 1354, Ap
c 13	513.5	11.5	3309400	9	US-09-738-626-1	Sequence 1, Appli
14	484.5	10.9	1877	10	US-09-974-300-653	Sequence 653, App
15	463.5	10.4	604	10	US-09-925-300-453	Sequence 453, App
16	453	10.1	2514	9	US-10-156-761-2792	Sequence 2792, Ap
17	453	10.1	9025608	9	US-10-156-761-1	Sequence 1, Appli
18	422.5	9.5	1776	9	US-10-156-761-7377	Sequence 7377, Ap
c 19	419	9.4	601	9	US-10-025-380-304	Sequence 304, App
c 20	419	9.4	601	10	US-09-922-217-304	Sequence 304, App
c 21	419	9.4	601	10	US-09-833-263-304	Sequence 304, App
22	317	7.1	441	10	US-09-770-444-893	Sequence 893, App
23	305.5	6.8	543	10	US-09-815-343-373	Sequence 373, App
24	261.5	5.9	1680	10	US-09-908-855-14	Sequence 14, Appl
25	249.5	5.6	1743	9	US-10-156-761-2147	Sequence 2147, Ap
c 26	247	5.5	310	9	US-10-102-524-1616	Sequence 1616, Ap
27	244.5	5.5	3033	9	US-10-212-219-5	Sequence 5, Appli
28	244.5	5.5	3309400	9	US-09-738-626-1	Sequence 1, Appli
29	240.5	5.4	204	10	US-09-878-574-12567	Sequence 12567, A
30	239.5	5.4	1785	9	US-09-738-626-2326	Sequence 2326, Ap
31	226	5.1	661	10	US-09-765-272-77	Sequence 77, Appl
32	226	5.1	6142	9	US-10-014-436-1	Sequence 1, Appli
33	223	5.0	2437	9	US-10-238-091-6	Sequence 6, Appli
34	210.5	4.7	976	10	US-09-765-272-79	Sequence 79, Appl
35	209.5	4.7	576	10	US-09-815-343-924	Sequence 924, App
36	207.5	4.6	2736	10	US-09-833-435A-14	Sequence 14, Appl
37	205	4.6	2106	9	US-10-156-761-2139	Sequence 2139, Ap
38	203	4.5	5058	9	US-09-252-088-22	Sequence 22, Appl
39	202.5	4.5	2352	9	US-09-938-842A-218	Sequence 218, App
40	195	4.4	2508	9	US-09-738-626-2305	Sequence 2305, Ap
41	194	4.3	2997	9	US-10-238-091-1	Sequence 1, Appli
42	194	4.3	2997	9	US-10-238-091-2	Sequence 2, Appli
43	187.5	4.2	1965	10	US-09-815-242-9714	Sequence 9714, Ap
44	184	4.1	2247	9	US-10-156-761-2776	Sequence 2776, Ap
45	182	4.1	2151	9	US-10-127-032-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-10-254-534-1
; Sequence 1, Application US/10254534
; Publication No: US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown

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Db 1773 TACTTTGGACTCGCAACTGATGGATGCTGTGTGTATCTGATGCTGCTCAACGATCTT 1832
QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
Db 1833 ATTATGGGCTTTTCCACAGATGCANTACCATGGTGAAGATTTAGCGGAATGCCGACA 1892
QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
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QY 541 AlaAspLysArgIleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
Db 1953 GCTGATAAATGATGTGCTCAAGAACCGGATGAGATTTGGAGATGGGTGTATAT 2012
QY 561 ValHisThrLeuThrAsnArgTrpSerGluLysCysValSerTyrAlaGluSerHis 580
Db 2013 GTTCATACACTGACAAATAGAAGATGGTCGGAAGTGTGTTTCATACGCTGAAGTCAT 2072
QY 581 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
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QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
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Db 2193 AAGATGATTAGCTTGTAACTATGGATTAGCAGAGAGGCTACCTAAATTCATGGCA 2252
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QY 801 LysThrAlaValValTyrAlaLeuValAspLysGluGluGluGluGluGluGlu 820
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RESULT 2

US-09-938-842A-872

; Sequence 872, Application US/09938842A

; Patent No. US20020160378A1

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: Wang, Xun

; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; TITLE OF INVENTION: SAME, AND METHODS OF USE

; FILE REFERENCE: SCRIPI300-3

; CURRENT APPLICATION NUMBER: US/09/938, 842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227, 866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264, 647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300, 111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 872

; LENGTH: 2418

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-872

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Query Match:	74.12%	Indels:	55
DB:	9	Gaps:	4

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QY	44	ProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAlaSerGln	63
Db	250	-----GATCTAGAAAGTCAACAATGGAATATATCTAGAGGCA	285
QY	64	IleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySerValGluGlu	83
Db	286	GTAAGAACAAGAAC	300
QY	84	LeuAspPheAlaSerSerLeuGlnGluGlyGlyLysLeuGluGluSerLysThr	103
Db	301	-----CAACA	306
QY	104	LeuAsnThrSerGluGluThrIleIleAspGluSerAspArgIleArgGluArgGlyIle	123
Db	307	ATGAACGTTGTCAAGAGAGA-----GGGTTGAACCAAGAATAGT	348
QY	124	ProProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArg	143
Db	349	CCCCCAGCGGTGATGGCAAGAAAAATTTATGATAGTAGACCCCATCTTACGAACCTTACA	408
QY	144	GlnHisLeuAspTyrArgTyrSerGlnTyrLysLeuArgGluAlaIleAspLysTyr	163
Db	409	AATCATCTTGATTCGGTATGACAGATATAAAGATTCCGTGAGGAATAGACAGATAT	468
QY	164	GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla	183
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QY	304	HisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGlu	323
DB	889	CATGTTGGCATGAGTAGCACGGAACCAATGGTCAATACGTATGCTAACTTTAGAGATGAT	948
QY	324	ValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlu	343
DB	949	GTCTCTCCCGCATCAAAAGCTTGGATATAATGCTGTTCAAATATATGGCCATACAAAGAA	1008
QY	344	HisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg	363
DB	1009	CATTCAATATATGCCAGCTTTGGGTACCATGTCACAAACTTTTTTGCCCAACGACGTCG	1068
QY	364	PheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal	383
DB	1069	TGTGGGACCCAGAGGAACATAAATCACTCATAGATAGAGCTCACGAGTTAGCGCTGGTA	1128
QY	384	ValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet	403
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QY	404	PheAspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrp	423
DB	1189	TTTGATGGAACATGATGCTCACTATTTTCACTCTGGACCTCGGGGATACCACTTGGATCGG	1248
QY	424	AspSerArgLeuPheAsnTyrGlyValTrpGluValLeuArgTyrLeuLeuSerAsnAla	443
DB	1249	GATTCAGCACTTTCAATATAGGAGCTGGGAAGTATTCAGATATCTCCCTTTCAAAATGCA	1308
QY	444	ArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMet	463
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QY	464	MetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGly	483
DB	1369	ATGTATTACTCATATGGACTCTCGTTGGATTACTGGGAACCTACACCGAATACTTTGGA	1428
QY	484	LeuAlaThrAspValAspAlaValValTyrLeuMetValAsnAspLeuIleHisGly	503
DB	1429	TTGGAAACTCATGPGATGCTGGTAATTACTCATGCTGGTTAATGATATGATTTCATGGG	1488
QY	504	LeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIle	523
DB	1489	CTCTACCTTGAAGCATACCGTTGGTGAAGATGTTAGTGGTATGCCAACATCTCTGTATT	1548
QY	524	ProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLys	543
DB	1549	CCGTCTCAAGATGGTGGCTTGGATTTGACTACCGTTTACATGGCTTACATGGCCATAGCTGATAG	1608

Qy	544	ArglleGluLeuLeuLysLysArgAspGluAspTrpArgValGlyAspIleValHisThr	563
Db	1609	TGATGAAGAAATGCTCAGAAAGAGAGATGAAGACTGGCAATGGCGACATCATTTACACA	1668
Qy	564	LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla	583
Db	1669	CTTACCAACAGAGAGGTGGTCAGAGAAAGTGATCTCTTATGCTGAAAGTCACGATCAAGCT	1728
Qy	584	LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMet	603
Db	1729	CTTGTGGTGATATAACAATGGCTTCTGGTTATGGACAAGGATATGTAATGATTTTCATG	1788
Qy	604	AlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIle	623
Db	1789	GCAGTCAGACAGACCACTCACTCTCTATCGATAGAGAGANTAGCTTTGCACAAAATGATT	1848
Qy	624	ArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPhe	643
Db	1849	AGGCTTATACTATGGGATTAGGCGGTGAAGGTTACTTAAATTTATGGGAAAGCAATTC	1908
Qy	644	GlyHisProGluTrpIleAspPheProArgAlaGluGluHisLeuSerAspGlySerVal	663
Db	1909	GGACATCCAGAAATGGATGATTTTCCAGAGGCGAGCAGCGCTCTTCTGATGGTAGCGTG	1968
Qy	664	IleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAla	683
Db	1969	ATTCTCGCAACAATTCAGTTATGACAAATGCCGCCGACAGTTTGATCTTGGGATGCA	2028
Qy	684	GluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAsp	703
Db	2029	GATTTATCTCAGATACCCGGGACTACAAGAATTTTGATCAGGCAATGCCAACATCTTGAAGAG	2088
Qy	704	LysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArg	723
Db	2089	AATTACGGTTTATGACTTCGGACACCAATTCATATCAGAAAGACGAGACAGATAGA	2148
Qy	724	MetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrpThrLysSer	743
Db	2149	GTAATCGTATTTCGAAAGAGGTGATCTCGTCTTTCTTAACTTTCTACTGGACACGACGC	2208
Qy	744	TyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSer	763
Db	2209	TACTTTGATTAACCCGATGGTGTCTCAAGCCCTGGAAAAATATAGATCGTATTGCACTCG	2268
Qy	764	AspAspProLeuPheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPhe	783
Db	2269	GACGATCCTCTCTTTGGTGGATTCAATAGGCTCGATCGCAAGGCGAGAGTACTTCACTTAT	2328
Qy	784	GluGlyTrpTyrAspAspArgProArgSerIleMetValTyrAlaProCysLysThrAla	803
Db	2329	GATGGCTTATACGACGACGACCCCTGCTTCATGGTGCTATGACCGGTGAGAACCCGCC	2388
Qy	804	ValValTyrAlaLeuValAspLysGlu	812
Db	2389	GTGGTTATGCTTTAGCAAAACACGAT	2415
RESULT 3			
US-09-938-842A-337			
; Sequence 337, Application US/09938842A			
; Patent No. US2002160378A1			
; GENERAL INFORMATION:			
; APPLICANT: Harper, Jeff			
; APPLICANT: Krebs, Joel			
; APPLICANT: Wang, Xun			
; APPLICANT: Zhu, Tong			
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING			
; TITLE OF INVENTION: SAME, AND METHODS OF USE			
; FILE REFERENCE: SCRIPT300-3			
; CURRENT APPLICATION NUMBER: US/09/938,842A			
; CURRENT FILING DATE: 2001-08-24			
; PRIOR APPLICATION NUMBER: US 60/227,866			
; PRIOR FILING DATE: 2000-08-24			
; PRIOR APPLICATION NUMBER: US 60/264,647			

; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 337
 ; LENGTH: 2577
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-337

Alignment Scores:
 Pred. No.: 0
 Score: 3266.00
 Length: 2577
 Matches: 602
 Percent Similarity: 83.25%
 Best local Similarity: 72.53%
 Mismatches: 89
 Query Match: 73.15%
 Indels: 26
 Gaps: 9

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-938-842A-337 (1-2577)

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 Db 160 AAGCCATCGTATGATTCATGAT-----TCGCTTCCTTAGCTACACCTGCAATCGAGAG 213
 QY 22 ValProGlyThrGlnSerAspSerSerSerSerSerThrAspGlnPheGlu 41
 Db 214 CTCGGTGGCCATCAGATGATAGCTTTCATCTGCTCTGATCAAGTACAATCTCGGGAT 273
 QY 42 ThrSerProGluAsnSerProAlaSerThrAspValAspSerSerThrMetGluHisAla 61
 Db 274 ACTGCTCTGACGATATCTACAGTCTCGGCAATGTAGACCTGACAAAACCTGAAGAAGCC 333
 QY 62 SerGlnIleLysThrGluAsnAspAspValGluProSerSerSerSerLeuThrGlySerVal 81
 Db 334 CAGGAA-----ACAGACACTAGATCAAACTCTGCATCTCAACATCTGGAAGCATA 387
 QY 82 Glu---GluLeuAspPheAlaSerSerLeuGlnLeuGlnGlyGlyLysLeuGlu 100
 Db 388 AGTTATAAAGAAAGATTTTGCA-----AAGATGTCACAC 420
 QY 101 SerLysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGlu 120
 Db 421 TCT-----GTGACCAA-----GAAGTTGGGCGAG 444
 QY 121 ArgGlyIleProProGlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThr 140
 Db 445 AGGAAGATTCACCTCTCGAGATGGGAAGAGATATATGATGATTCATGCTATGTTGAC 504
 QY 141 AsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIle 160
 Db 505 AGTCATCGTAATCATCTTGATACCGATATGGCAGTACAGAAAACCTGCGTGAAGAAAT 564
 QY 161 AspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThr 180
 Db 565 GACAAGATGAAGTGTGTTGGAGCAATTTCTCGTGTATGAAATATTTGGCTTCAT 624
 QY 181 ArgSerAlaThrGlyIleThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeu 200
 Db 625 CGAAGCGCCACTGGTATCACTTACCGGAATGGCACCAGGAGTACAGGAGCATCACTG 684
 QY 201 IleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGly 220
 Db 685 ATCGGAGATTTTAACTACTGGAATCGGAAATCTGATGTTATGGCTCGGAACGACTTTGGT 744
 QY 221 ValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySer 240
 Db 745 GTGGGAATATTTCTGCCAATATATGCTGATGGCTCACCAGCAATTCGCCATGGCTCC 804
 QY 241 ArgValLysIleArgMetAspThrProSerGlyValLysAspSerIleProAlaTrpIle 260
 Db 805 CGTGTGAAGATCCGATGATACCCATCTGGTATTAAGACACCTCAATCCAGCTTTGATC 864
 QY 261 AsnTyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProPro 280

Db 865 AAGTATTCCTCCAGCCACCTGGCAGATCCCATATAATGGATATATATGACCCCTCT 924
 QY 281 GluGluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIle 300
 Db 925 GAGGAGGATAATATGCGTTCAACATCTCTGFCCAAAGAAACCCACATCGCTGCCTATATA 984
 QY 301 TyrGluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPhe 320
 Db 985 TATGAATCATCTGTTGAATGAGTAGTAGCGAACCAAGATAATATATATGCAACTTT 1044
 QY 321 ArgAspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAla 340
 Db 1045 AGAGATGATGATCTTCCCGGTATAAAAGCTAGGCTATATGCTGTGAGATAATGGCC 1104
 QY 341 IleGlnGluHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPheAlaPro 360
 Db 1105 ATCAAGACATGCGCTACTATGCCAGCTTGGGTATCATGTGACAAATTTTTCGCACCT 1164
 QY 361 SerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeu 380
 Db 1165 AGCAGCCGCTTTGGAACACCTGATGACCTTAATCTTTCATAGACAAAGCTCATGAGCTA 1224
 QY 381 GlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGly 400
 Db 1225 GGTCTGGTGTCTCTGATGATATGTGCACAGCCATGCAATCAAAAACACACATGGATGGC 1284
 QY 401 LeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyValArgGlyTyrHis 420
 Db 1285 CTGGACATGTTTGATGGTACTGATGTCATATTTCCACTCTGGATCGCGTGGTATCAT 1344
 QY 421 TrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeu 440
 Db 1345 TGGATGTGGGATTCGCTCTTTTCAATTCAGGAAGCTGGGAAGTCTTAGTATCTCTT 1404
 QY 441 SerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyVal 460
 Db 1405 TCCACGCGAGATGGTGGCTGGGAAGAAATAGTTTGTAGTGGTTCAGATTTGATGTTG 1464
 QY 461 ThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGlu 480
 Db 1465 ACTTCATGATGTCACATCATCATGCTGACCTGCGAGTCAATTTACTGGGAATTCATAGAG 1524
 QY 481 TyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeu 500
 Db 1525 TACTTTGGATATCTTACTGATGTTGACGCTCTGCTCTATCTAATGCTGCTGAACGATTTG 1584
 QY 501 IleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThr 520
 Db 1585 ATTCATGGGCTATACCTTGAGGCTATTTGTCGGCGAAGATGTTAGCGGATGCCAGCT 1644
 QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
 Db 1645 ITTTGCGTCTCTCGAAGACGGTGTGTTGGGTTTGGACTACCGCTACACATGCCAGTG 1704
 QY 541 AlaAspLysArgIleGluLeuLysLysArgAspGluAspTrpArgValGlyAspIle 560
 Db 1705 GCATATAATGGATTGAGCTTCTTAAGAAGAGACAGGAGTCTGCGAGTTGGTGATATA 1764
 QY 561 ValHisThrLeuThrAsnArgTyrTrpSerGluLysCysValSerTyrAlaGluSerHis 580
 Db 1765 ACTTTCAGCTTACCAACAGAGGTGGGAGAAAATGTGTCGTCTATGCGAGAGATCAT 1824
 QY 561 AspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr 600
 Db 1825 GATCAAGCCCTTGTGGAGACAAACGATAGCTTCTGGCTAATGGAATAGGACATGTAT 1884
 QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
 Db 1885 GATTTCATGCGCGTTGATAGACAGGCCACTCCGCGTGTAGACCGTGGGATGCTTTACAC 1944
 QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeuAsnPheMetGly 640

Db 1945 AAAATGATCGCTCTCATTACGATGGGATGGGAGGAGGATACCTCAATTCATGGGA 2004
Qy 641 AsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 2005 AACGAATTTGGACACCCAGAAATGGATCGACTTCCCAAGACCCGACACCTTCTCGAT 2064
Qy 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeu 680
Db 2065 GGCAGAGTCATCGCTGGGAATATGGTAGTTATGATTAATGCCGACGAGGATTTGATG 2124
Qy 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db 2125 GGAGATGAGATATCTTAGATACCATGGACTCAAGAGTTTGTATCGAGCAATGCAAAAT 2184
Qy 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db 2185 CTAGAGGAGAGCTATGGTTTCATGACTTCAGAGCACCAGATACATATCCGCAAGGATGAA 2244
Qy 721 GlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPheAsnPheHisTrp 740
Db 2245 GGACACAGAGCATGTTATTCAGAGAGGTAACTGCTCTTCGCTTCACTTCCACTGG 2304
Qy 741 ThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysProGlyLysTyrLysValAla 760
Db 2305 ACCAACAGTTACTCTGACTACCGTATCGGTTGCTCTGTTCGGGAAAGTACAAATATCGTT 2364
Qy 761 LeuAspSerAspProLeuPheGlyPheGlyArgIleAspHisAsnAlaGluTyr 780
Db 2365 TTGACTCTGATACTCTTTATTTGGAGGCTTCAACCGGCTAGATGACTCCGCGGAGTTT 2424
Qy 781 PheThrPheGluGlyTrpTyrAspArgProArgSerIleMetValTyrAlaProCys 800
Db 2425 TTCACCTCTGATGGAAGCAGCAGATAGGCTTCTCTTCATCGTGTATGACCCGTC 2484
Qy 801 LysThrAlaValTyrAlaLeuValAspLysGluGluGluGluGluGluGluGlu 820
Db 2485 AGAACCGCTGAGTTTACGCTGCGATGATGATGATGATGATGATGATGATGATGATGAT 2544
Qy 821 GluGluValAlaAlaValGluValVal 830
Db 2545 GTCCCATGAGGCTGTTACCCGAGATGTT 2574

RESULT 4

US-09-792-127-3

; Sequence 3, Application US/09792127

; Patent No. US20020002713A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Beckles, Diane M.

; APPLICANT: Butler, Karla

; APPLICANT: Pearlstein, Rich

; TITLE OF INVENTION: Starch Branching Enzyme IIB

; FILE REFERENCE: BBL439 US NA

; CURRENT APPLICATION NUMBER: US/09/792,127

; CURRENT FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: 60/186098

; PRIOR FILING DATE: 2000-03-01

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 3

; LENGTH: 3039

; TYPE: DNA

; ORGANISM: Triticum aestivum

US-09-792-127-3

Alignment Scores:

Pred. No.:

Score: 0

Length: 3039.00

Matches: 538

Conservative: 95

Best Similarity: 81.52%

Best Local Similarity: 69.66%

Query Match: 68.02%

Indels: 46

Gaps: 10

DB: 8

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-792-127-3 (1-3039)
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Db 264 TCCGGGGAGGATGATGATCCCT-----GACGGCGGTAGTGGCGGRACA----- 305
Qy 37 PheGluPheThrGluThrSerProGluAsnSerProAlaSerThrAspValAspSerSer 56
Db 306 -----CCGCTTCCATCGAC----- 320
Qy 57 ThrMetGluHisAlaSerGlnIleLysThrGluAsnAspValGluProSerSerAsp 76
Db 321 -----GGTCCCGTTTCAGTTCTGATGATCTGAAG----- 353
Qy 77 LeuThrGlySerValGluLeuAspPheAlaSerSerLeuGlnGluGluGlyGly 96
Db 354 -----GTCCCATTCATTGATGATGAACAAGC-----CTACAGATGGAGGT 395
Qy 97 Lys-----LeuGluGluSerLysThrLeuAsnThrSerGluGluThrIleLeuAspGlu 114
Db 396 GAAAGATAGTATTGTTGCTTCAGAGACAAATCAGTTAGTGAAGAAATTTGATGCTGAAGAC 455
Qy 115 SerAspArgIle-----ArgGlu-----ArgGlyIleProProPro 126
Db 456 ACGACGACGAATGGCAAAAGATCATCTACGAGGGAGAAATACGCATTTCTGCCACACCG 515
Qy 127 GlyLeuGlyGlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeu 146
Db 516 GGAATGACACCAATATACGAGATTGACCAACGCTCCGAGACTTTAAGTACCATCTT 575
Qy 147 AspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGly 166
Db 576 GAGTATCGATATAGCTATACAGAGAAATACGTTACACATTTGATGAACACCAAGAGAGC 635
Qy 167 LeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIle 186
Db 636 ATGGATGTATTTTCCCGCGTTACGAGAAAGTTTGGATTATGCGCAGCGCTGAAGGTATC 695
Qy 187 ThrTyrArgGluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnAsn 206
Db 696 ACTTACCGAGAAATGGCTCTCGAGCAGATTTCTGCAGCATTTAGTTGCGGACTTCAACAAT 755
Qy 207 TrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeu 226
Db 756 TGGGATCCAAATGCAGACCATATAGCAAAATACCTTGGTGGTGGGAGATTTTCTTG 815
Qy 227 ProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValIysIleArgMet 246
Db 816 CCAACAATGCAGATGGTTCCGCCCAATTCCTCAGCGCTCAGCGGTGAAGGTGAATG 875
Qy 247 AspThrProSerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeu 266
Db 876 GATACCTCCATCTGGGATAAAGGATTCATTCCTGCTGGATCAAGTACTCCGTCGAGACT 935
Qy 267 ProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGluArgTyrIle 286
Db 936 CCAGGAGATATACCATACATGGAATATATTATGATCTCCCTCCCAAGAGAGATGATGA 995
Qy 287 PheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGly 306
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Qy 307 MetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuPro 326
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Qy 327 ArgIleLysLysLeuGlyTyrAsnAlaLeuGluIleMetAlaIleGlnGluHisSerTyr 346
Db 1116 AGAATTAAAGACTTGGATACAAATGAGTGCATTAATATGCAATTCACAGACACTCATAC 1175
Qy 347 TyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPheGlyThr 366
Db 1176 TATGGAAGCTTTGGGTACCATGTTACCAATTTCTTTCACCAAGTAGCCGTTTGGGTCC 1235

217 AsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySerProAlaIle 236
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306 AATGACCTGGTGGTGGAGATTTCTGCCAACAATGCAGATGGTTCGCCACCAAT 365
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237 ProHisGlySerArgValIleArgMetAspThrProSerGlyValIleAspSerIle 256
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366 CCTCAGCCTCAGGGGTGAAGGTGAGATGGATCTCCATCTGGGATAAAGGATTCAT 425
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257 ProAlaTrpIleAsnTyrSerLeuGlnProAspGluIleProTyrAsnGlyIleHis 276
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426 CCGTCTGGATCAAGTACTCCGTCCGAGACTCCAGGAGATATACCAATCAATGGAATAT 485
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277 TyrAspProProGluGluGluArgTyrIlePheGlnHisProArgProIleLysProLys 296
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377 AlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsn 396
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397 ThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAla 416
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846 ACCTTGGACGGGTGAATGGTTTGTGATGGCAGGATACACATTCATTCCTGATGGTTCGA 905
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417 ArgGlyTyrHisTrpMetIrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeu 436
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906 CGGGGCCATCACTGGATGGGATCCCGTGTGTTAACTATGGGAATAAGGAAGTTATA 965
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497 ValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSer 516
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1146 ATCAATGATCTAATTCATGGTTTATCTCTGAAGCCGTAACTATCGGTGAAGATGTTAGT 1205
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517 GlyMetProThrPheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeu 536
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1206 GGAATGCTACATTTGCCCTTCCTGTTCAAGTTGGTGGGTGGTGGTGGTGGTGGTGGT 1265
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537 HisMetAlaIleAlaAspLysArgIleGluLeuLeuLysArgAspGluAspTrpArg 556
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1266 CATATGGCTGTCCGCAAAATGGATGAACTTCTCAAGGAAACGAATGAAGCTTGGGAG 1325
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557 ValClyAspIleValHisThrLeuThrAsnArgTrpSerGluLysCysValSerTyr 576
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1326 ATGGGTAAATATTGCACACACATTAACAACAGAGGTGGCTGGAAAAAGTGTGTACTTAT 1385
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577 AlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLeuMetAsp 596
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Db 1386 GGTGAAGTCAAGATCAAGCACTTGTGGAGACAGACTATTGCAATCTGGTGTGAGGAC 1445
QY 597 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGly 616
Db 1446 AAGGATATGATGATTTTCATGGCTGACGACCTTCGACCCCAATATTCATGCTGGA 1505
QY 617 IleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlyGluGlyTyrLeu 636
Db 1506 ATGACACTGCATAAAATGATTAGACTTATCAATCGGTCTAGGAGAGAGGTTATCTT 1565
QY 637 AsnPheMetGlyAsnGluPheGlyHisProGluTrpIleAspPheProArgAlaGluGln 656
Db 1566 AACTTTATGGAAATGAGTTCGGCATCTGTAATGATAGACTTCCCAAGAGCCCAACA 1625
QY 657 HisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArg 676
Db 1626 GTACTTCAAGTGGTAACTTCATCCAGGAACAACAACAGATACGACAAATGCCGTGCA 1685
QY 677 ArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArg 696
Db 1686 AGATTTGACCTGGGTGATGCAAAATTTCTTAGGTATCATGGTATGACAGAGTTGATCAG 1745
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Db 1746 GCAATGCACTTTCAGGAAATAATGTTTATGACATCAGACCAACAGTACGTATCT 1805
QY 717 ArgLysAspGlyAspArgMetIleValPheGluLysGlyAsnLeuValPheValPhe 736
Db 1806 CGGAACATGAGAAATAGGTGATCGTGTGTAAGAGGACATGTTGTTGTTGTTGTT 1865
QY 737 AsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaLysLeuLysProGlyLys 756
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QY 757 TyrLysValAlaLeuAspSerAspProLeuPheGlyPheGlyPheGlyArgIleAspHis 776
Db 1926 TACAGGTGCTTACAGTCGACGCTGGACTCTTGGTGATTTGGTAGATTCATCTCAGT 1985
QY 777 AsnAlaGluTyrPheThrPheGluGlyTyrTyrAspArgProArgSerIleMetVal 796
Db 1986 ACTGCAGACGACGCTCACTTCTGACTGCCAACAATGACAACAGGCCCATTCATCTCAGT 2045
QY 797 TyrAlaProCysLysThrAlaValValTyrAla 807
Db 2046 TACACTCTAGCAGAACCTGTGTGTCTATGCT 2078
RESULT 6
US-10-254-534-3
; Sequence 3, Application US/10254534
; Publication NO. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393

; PRIOR APPLICATION NUMBER: 60/222,470
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PERL Program
; SEQ ID NO 30

; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030113720A1 g184025
US-09-918-624B-30

Alignment Scores:
Pred. No.: 5,26e-227 Length: 2955
Score: 2058.00 Matches: 383
Percent Similarity: 71.82% Conservative: 119
Best Local Similarity: 54.79% Mismatches: 176
Query Match: 46.09% Indels: 22
DB: 9 Gaps: 7

US-10-056-454A-15_COPY_49_882 (1-834) x US-09-918-624B-30 (1-2955)

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Db 134 AGCGCGCGCTCAATCGCGCGCTGGCTGACGTGCGGAA-CTGGCC---AGACTCCTGGAG 189

QY 135 IleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLys 154
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Db 190 ATCGACCCCTACTTGAAGCCCTGACGCGCTGGACTCCAGCGGAGTAAAGCATTAGC 249

QY 155 LysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAlaPheSerArgGlyTyr 174
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Db 250 CAAATTTGAAGAATCGGAGAAATGAAGTGGTATTGATAAGTTTCCAGAGCTAT 309

QY 175 GluLysMetGlyPheThrArgSerAlaThrGlylleThrTyr---ArgGluTrpAlaLeu 193
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Db 310 GAATCATTTGGCGCTCACAGATGCTGATGGTGGTATTACTCCAAAGAAATGGGCGCG 369

QY 194 GlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnTyrAspAlaAsnAlaAspIle 213
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Db 370 GGAGCAGAGAGAGTTTCTTACTGGAGATTATTAATGGTGGTAAATCCATTTTCGTACCCA 429

QY 214 MetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsnValAspGlySer 233
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QY 234 ProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGly---Val 252
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QY 253 LysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyr 272
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QY 273 AsnGlyIleHisTyrAspProGluGluGluArgTyrIlePheGlnHisProArgPro 292
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Db 610 GATTGGATACACTGGGATCCA-----GAACACTCATATGAGTTTAAGCATTCACAGACCA 663

QY 293 LysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerProGluPro 312
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Db 664 AAGAAGCCAGGAGTCTAAGAAATTAAGATCTCATGTTGGGAATTTCTCCCATGAGGA 733

QY 313 LysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGly 332
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Db 724 AAGTAGCTCTCTATAAACATTTTATACATGCAATGTACTACCAAGATCAAGGCCITGGA 783

QY 333 TyrAsnAlaLeuGlnIleMetAlaIleGlnIleHisSerTyrTrpAlaSerPheGlyTyr 352
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Db 784 TACAACCTGCTCAGTTGATGGCAATCATGAGCAGTCTTACTATGCGACTTGGTTTAC 843

QY 353 HisValThrAsnPheAlaProSerSerArgPheGlyThrProAspLeuLysSer 372
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Db 844 CAAATCACAAAGCTTCTTTGCAGCTTCCAGCCGTTATGGAAACACCTGTAAGAGCTACAGAA 903

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Db 904 CHGGTAGACACAGCTCAITCCATGGGTATCATAGTCTCTTAGATGTGTACACAGCCAT 963

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QY 453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
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QY 473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAlaValVal 492
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Db 481 TCGGAGCAGCAATTCATATCAGAAAGACGAGCAGATAGAGTATCGTATTCGAAAGA 422
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QY 750 AlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspAspProLeuPheGly 769
Db 361 GGTGCTCCAGCCTGGAATAATAGATCGTATGGACTCGGACGATCCTCTCTTGT 302
QY 770 GlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTrrPyrAspAsp 789
Db 301 GGATTCATAGGCTCGATCGCAAGCAGAGTACTTCACCTATGATGGCTTATACGACGAA 242
QY 790 ArgProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyrAlaLeuVal 809
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QY 810 AspLysGlu 812
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RESULT 11
US-10-329-960-1
; Sequence 1, Application US/10329960
; Publication No. US2003009277A1
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Frag
; FILE OF INVENTION: Thereof, and Uses Thereof
; FILE REFERENCE: PB186PI
; CURRENT APPLICATION NUMBER: US/10/329,960
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 09/643,990
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: US 08/487,429
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/426,787
; PRIOR FILING DATE: 1995-04-21
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1830121
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72 / NAME/KEY: misc_feature
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QY 340 AlaIleGlnGlnHisSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAla 359
Db 1437031 CGCCTTCTGAATTCGCTTTGATGGTTCTTGGGTTATCAACCACTTGGCCTTATTCG 1437090
QY 360 ProSerSerArgPheGlyThrProAspAspLeuLysSerLeulleAspLysAlaHisGlu 379
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QY 380 LeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAsp 399
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QY 400 GlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArg---Gly 418
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QY 479 GluGluTyr-----PheGlyLeuAlaThrAspValAspAlaValValTyrLeu 494
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QY 495 MetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAsp 514
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QY 515 ValSerGlyMetProThrPheCysIleProValGlnGluGlyValGlyPheAspTyr 534
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QY 555 TrpArgValGlyAspIleValHisThrLeuThrAsnArgArgTirpSerGluLysCysVal 574
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QY 575 SerTyrAlaGlu-----SerHisAspGlnAlaLeuValGlyAspLys 588
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QY 589 ThrIleAlaPheTirpLeuMetAspLysAspMetIyrAspPheMetAlaLeuAspArgPro 608
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QY 609 SerThrSerLeuIleAspArg-----GlyIleAlaLeuHisLysMetIleArgLeu--- 625
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US-09-738-626-1354
; Sequence 1354, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738, 626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 1354
; LENGTH: 2193
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1354
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Alignment Scores: 1.06e-48 Length: 2193
Pred. No.: 513.50 Matches: 198
Score:

Percent Similarity:	41.07%	Conservative:	133
Best Local Similarity:	24.57%	Mismatches:	328
Query Match:	11.50%	Indels:	147
DB:	9	Gaps:	35

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Dd	121	GTTATCCGACCGCGCAGGTGGCGCGACGAGGTAAATTGCTTATGACACACACTCC 180	:::	
QY	117	ArgIleArGluArGlyLeuProProGlyLeuGlyGlnLysIleTyrgluileAsp 136	:::	
Dd	181	CACGTC-----ATGACCCT-----ATCGGCGACGACATTTCGCAATTGAC 222	:::	
QY	137	ProLeuLeuThrAsnTyArgGlnHisLeuAspTyArgTyr-----Ser 151	:::	
Dd	223	-----TTAGGTCAACCGGAGCGCGCTGACTATCGCTTGGAACTCACCTGGCTGAT 273	:::	
QY	152	GlnTyrLysLeuArGluAlaIleAspLysTyr-----Glu 164	:::	
Dd	274	CAAGAACCGCAGGTCAAG---CGTGATCATACTACTTCCTCCGACCGCATAGGCGAG 327	:::	
QY	165	GlyGlyLeuGluAlaPheSerArgLy-----TyrGluLysMetGlyPhe 179	:::	
Dd	328	ATGGATAATTACCTCTTCTCTGAGGACCGCCATGAGCGTTTCTGGGAGATTCTCGGTGCC 387	:::	
QY	180	Thr-----ArgSerAlaThrGlyIleThrTyArgGluTrp 191	::: ::::	
Dd	388	AACATCAAGACCTACCAACATCGCTCGGAACAGTTCTGTGCACCGCATTTACTGTGTG 447	::: ::::	
QY	192	AlaLeuGlyAlaGlnSerAlaAlaIleGlyAspPheAsnAsnTrpAspAlaAsnAla 211	:::	
Dd	448	GCTCCAACGCAATVGCTGCGCAGTGGTCGGTGTTCACAGGTTGGAATTCATCCCGAG 507	:::	
QY	212	AspIleMet---ThrArGsnGluPheGlyValTrpGluIlePheLeuProAsnAsnVal 230	:::	
Dd	508	CATCCGATGCGTTCTATGGGTGGTTTCGGCTCTGTGGAGCGTTCATCCCGACGATACAG 567	:::	
QY	231	AspGly-----SerProala 235	:::	
Dd	568	GAAGCGCAAGTGTAACAATWCGCGCTCCAAACACGGAAGGCCAACGTCGTGATAAGGCC 627	:::	
QY	236	IleProHisGlySerArqValLysIleArgMetAspThrProSerGlyValLysAspSer 255	::: ::::	
Dd	628	GATCCGATGCTCGTCGCGCAGAACTGGCGCGGACACCGAGATCTATGTGCGTCTCCTCT 687	::: ::::	
QY	256	IleProAlaTrpIleAsnTySerLeuGlnLeuProAspGluIleProTyArgsnGlyIle 275	:::	
Dd	688	GAGTACAGTGG-----	:::	
QY	276	HISTyAspProProGluGluGluAtqTyIlePheGlnHisProArgProLysLysPro 295	:::	
Dd	700	-----CAGATTCCGAGTGGTCGCGGAGCGGTGCCAAAAGCTGATCTCGCATCCAGCCA 753	:::	
QY	296	LysSerLeuArgIleTyrgluSerHisIleGlyMetSerSerProGluProLysIleAsn 315	::: ::::	
Dd	754	ATGAGT-----GTCTACGAGGTCCACCTCGGTCTCTGGCGTGGGGT-----AAG 798	::: ::::	
QY	316	SerTyrrValasnPheArspGluValLeuProArGlieLysLysLeuGlyTyrrAsnAla 335	::: ::::	
Dd	799	AAGTATGAGGATTTGGCTACTGAGCTGGTTGATACGTCGCGAGATCTTGCTACACCCCAC 858	::: ::::	
QY	336	LeuGlnIleMetaIleGlnGluHisSerTyTyrrAlaSerPheGlyTyrrHisValThr 355	::: ::::	

448 ATCTACGAGCTTCATATCGGTTCTGCGAAGAAAGCGGATGGAGCGTTTTTTCACATAC 507
QY
318 VallasnPheArgAspGluValLeuProArgIleHisLysLeuGlyTyrAsnAlaLeuGln 337
Db
508 CGGNACTGACGGAACCGGTCATCTTACGTCAAAGAACACAGGATTCACACATATCGAG 567
Db
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358 PheAlaProSerSerArgPheGlyThrProAspAspLeuLysSerLeuIleAspLysAla 377
QY
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Db
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QY
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Db
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QY
748 CACGCGCTGTATTTGACGGGTATGCTCTGTATGAA-----TATAAA 792
Db
413 HisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsn 432
QY
793 CACGAGCATGACAGG---GAAATTTGGGAATGGGGACCGCCCAATTTTGACCTCGGAAAA 849
Db
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Db
453 AspGlyPheArgPheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerVal 472
QY
910 GATGATTTTCGAGTCGATCGCGTTCCGAACTCTGATTTGCCCAACCGCTCCAGCCT 969
Db
473 GlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValVal 492
QY
970 GAAGCGAAGCGC-----TTTGCATGCGAA 993
Db
493 TyrLeuMetLeuValAsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGly 512
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994 TTTATTCACAGCTTTAAATGACAGCGTTTTTGCAAAAGATCCCGACTTTTGATGATGCA 1053
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QY
1348 TATTTTATGATGACCCCGGAAAAAG-----CTCTTTTATGCGCGGTGAGTTGCT 1401
Db

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 6, 2003, 02:17:31 ; Search time 2890 seconds
(without alignments)
4673.715 Million cell updates/sec

Title: US-10-056-454A-15_COPY_49_882
Perfect score: 4465
Sequence: 1 EKSYSNSEFRSTVAAGKV.....EEEEEEVAAVEVVVEE 834

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Database :

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2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
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8: em_hic:*
9: gb_est1:*
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11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estcom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2987.5	66.9	2766	11	AY109521	Zea mays
2	2809.5	62.9	2732	11	AY109532	Zea mays
3	2082	45.6	3012	11	AY105679	Zea mays
4	2038	45.6	2738	11	AK009815	Mus muscu
5	1136	25.4	728	14	BU008463	BU008463 QGH7K17.Y
6	1123	25.2	713	14	BQ986883	BQ986883 QGF10L08.Y
7	1121.5	25.1	1524	10	B636603	rockefell
8	1063	23.8	689	13	B1308555	EST529965
9	1062	23.8	801	10	BE195628	HVSMEH008
10	1060	23.7	1482	17	BH770747	LLMtag49
11	1044	23.4	678	10	AV939010	AV939010
12	1035.5	23.2	898	14	BQ716536	AGENCOURT
13	1027.5	23.0	731	10	BE602527	B6602527 HVSMEH009
14	989.5	22.2	717	14	BU005876	BU005876 QGG9F08.Y
15	976	21.9	639	10	AW065909	AW065909 687002609
16	973.5	21.8	621	12	BG521671	BG521671 13-3 Stev
17	971	21.7	1088	14	BQ232004	AGENCOURT
18	970	21.7	825	12	BF065047	BF065047 HV_CEP002
19	959	21.5	646	9	AU238577	AU238577
20	956.5	21.4	695	14	BQ240494	BQ240494 TA05016F
21	951	21.3	573	13	BM526229	BM526229 sal38f02.
22	950	21.3	651	12	BG526727	BG526727 63-11 Ste
23	944.5	21.2	761	13	BM411030	BM411030 EST585357
24	937.5	21.0	918	17	CNS06W72	AL418101 T3 end of
25	934.5	20.9	751	13	BI920158	BI920158 EST540093
26	934	20.9	569	10	AV442128	AV442128 AV442128
27	931	20.9	571	13	BI69680	BI69680 sal125q09.
28	927	20.8	650	9	BE427534	BE427534 PSR7153 I
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31	914	20.5	962	17	CNS0607J	AL408509 T7 end of
32	907	20.3	560	14	BM885252	BM885252 sal197a08.
33	897.5	20.1	967	17	BH132946	BH132946 ENTPC72TF
34	897	20.1	571	13	BI469105	BI469105 sal107e09.
35	895	20.0	589	10	AW596011	AW596011 sal96g03.Y
36	894	20.0	576	10	AW244197	AW244197 687050F06
37	891.5	20.0	693	13	BI091718	BI091718 602859457
38	881	19.7	575	13	BI425610	BI425610 sah69a11.
39	878	19.7	582	13	BM309136	BM309136 sak55b02.
40	872	19.5	801	12	BG741971	BG741971 602633412
41	866	19.4	592	13	BJ268430	BJ268430
42	863	19.3	774	9	AU139463	AU139463
43	861.5	19.3	671	13	BI719233	BI719233 1031042C0
44	860.5	19.3	602	12	BG524041	BG524041 38-25 Ste
45	860	19.3	739	9	AU004044	AU004044

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
AY109521	AY109521	Zea mays	AY109521	AY109521.1	GI:21213273	HTC	Zea mays		
							Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.		
							1 (bases 1 to 2766)		
							Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whittitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.		

TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of
JOURNAL	Overgo Probes
REFERENCE	Unpublished (2002)
AUTHORS	2 (bases 1 to 2766)
TITLE	Coe, E.C.
JOURNAL	Direct Submission
FEATURES	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
source	Location/Qualifiers
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	/organism="Zea mays"
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	/db_xref="taxon:4577"
	/clone="C11245_1"
	/clone.lib="Maize Mapping Project/DuPont Consensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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ORIGIN	
Alignment Scores:	
Pred. No.:	0 Length: 2766
Score:	2987.50 Matches: 562
Percent Similarity:	79.04% Conservative: 79
Best Local Similarity:	69.30% Mismatches: 147
Query Match:	66.91% Indels: 23
DB:	11 Gaps: 6
US-10-056-454A-15_COPY_49_882 (1-834) x AY109521 (1-2766)	
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Db	56 AGCTGCCTGTGTCTCTCGAAGGTAAGTACTGTGCTGGAGCTGGAGCTGACATGCT 115
Qy	32 SerSerThrAspGlnPheGluPheThrGluThrSerProGluAsnSerProAlaSerThr 51
Db	116 TCCTCCGACAG-----CGGTCGTGGACACTCAACCTGAAGAA-----CTACAGATA 163
Qy	52 AspValAspSerSerThrMetGluHisAlaSerGlnLysThrGluAsnAspVal 71
Db	164 CCTGAACGACAGACTGCTGTGGAGAAGACATCTCTCACCACACTCAACAA----- 214
Qy	72 GluProSerSerAspLeuThrGlySerValGluGluLeuAspPheAlaSerSerLeuGln 91
Db	215 -----ACATCAGCATGGCTGAAGCA-----AGTCAGAGATTGAG 250
Qy	92 LeuGlnGluGlyLysLeuGluGluSerLysThrLeuAsnThrSerGluGluThrIle 111
Db	251 GCTGAGAGAGCGCTGACCTCTCAGAGATTGAGTTGGAGTTGGAGGTACTGGTGAACCAAA 310
Qy	112 IleAsp-----GluSerAspArgIleArgGlu-----ArgGlyIle 123
Db	311 ATTGATGTCAGGCATCAAAAGCCAAAGCACCATCTCGTGAGGAGAAACACACGAGTTATC 370
Qy	124 ProProGlyLeuGlyClnLysIleThrGluIleAspProLeuLeuThrAsnTyrArg 143
Db	371 CCACCACGAGAGATGGCCACGAAATATAGATTGACCCAAATGTTGAAGAGGTTTCGG 430
Qy	144 GlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyr 163
Db	431 GGTCACCTTGACTACCGATACAGTCAATATAAGAGATTACGTGGCGCTATTGATCAACAT 490
Qy	164 GluGlyGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArgSerAla 183
Db	491 GAAGGTGGTTGGATGCAATTTACGCGGTTACGAAAGCTGGATTACTGCGACGGCT 550
Qy	184 ThrGlyIleThrTyrArgGluThrPalaLeuGlyValaGlnSerAlaAlaLeuIleGlyAsp 203

BASE COUNT	837 a	628 c	790 g	756 t	1 others
ORIGIN					

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Score: 2082.00
Percent Similarity: 66.00%
Best Local Similarity: 50.44%
Query Match: 46.63%
DB: 11
Length: 3012
Matches: 402
Conservative: 124
Mismatches: 208
Indels: 63
Gaps: 10

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US-10-056-454A-15_COPY_49_882 (1-834) x AY105679 (1-3012)

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QY	63	GlnIleLysThrGluAsnAspValGluProSerSerAspLeuThrGlySerValGlu	82
Db	227		268
QY	83	GluLeuAspPheAlaSer	89
Db	269	CGCCTGAGTGTTGTCCTCCAGTGCAGAGGCTCCCGGTGAGGGGTGCGAAGGTCAAG	328
QY	90	LeuGlnLeuGlnGluGlyLysLeuGluSerLysThrLeuAsnThrSerGluGlu	109
Db	329	ASCAAAATTCGCACCTGCAGCTACTGTGCAAGAAGATAAACTATGCGCACTGCCAAGGC	388
QY	110	ThrIleIleAspGluSerAspArgIleArgGluArgGlyIleProProProGlyLeuGly	129
Db	389	GATGTC-----GACCATCTC-----	403
QY	130	GlnLysIleTyrGluIleAspProLeuLeuThrAsnTyrArgGlnHisLeuAspTyrArg	149
Db	404	---CCCATATAGCACTGGCCCCAAGCTGGAGATATTCAGGACCATTTCAGGTACCGG	460
QY	150	TyrSerGlnTyrLysLysLeuArgGluAlaIleAspLysTyrGluGlyGlyLeuGluAla	169
Db	461	ATGAAAAGATTCTTAGACGACAGAGGATCAATTGAAGAAATGAGGAAGTCTTGAATCT	520
QY	170	PheSerArgGlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArg	189
Db	521	TTTTCTAAAGCTATTGAAATTTGGATTAAATACAAATGAGGATGGAACCTGTATACGT	580
QY	190	GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnThrAspAla	209
Db	581	GAATGGCACCTGCTGCGCAGGAGCGACAGCTTAATGGTGACTTCAATGACTGGAATGGT	640
QY	210	AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn	229
Db	641	GCAACCATTAAGATGGAGAGGATAAATTTGGTTTGGTCGATCAAAAT---GACCAT	697
QY	230	ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro	249
Db	698	GTCNAAAGGAAACCTGCCTCCCTTCAAAATCCCAAGGTTAAATTCGCTTTCACATGGT	757
QY	250	SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu	269
Db	758	GGAGTAGTGGTTGATCGTATTCACGACATTCGTTATCGGACTGTTGAGCGCTCTAAA	817
QY	270	Ile-----ProTyrAsnGlyIleHisTyrAspProProGluGluArgTyrIlePhe	287
Db	818	TTTGGAGCTCCCTATGATGTGTTCATTTGGATCTCTCTCTCTCTCTCTCTCTCTCTCT	877
QY	288	GlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMet	307
Db	878	AAGCATCTCGGCCTTCAAGCCTGCTGCTCCAGGTATCTATGAAGCCCATGTAGGTATG	937
QY	308	SerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArg	327
Db	938	AGTGGTGAAGAGCCAGCAGTAGCACCATATAGGGAATTTCCAGACAAATGTGTGCCACGC	997

QY	328	IleYsLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyr	347
DB	998	ATACGAGCAAAATAACTACAACACAGTTCAGTTCATGGCGAGTTATGGAGCATTCGGACAT	1057
QY	348	AlaSerPheGlyTyrHisValThrAsnPheAlaProSerSerArgPheGlyThrPro	367
DB	1058	GCTTCCTTCGGGTACCATGTGCAAAATTCCTTTCGGTTCAGCAGCAGATCAGGCACCA	1117
QY	368	AspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAsp	387
DB	1118	GAGGACTCAATATCTTGATAGGCACACAGTTGGTTCGAGTTCGTGATGAT	1177
QY	388	IleValHisSerHisAlaSerAsnThrLeuAspGlyLeuAsnMetPheAsp	405
DB	1178	GTTTCATAGCATGCAAGTAAATATGTCACAGATGTTTAAATGGCTATGATGTGGA	1237
QY	406	--CysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTyrMetTyrAsp	424
DB	1238	CAAAGCACCAAGAGTCCATTTTCATCGGGAGATAGAGTTATCATAAACTTTGGAT	1297
QY	425	SerArgLeu-PheAsnTyrGlyAsnTyrGluValLeuArgTyrLeuLeuSerAsnAlaAr	444
DB	1298	AGTCGCGTGTTCACATATGCTAACTGGGAGTATTAACGTTCTCTTCTTAACCTGAG	1357
QY	444	GTrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetIle	464
DB	1358	ATATTTGGTTGGATGAATTCATGTTTGATGCTCCGATTTGATGSAGTTACATCAATGCT	1417
QY	464	TyrIleHisHisGlyLeuSerValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLe	484
DB	1418	GTATCATCACCATGGTATCAATGGGGCTTACTGGAACTACACAGAAATATTTCAGTTT	1477
QY	484	uAlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuIleHisGlyLe	504
DB	1478	GGACACAGCTGTGGATGCAGTTGTTACATGATGCTGTCGAACCATTTAATGCAAACT	1537
QY	504	uPheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePr	524
DB	1538	CTTGCCAAAGCAACTGTGTGTGCTGAAGATGTTTCAGGATGCGGCTCCTTTGCGGCG	1597
QY	524	oValGlnGluGlyGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysAr	544
DB	1598	AGTTCATGAAGGTGGGTGGTTTGACTATCGGCTGGCAATGGCTATCCCTCATAGATG	1657
QY	544	gIleGluLeuLysLysArgAspGlu--AspTrpArgValGlyAspIleValHisIsth	563
DB	1658	GATTCACTACCTGAAGAATAAAGATGACTCTGAGTGTTCGATGGGTCAATACCGCATAC	1717
QY	563	rLeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAl	583
DB	1718	TTTGACATACAGGAGATATACTGAAAATGCATCGCATGTCGTAGAGGCATGATCAGTC	1777
QY	583	aLeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyrAspPheMe	603
DB	1778	TATGTTGGCGACAARAATTCATTTCTCCGTGACACAGGAAATGTACACTGGCAT	1837
QY	603	tAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHisLysMetIl	623
DB	1838	GTCAGACTTGCAGCGCTTCACTCACTCAATGATCGAGGATGTCATCTCAAAAGATGAT	1897
QY	623	eArgLeuValThrMetClyLeuGlyGlyGluGlyTyrLeuAsnPheMetGlyAsnGluPh	643
DB	1988	TCATCTCAACAAATGGCCCTTGGAGGTGATGGCTACTTGAATTTTATGGGAAATGAGTT	1957
QY	643	eGlyHisProGluTrpIleAspPheProArgAlaGluGlnHisLeuSerAspGlySerVa	663
DB	1958	TGTCACCCCAAGATGGATTCCTTCCAGA-----1988	
QY	663	lIleProGlyAsnGlnPheSerTyrAspLysCysArgArgArgPheAspLeuGlyAspAl	683
DB	1989	----GAAGGGAACAACCTGGAGCTATGATAAATGCAGCACACAGTGGAGCCTTGTGCACAC	2044
QY	683	aGluTyrLeuArgTyrArgClyLeuGlnGluPheAspArgProMetGlnTyrLeuGluAs	703

QY 668 GlnPheSerTyrAspLysCysArgArgPheAspLeuGlyAspAlaGluTyrLeuArg 687
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 1689 AATGAGAGTATACCATATGCGAGAGCGAGTTTAAATTRACCGAGCATGACCTTCCTCGC 1748
 QY 688 TyrArgGlyLeuGlnGluPheAspArgPrometGlnTyrLeuGluAspLysTyrGluPhe 707
 |||: ||| ||||| ||| |||||:||||: |||
 Db 1749 TATAAGTTCTAAATAACTTTGACAGAGATATGAATAGACTGGAAGAAGATGCGTTGG 1808
 QY 708 MetThrSerGluHisGlnPheIleSerArgLysAspGluGlyAspArgMetIleValPhe 727
 :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
 Db 1809 CTTTCAGCTCCACAGCGCTACGTTGAGTGAAGAAATGAAGCCCAATAGACAATCACTTT 1868
 QY 728 GluLysGlyAsnLeuValPheValPheAsnPheHisThrPheThrLysSerTyrSerAspTyr 747
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
 Db 1869 GAGAGCAGGAGCTTCCTTTTATTTCACTCCACCCCAAGCAAGACTATACGGACTAC 1928
 QY 748 ArgIleAlaCysLeuLysProGlyLysTyrLysValAlaLeuAspSerAspProLeu 767
 |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
 Db 1929 CGAGTCGGGACACCAACACCGAGGAGTTCAAAATTTGACTAGATTCTGACGCGGAG 1988
 QY 768 PheGlyGlyPheGlyArgIleAspHisAsnAlaGluTyrPheThrPheGluGlyTyrTyr 787
 :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
 Db 1989 TATGGAGGTATCAGACAGCTGGACCAACACCACTACTTTGCTGAGGCTTTTGACAT 2048
 QY 788 AspAspArgProArgSerIleMetValTyrAlaProCysLysThrAlaValTyrAla 807
 :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||
 Db 2049 AATGGGCGCCCTATCTCTCTGTTGTTAGATCCCAAGCGGAGTGGCTCTCATCTTCAG 2108
 QY 808 LeuValAsp 810
 |||||
 Db 2109 AATGTGGAT 2117

RESULT 5

BU008463

LOCUS

DEFINITION QGH7K17.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
 QGH7K17, mRNA sequence.

ACCESSION

BU008463

VERSION

BU008463.1

KEYWORDS

EST.

SOURCE

Lactuca sativa.

ORGANISM

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.

REFERENCE

1 (bases 1 to 728)

AUTHORS

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Riesberg,L.,
 Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
 P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lal,Z.,
 Church,S., Jackson,L. and Bradford,K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://comphenomics.ucdavis.edu/
 Unpublished (2002)

TITLE

JOURNAL

COMMENT

Contact: Alexander Kozik [R.W.Michelmore]
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 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
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 Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
 Belongs to contig QG_CA.Contig96851, see http://cypdb.ucdavis.edu/
 for details.

Plate: OGH7

row: K

column: 17.

Location/Qualifiers

1. 728

/organism="Lactuca sativa"

/cultivar="L.serriola"

/db_xref="taxon:4236"

/clone="QGH7K17"

/clone_lib="QG_EFGHJ lettuce serriola"

/lab_host="E.coli"

/note="Vector: pBRCDNASfiab; The library was constructed

FEATURES

Source

from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at <http://cypdb.ucdavis.edu/>
 TAG_LTB-QG_EFGHJ lettuce serriola
 TAG_TISSUE=leaves dark grow

BASE COUNT 227 a 133 c 149 g 218 t 1 others
 ORIGIN

Alignment Scores:

Pred. No.: 4.27e-123 Length: 728
 Score: 1136.00 Matches: 205
 Percent Similarity: 92.98% Conservative: 20
 Best Local Similarity: 84.71% Mismatches: 17
 Query Match: 25.44% Indels: 0
 DB: 14 Gaps: 0

US-10-056-454a-15_COPY_49_882 (1-834) x BU008463 (1-728)

QY 173 GlyTyrGluLysMetGlyPheThrArgSerAlaThrGlyIleThrTyrArgGluTrpAla 192
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 1 GGTATGAAATAATAGCTTTTCACTCGAGCAAAACAGTATCATCTTATAGAGAATGGCA 60
 QY 193 LeuGlyAlaGlnSerAlaLeuIleGlyAspPheAsnAsnTyrAspAlaAsnAlaAsp 212
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 61 CCTGGGCAAGTCTGCTTCACTTACTGGAGATTTCACAACTGGAATCCAATGCTCAT 120
 QY 213 IleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnValAspGly 232
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 121 GTTATGACCGCAATGAAATTTGGTGTGTGGGAGATCTTTTGGCAACAATGTCATCAT 180
 QY 233 SerProAlaIleProHisGlySerArgValLysIleArgMetAspThrProSerGlyVal 252
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 181 TCTTCACCTATTCCTCATGTTCTCGAGTAAAGATTCTGATGGATACCCATCGGCATT 240
 QY 253 LysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGluIleProTyr 272
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 241 AAAGACTCGATTCCTGCTTGGATCAAGTTTTCAGTACAAAGCACCTGGTGAGATTCCTTAT 300
 QY 273 AsnGlyIleHisTyrAspProGluGluGluArgTyrIlePheGlnHisProArgPro 292
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 301 AATGGAATATATCTATGATCCCCACACAGAGAAAATACGTGTTTCAACATCCAAAGACCA 360
 QY 293 LysLysProLysSerLeuArgIleThrGluSerHisIleGlyMetSerSerProGluPro 312
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 361 AAGAGCGCAATCTCTTAGGATTATAGGCACATGTTGGAATGAGTAGTAGTACGGAACCA 420
 QY 313 LysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLysLysLeuGly 332
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 421 ATGATCAACACGATGCTAACTTTAGACAGCATGTTCTCCCTCGCATAAAAAACTCGGT 480
 QY 333 TyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSerPheGlyTyr 352
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 481 TACAATGCAATCTCAATCATGCTATTCAAGAGCATTCATATTATGCTAGCTTTGGGTAC 540
 QY 353 HisValThrAsnPhePheAlaProSerSerArgPheGlyThrProAspAspLeuLysSer 372
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 541 CATGTGACAAATTTTTTGGCACCAGTAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 600
 QY 373 LeuIleAspLysAlaHisGluLeuGlyIleValValLeuMetAspIleValHisSerHis 392
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 601 ATGATTGATAAAGCACATGAATTAGTCTTGTGTTCTCATGGATATTGTGCATAGTCAT 660
 QY 393 AlaSerAsnAsnThrLeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPhe 412
 ||||| |||||:||||:|||| ||| :||| |||||
 Db 661 TCATCAACAACACATATAGATGGATTANATATGTTTGAAGAACATGATGATGATGATGAT 720
 QY 413 HisSer 414

Db	721	CAATCT	726		
RESULT 6	BQ986883				
LOCUS	QGF10L08.yg.ab1	QGF10L08	713 bp	mRNA	linear
DEFINITION	QGF10L08.yg.ab1	QGF10L08	lettuce serriola	Lactuca sativa	cdna clone
ACCESSION	BQ986883				
VERSION	BQ986883.1	GI:22404408			
KEYWORDS	EST				
SOURCE	Lactuca sativa.				
ORGANISM	Lactuca sativa				
REFERENCE	1 (bases 1 to 713)				
AUTHORS	Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavellie,D., Chevallier,P., Ziegler,J., Ellison ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.				
TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project				
JOURNAL	http://compgenomics.ucdavis.edu/				
COMMENT	Unpublished (2002)				
	Contact: Alexander Kozik [R.W.Michelmore]				
	Department of Vegetable Crops, R.W.Michelmore Lab				
	University of California at Davis (UCD)				
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	Tel: 1-(530)-742-1742				
	Fax: 1-(530)-752-9659				
	Email: akozika@ucdavis.edu [michelmore@vegmail.ucdavis.edu]				
	belongs to contig QG_CA.Contig6851, see http://cgdb.ucdavis.edu/				
	for details.				
	Plate: QGF10 row: L column: 08.				
FEATURES	Location/Qualifiers				
source	1..713				
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	/cultivar="L.serriola"				
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	/clone_lib="QGF10L08"				
	/lab_host="E.coli"				
	/note="Vector: pBRCNDSfiAB; The library was constructed				
	from 10 different sources of RNA from a single genotype.				
	Separate cDNAs were generated using primers that				
	incorporated unique 5' and 3' tags to distinguish each				
	source of RNA. cDNAs were then pooled, size-fractionated,				
	directionally cloned into a custom medium-copy vector and				
	transformations made with four size classes to minimize				
	size bias. Details of each source of RNA and library				
	construction can be obtained at http://cgdb.ucdavis.edu/				
	TAG_LIB=QG.FFGHJ lettuce serriola				
	TAG_TISSUE=flowers post-fertilized				
	TAG_SEQ=TGCCATCGG				
BASE COUNT	221 a	132 c	146 g	214 t	
ORIGIN					
Alignment Scores:					
Pred. No.:	1..41e-121	Length:	713		
Score:	1123.00	Matches:	203		
Percent Similarity:	93.67%	Conservative:	19		
Best Local Similarity:	85.65%	Mismatches:	15		
Query Match:	25.15%	Indels:	0		
DB:	14	Gaps:	0		
US-10-056-454a-15_COPY_49_882 (1-834) x BQ986883 (1-713)					
QY	178	GlyPheThrArgSerAlaThrGlyIleThrTyArgGluTrpAlaLeuGlyAlaGlnSer	197		
Db	1	GGTTTCACTCGAAGCAACAGGTATCACTTATAGAGATGGCCACCTGGGGCAAGTCT	60		
QY	198	AlaAlaLeuIleGlyAspPheAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsn	217		

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/db_xref="taxon:108607"
/clone_lib="Wastigamoeba balamuthi lambda ZAP II Library"
/notes="syn: Phreatamoeba balamuthi"
BASE COUNT 277 a 525 c 461 g 261 t
ORIGIN

Alignment Scores:
Pred. No.: 7,99e-121 Length: 1524
Score: 1121.50 Matches: 213
Percent Similarity: 69.77% Conservative: 64
Best Local Similarity: 53.65% Mismatch: 98
Query Match: 25.12% Indels: 22
DB: 10 Gaps: 5

US-10-056-454A-15_COPY_49_882 (1-834) x BE636603 (1-1524)

QY 417 ArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGlyAsnTrpGluValLeu 436
Db 8 AAGGGCGGCGACAGCTGTGGACAGCGGCTGTCAACTACGCAACTGGGAGAGCGTG 67

QY 437 ArgTyrLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLysPheAspGlyPheArg 456
Db 68 CGGTTCTCTGAGCAACAGTGGGTGTATACGAGGAGTACCGCTTCGACGCTTCCGC 127

QY 457 PheAspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGly 476
Db 128 TTGACGGGTGACCTGCTGCTACGTCACCGACCGGACGCGGACGCGGACGCGG 184

QY 477 AsnTyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeu 496
Db 185 GACTACCGGACCTTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 244

QY 497 ValAspAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSer 516
Db 245 GCAACACCGTCAATCAGGAGATCAACCGGAGCGGCGGTGTCACCGGAGGAGCGG 304

QY 517 GlyMetProThrPheCysIleProValGlnGlnGlyValGlyPheAspTyrArgLeu 536
Db 305 GGGTTCCGGGGGCTGTGACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364

QY 537 HisMetAlaIleAlaAsp-LysArgIleGluLeuLeuLysLys-----ArgaspGluAs 554
Db 365 GCGATGGCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 424

QY 554 pTTPArgValGlyAspIleValHisThrLeuThrAsnArgArgTrpSerGlyLysCysVa 574
Db 425 CTGGGACATGGACGATCTCAACACCCCTCGCCACCGCGGCGGCGGCGGCGGCGG 484

QY 574 lSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTrpLe 594
Db 485 CGGCTACGGCGGATCCCGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 544

QY 594 uMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuIleAs 614
Db 545 GATGGACAGGAGATGTACGACGGGATGATGATGATGATGATGATGATGATGATG 604

QY 614 pArgGlyIleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGluGlu 634
Db 605 GCGGGCATGGCGCTGCACAGATGATCCGGCTGCTGACGCGGCGGCGGCGGCGG 664

QY 634 yTyrLeuAsnPheMetGlyAsnGluPheGlyHisProGluTrpTrpIleAspPheProArgAl 654
Db 665 CTACCTGACGTTTATGGGCAACGAGTTGGGCGGCGGCGGCGGCGGCGGCGGCGG 722

QY 654 aGluGlnHisLeuSerAspGlySerValIleProGlyAsnGlnPheSerTyrAspLysCy 674
Db 723 -----CCGGGCAACAAACCGGAGCTACCACTACGC 751

QY 674 sArgArgArgPheAspLeuGlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPh 694
Db 752 GCGGGCGCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 811

```

```

694 eAspArgProMetGluTyrLeuGluAspLysTyrGluPheMetThrSerGluHisGlnPh 714
Db 812 IGACGGCGGCGATGCTGCACCTCGAGGAGAGTCCACTGCTCAGCGCGGCAACGCTA 871

QY 714 eIleSerArgLysAspGluGlyAspArgMetIleValPheGluGlyAsnLeuValPh 734
Db 872 CGTCTGCTGCGCCACGCGCTCGACAGGTCATCGTCTTTGAGCGCGCGCGCGCTT 931

QY 734 eValPheAsnPheHisTrpThrLysSerTyrSerAspTyrArgIleAlaCysLeuLysPr 754
Db 932 TGCTTCAACTTCACCCGAGCTGAGCTGCGGAGTACGGGTGCGCTGCTGCGAGGCC 991

QY 754 oGlyLysTyrLysValAlaLeuAspSerAspProLeuPheGlyGlyPheGlyArgIle 774
Db 992 CGGAGGTACCGCTGCGCTGCTGCTGCGGAGCTGCGCTGCGGCGGCGGCGGCGG 1051

QY 774 eAspHisAsn-----AlaGluTyrPheThrPheGluGlyTyrTrpAspAspAr 790
Db 1052 CGACAGCGGTCGCCGCGGAGAGTACAGGTCTACGGCTGCTGCGTTCGAC----- 1106

QY 790 gProArgSerIleMetValTyrAlaProCysLysThrAlaValValTyr 806
Db 1107 ---TACTCGCTCAIGATCTACGCGCTCGCGCAGCGCTCGCTCTTT 1151

RESULT 8
LOCUS BI308555 689 bp mRNA linear EST 20-JUL-2001
DEFINITION EST529965 GP0D Medicago truncatula cDNA clone pgPOD-7017 5' end,
mRNA sequence.
ACCESSION BI308555
VERSION BI308555.1 GI:14982882
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 689)
AUTHORS Grusak,M.A., Samac,D.A., Town,C.D., Van Aken,S., Utterback,T., Cho
,J. and Fraser,C.M.
ESTs from developing reproductive tissues of Medicago truncatula
Unpublished (2001)
Contact: Michael A. Grusak
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1100 Bates Street, Houston, TX 77030-2600, USA
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Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
B3954106
TIGR sequence name: MTOAQ93TX
More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gta gat CC).
FEATURES
location/Qualifiers
1..689
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/cultivar="Al7"
/db_xref="taxon:3880"
/clone="pgPOD-7017"
/clone_lib="GP0D"
/tissue_type="immature pod walls"
/dev_stage="immature pods, ranging in age from 15 to 30
days after pollination"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Immature pods, ranging in age from 15 to 30 days
after pollination, were collected from greenhouse-grown
plants. At harvest, seeds were removed from pods and
isolated pod walls were collected and immediately frozen
in liquid nitrogen. Pod walls were pooled for mRNA
extraction. cDNA was prepared from polyA+ enriched RNA.
The cDNA was directionally ligated into the Unizap XR
vector from Stratagene and packaged using Gigapack III

```


Db 2 ATTCAAGGACTTTATCCGGATGCTGTATCCATGGTGAAGATGTCAGCGGAATGCTTACA 61
QY 521 PheCysIleProValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIle 540
Db 62 TTTTGGATCCCTGCCAGATGGTGTGTGGTTTCACTATCCCTGCATATGGCTGTA 121
QY 541 AlaAspIleArgIleGluLeuLeuLysArgAspGluAspTyrArgValGlyAspIle 560
Db 122 GCAGATAAATGGATTGAATCCCAAGCAAGTGAAGATCTGGAAATGGCGGATATT 181
QY 561 ValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyrAlaGluSerHis 580
Db 182 GTCCACACCCCTAACAAAGAGTGGCTTGAGAGTGTCTCACTTAAGCAGAAAGTCAT 241
QY 581 AspGluAlaLeuValGlyAspLysThrIleAlaPheThrLeuMetAspLysAspMetTyr 600
Db 242 GATCAAGCACTAGTTGGTGAAGACTATTGCAATCTGGTTGATGGATAAGGATATGAT 301
QY 601 AspPheMetAlaLeuAspArgProSerThrSerLeuIleAspArgGlyIleAlaLeuHis 620
Db 302 GATTTCATGCTCTGGATAGACCTTCAACCCCTCGCATTTGATGTCATAGCATTTACAT 361
QY 621 LysMetIleArgLeuValThrMetGlyLeuGlyClyGluGlyTyrLeuAsnPheMetGly 640
Db 362 AAAATGATCAGGCTTGTACCATGGGTTTAGGTGGCAGAGGCTATCTTAATTTTCATGGGA 421
QY 641 AsnGluPheGlyHisProGluTyrIleAspPheProArgAlaGluGlnHisLeuSerAsp 660
Db 422 AATGAGTTTGGGCATCTCGAATGATAGATTTCGAAGGGGTCCGCAACTCTTCCAACC 481
QY 661 GlySerValIleProGlyAsnGlnPheSerTyrAspLysCysArgArgPheAspLeu 680
Db 482 GGCAAGTCTCTCCCTGGCATAACATAGTATGATAAATGCCCGCTAAATTTGATCTT 541
QY 681 GlyAspAlaGluTyrLeuArgTyrArgGlyLeuGlnGluPheAspArgProMetGlnTyr 700
Db 542 GGAGATGCAGATTTCTTAGATATCGTGAATGCAAGAGTTCGATCAGCAATCCGCCAT 601
QY 701 LeuGluAspLysTyrGluPheMetThrSerGluHisGlnPheIleSerArgLysAspGlu 720
Db 602 CTGAGGGAATAATAGCGTTTATGACATCTGAGCACCACGATGTTCTCGGAAACTTCAG 661
QY 721 GlyAspArgMetIleVal-PheGluLysGlyAsnLeuValPheValPheAsnPheHisTyr 740
Db 662 GAAGATAAGGTGAACATCTTTTGAAGAGGAAATTTGCTATTTCTTCAACTTTCCTCG 721
QY 740 p-ThrLysSerTyrSerAspTyr--ArgIleAlaCysLeuLysPro-GlyLysTyr-Lys 758
Db 722 GGAGCAATAACTTTTGTACTACCCCGGTTGGGGGTTTCCAAAGCCTTGGGAAATACCAAG 781
QY 759 ValAlaLeuAspSer 763
Db 782 GTGGCCCTTAAATCT 796

RESULT 10
BH770747/c
LOCUS
DEFINITION
LLMtag494 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, DNA sequence.
BH770747
BH770747.1 GI:20373704
GSS.
Lactococcus lactis subsp. cremoris.
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
1 (bases 1 to 1482)
Boltin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments, (2002) In press
Contact: Sorokin A
Genetique Microbienne
INRA

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain ILL403 is glgB (88%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 1454.
Location/Qualifiers
1..1482
/organism="Lactococcus lactis subsp. cremoris"
/strain="MG1363"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGM2; Site 1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
BASE COUNT 455 a 304 c 257 g 465 t 1 others

FEATURES
source

Alignment Scores:
Pred. No.: 1,41e-113 Length: 1482
Score: 1060.00 Matches: 220
Percent Similarity: 65.90% Conservative: 68
Best Local Similarity: 50.34% Mismatches: 125
Query Match: 23.74% Indels: 24
DB: 17 Gaps: 9

US-10-056-454a-15_COPY_49_882 (1-834) x BH770747 (1-1482)

QY 187 ThrTyrArgGluTyrPalaLeuGlyAlaGlnSerAlaLeuIleGlyAspPheAsnAsn 206
Db 1311 ACTTCCGCGAATGGCACCATAATCTAAAAAGCTTGGCTTGTGTGACTTTAACCAAT 1252
QY 207 TrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTyrGluIlePheLeu 226
Db 1251 TGGGAACAACACTATGAA---CTAAACAGCGCTTATGCGGAGACTTGGGAAATTCAGTT 1195
QY 227 ProAsnValAspGlySerProAlaIleProHisGlySerArgValIleArgMet 246
Db 1194 CCTGGA-----TTATTACCTGTGGTCTTAAAGTAAAAATAAGTTG 1153
QY 247 AspThrProSerGly---ValLysAspSerIleProAlaTyrPheAsnTyrSerLeuGln 265
Db 1152 CTTTGGCAACTGGAGAGTTGTTATCGTGTCTTCTTACATATGATGCT----- 1099
QY 266 LeuProAspGlu--IleProTyrAsnGlyIleHisTyrAspProGluGluArg 284
Db 1098 CTTCTTAATGAATCATCTAGTTAGACGGGTTATTACTACGCT-----AAG 1051
QY 285 TyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyrGluSerHis 304
Db 1050 TACGAATGGAATAATAAAAGCCCTAAACCTAAACGAGCACCCTTTGATTATCAAGACAT 991
QY 305 IleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArgAspGluVal 324
Db 990 ATTGGGATTTCAACCGAAGATACAAATAATCTTACAAAGAAATCAGCGCATGTT 931
QY 325 LeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHis 344
Db 930 TTACCCAGAAATAAAGATGGTTACATACCATCAGCTGATGCGCAATTATGGAACAC 871
QY 345 SerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArgPhe 364
Db 870 CGGCTCTATGCTAGTTTGGTTATCAAGTTTCCCAATTTTTCATCTCTAGTCGCTT 811
QY 365 GlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleValVal 384
Db 810 GGTACGCCAGAGATTTAATGGAATTTGATGATAAAGCAGCATGTTTGGGTTTGAAGTG 751
QY 385 LeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMetPhe 404
Db 750 CTTTGTAGCGTGGTTTCATTCACATGCTGTAAATAATATTGAGGATGGGCTCACTATTT 691

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405 AspCysThrAspSerCysTyrPheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAsp 424
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690 GATGAACAGAAATCAGTATTTTCATGAAGCGAAGCGGGAATCATCCAGCTTGAGAG 631
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
425 SerArgLeuPheAsnTyrGlyAsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArg 444
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
630 ACGAAACATTTTAAATATGCAAGATGAAGTCTTCATTTTACTATCAATCAATAA 571
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
445 TrpTrpLeuAspAlaPheLysPheAspGlyPheArgPheAspGlyValThrSerMetMet 464
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
570 TTTTGGCTAGACATTTATCATTTTCATGAGCTTTCGTTTGTGAGTAAATTTCAATGCTT 511
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
465 TyrIleHisHisGlyLeuSerValGlyPheTrpGlyAsnTyrGluGluTrpPheGlyLeu 484
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
510 TATCATGACCATGGTTAGGAACCTGCTTTTACA---GATATAGTAAATTTTTCACCT 454
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
485 AlaThrAspValAspAlaValValTyrLeuMetLeuValAsnAspLeuHisGlyLeu 504
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
453 AATACAGATGTTGAAGCGCTGACATATTTGATGCTGGCTAATGAATCACTCATCTCTT 394
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
505 PheProAspAlaIleThrIleGlyGluAspValSerGlyMetProThrPheCysIlePro 524
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
393 ATCCATCAGCAACAACATCCCGAAGACATGCTGCCATGCGCTGGGATGCCACTACCT 334
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
525 ValGlnGluGlyValGlyPheAspTyrArgLeuHisMetAlaIleAlaAspLysArg 544
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
333 ATCTCGGCTGGCGGAATGTTTTCATTATGCTTTGTCATGGAATTCCTGATTTTGG 274
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
545 IleGluLeuLeuLys---LysArgAspGluAspTrpArgValGlyAspIleValHisThr 563
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
273 ATTAACAATTTGAAGAAACAAACAGATATATAGTTTGTAAAGTTTATGTTGGGAA 214
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
564 LeuThrAsnArgArgTrpSerGluLysCysValSerTyrAlaGluSerHisAspGlnAla 583
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
213 TTGACGACCAAGCCTGGAGAAAATATCGGTTATTCAGAAAGTCATGACCAAGCT 154
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
584 LeuValGlyAspLysThrIleAlaPheTrpLeuMetAspLysAspMetTyr----- 600
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
153 TTAGTTGGTGATAAAACACTGATGCTGGCTAGCTAATGAAGAAATCTATGGACATG 94
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 -----AspPheMetAlaLeuAspArgProSerThrSerLeuIle 613
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
93 TACATCAATAGTCAATCTATCATGATTGACCGCAATGCTTCCCTTAGTT 43
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
AV939010
LOCUS
DEFINITION
AV939010 K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah20e24 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 678)
Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .678
/organism="Hordeum vulgare subsp. spontaneum"

FEATURES
source

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/strain="H602"
/db_xref="taxon:77009"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 193 a 135 c 154 g 194 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 2,81e-112 Length: 678
Score: 1044.00 Matches: 190
Percent Similarity: 93.78% Conservative: 21
Best Local Similarity: 84.44% Mismatches: 13
Query Match: 23.38% Indels: 1
DB: 10 Gaps: 0
US-10-056-454a-15_COPY_49_882 (1-834) x AV939010 (1-678)
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    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 GGTATCATTACCGAGNAATGGCTCTCTGGNGCGCATTTCTGCAGCATTTAGTAGTACT 64
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 204 eAsnAsnTrpAspAlaAsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGlu 224
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Db 65 CAACAATTTGAAGCCCAATATGCAGTACTATGACCAGAGATGATTATGTTGGAGAT 124
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 224 ePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArgValLys 244
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 TTTCTCCTTACATGCTGATGGATCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 eArgMetAspThrProSerGlyValLysAspSerIleProAlaIleAsnTyrSerLe 264
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 185 ACGGATGATGATCTCCATCTGTTGTAAGGATTCATTTCTGCTGGATCAAGTTCTCT 244
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 264 uGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGluArg 284
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 245 CGAGGCTCCAGTGAAATACCATTCATGTCATATATTATGATCCACCTGAAGAGAA 304
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 284 gTyrIlePheGlnHisProArgProLysLysProLysLysSerLeuArgIleTyrGlu 304
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 305 GTATCTCTCCACATCTCTCAACCTAAGCAGATCAGTCAAGATATATGATATACA 364
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 sIleGlyMetSerSerProGluProLysLysIleAsnSerTyrValAsnPheArgAsp 324
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Db 365 CATTGGAATGACGAGCCGGAACCAAGATAAATTCATATGCTAATTTTAGGGATGAG 424
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 324 lIleProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGlu 344
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 GCTGCCAAGAATTTAAAGGCTTGGATACATGTCAGTGCAGATAATGGCAATCCAG 484
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 344 sSerTyrTyrAlaSerPheGlyTyrHisValThrAsnPhePheAlaProSerSerArg 364
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 485 TTCATACATGCGAGCTTTGGTACCATGTTACTAATTTTTTTCGCAAGTAGCCGTT 544
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 364 eGlyThrProAspAspLeuLysSerLeuIleAspLysAlaHisGluLeuGlyIleVal 384
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 545 TGSAACTCCAGAGACTTAAATCTTGTATCGATGAGACACATGAGCTTGCTTGTGT 604
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 384 lLeuMetAspIleValHisSerHisAlaSerAsnAsnThrLeuAspGlyLeuAsnMet 404
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 505 TCTTATGATATGTTTTCATGTCATGCTCAATAATACCTTACCGTTTGAATGGTTT 664
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 404 eAspCysThrAsp 408
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 665 CGATGGCACATGAT 677
    ||| |||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
BQ716536
LOCUS
DEFINITION
BQ716536 898 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8478168 lupski_sympathetic_trunk Homo sapiens cDNA clone
IMAGE:6196860 5', mRNA sequence.

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ACCESSION BQ716536
VERSION BQ716536.1 GI:21855433
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 898)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-f@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13605 row: p column: 13
High quality sequence stop: 595.
FEATURES
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        1..898
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                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone="IMAGE:6196860"
                /clone_lib="Lupski-sympathetic_trunk"
                /sex="male"
                /tissue_type="sympathetic trunk"
                /dev_stage="adult, 16 yr"
                /lab_host="DH10B"
                /note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
                NotI; Site_2: SalI; cDNA made by oligo-dT priming.
                Directionally cloned using the following adaptors:
                5'-TCGAGTCTAGATCGGCGGCGCCCT(15)-3'. Size selected >
                1 kb for average insert length 1.9 kb. This is a primary
                library, non-amplified. Library constructed by Life
                Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
                College of Medicine); available through Life
                Technologies."
BASE COUNT 234 a 171 c 225 g 268 t
ORIGIN
Alignment Scores: 4.64e-111 Length: 898
Pred. No.: 1035.50 Matches: 189
Score: 80.14% Conservative: 45
Percent Similarity: 64.73% Mismatches: 54
Best local Similarity: 23.19% Indels: 4
Query Match: 14 Gaps: 3
DB:
US-10-056-454a-15_copy_49_882 (1-834) x BQ716536 (1-898)
Qy 378 HisGluLeuGlyIleValValLeuMetAspIleValHisSerHisAlaSerAsnThr 397
Db 2 CATTCATGGGTATCATAGTCTCTTAGATGGGTACACGCCATGCTTCAAAAATTC 61
Qy 398 LeuAspGlyLeuAsnMetPheAspCysThrAspSerCysTyrPheHisSerGlyAlaArg 417
Db 62 GCAGATGGGATGAATATCTTTGATGGGACAGATTCCTGTTATTTTCATCTGGACCTAGA 121
Qy 418 GlyTyrHisTyrMetTyrAspSerArgLeuPheAsnTyrGlyAsnTyrGluValLeuArg 437
Db 122 GGGACTCAATGATCTTTGGGATAGCAGATGTTGGCTACTCCAGCTGGGAAGTTTAGA 181
Qy 438 TyrLeuLeuSerAsnAlaArgTyrTrpLeuAspAlaPheLysPheAspGlyPheArgPhe 457
Db 182 TTCCTTCGTCAACATAAGATGGTGGTGGGAAGATATCGCTTTGATGGATTCGTTTT 241
Qy 458 AspGlyValThrSerMetMetTyrIleHisHisGlyLeuSerValGlyPheThrGlyAsn 477
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Db 242 GATGGTGTACCTCCATGCTTTATCATCACCATGGAGTGGGTCAAGGTTCTTCAGGTGAT 301
Qy 478 TyrGluGluTyrPheGlyLeuAlaThrAspValAspAlaValValTyrLeuMetLeuVal 497
Db 302 TACAGTGAATATTTCCGACTACAAGTAGATGCTTGCCTGACTTACCTCATCTTGCA 361
Qy 498 AsnAspLeuIleHisGlyLeuPheProAspAlaIleThrIleGlyGluAspValSerGly 517
Db 362 AATCATTTGGTTACACAGCTGTGTCGCGATTTCTAAACAATAGTAGTAGGATGTATCAGGA 421
Qy 518 MetProThrPheCysIleProValGluGluGlyValGlyPheAspTyrArgLeuHis 537
Db 422 ATGCCAGCTCTGTGCTCTCCAAATTTCCCGAGGAGGGGTGTTTGTACTATCGACTAGCC 481
Qy 538 MetAlaIleAlaAspLysArgIleGluLeuLeuLysLys---ArgAspGluAspTyrArg 556
Db 482 ATGCCAATTCAGATAAGTGCATTCAAGAGTTTAAAGAGTTTAAAGATGAAGATGGAAC 541
Qy 557 ValGlyAspIleValHisThrLeuThrAsnArgArgTyrSerGluLysCysValSerTyr 576
Db 542 ATGGCGGATATAGTATACGCTCACAAACAGGGGCTACCTTGAAGAGTGCATTGCTTAT 601
Qy 577 AlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAlaPheTyrLeuMetAsp 596
Db 602 GCAGAGAGCCCATGATCAGGCATTGTTGGGATAGTCGCTGGCATTTTGGTTGATGGAT 661
Qy 597 LysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSerLeuLeuAspArgGly 616
Db 662 GCCGAATGTATACAAACATGAGTCTCTGACTCCCTTACTCCAGTTATTGATGCGCGGA 721
Qy 617 IleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGlyGlu---GlyTyr 635
Db 722 ATACAGCTTCAATAATGATTCGAGCTCATTCAGCATGGGGCTGGGAGAAAGGCTAT 781
Qy 636 LeuAsnPheMetGlyAsnGlu---PheGlyHisProGluTyrIle-AspPheProArgAl 654
Db 782 TCCATTTTCTGGGGAGAAAGAAATTTGGGGCAATTCCTGAATGGGTAGAGATTCCCCAGGA 841
Qy 654 aGluGlnHisLeuSerAspGlySerValIlePro 665
Db 842 AAGGAAAAAATGGGAGAGTCCCTTAATGCC 875
RESULT 13
BE602527 731 bp mRNA linear EST 22-OCT-2001
LOCUS HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
mRNA sequence.
ACCESSION BE602527 GI:13190371
VERSION BE602527.2
KEYWORDS EST.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 731)
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:9860088.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bq bases = 322
Seq primer: AATTAACCTCCTACTAAAGGG

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FEATURES
source

High quality sequence stop: 680.
Location/Qualifiers
1. .731
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH009922f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCN0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
<http://www.genome.clemson.edu/projects/barley/>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/g9ppages/bgn/31/cover.html>)"

BASE COUNT 194 a 132 c 186 g 216 t 3 others
ORIGIN

Alignment Scores:

Pred. No.: 2.86e-110 Length: 731
Score: 1027.50 Matches: 194
Percent Similarity: 86.78% Conservative: 16
Best Local Similarity: 80.17% Mismatches: 32
Query Match: 23.01% Indels: 2
DB: 10 Gaps: 0

US-10-056-454A-15_COPY_49_882 (1-834) x BE602527 (1-731)

QY 412 PheHisSerGlyAlaArgGlyTyrHisTrpMetTrpAspSerArgLeuPheAsnTyrGly 431
Db 8 TTTTCATGGCGGCTCACGGGCCATCACTGGATGGGATTCCTGTGTGTTCAACTACGGG 67
QY 432 AsnTrpGluValLeuArgTyrLeuLeuSerAsnAlaArgTrpTrpLeuAspAlaPheLys 451
Db 68 AATAAGGAAGTATAGGGTTCTACTTCCATGCCAGATGGGGCTTGAGGAATATAAG 127
QY 452 PheAspGlyPheArgPheAspGlyValThrSerMetMetTyrTrleHisHisGlyLeuSer 471
Db 128 TTCCATGGGTCCCATTCGACGGGCCACCTTCATGATGTATACCCCAAGGATTACAA 187
QY 472 ValGlyPheThrGlyAsnTyrGluGluTyrPheGlyLeuAlaThrAspAlaVal 491
Db 188 GTACC-TTTACAGGAGC-TACCATGAATATTTGGCTTTCACCGGATGATGATGATGATG 245
QY 492 ValTyrLeuMetLeuValAsnLeuLeuHisGlyLeuPheProAspAlaThrLe 511
Db 246 GTTACTGATGCTGGTGAATGATCTAATTCACGGCTTATCTCTGAAGCCGTACTATT 305
QY 512 GlyGluAspValSerGlyMetProThrPheCysIleProValGlnGluGlyValGly 531
Db 306 GGTGAGATGTTAGTGAATGCTACATTGGCCCTTCCTGTTCAAGTTGGTGGGTGGT 365

QY 532 PheAspTyrArgLeuHisMetAlaLeuAlaAspLysArgLleGluLeuLeuLysLysArg 551
Db 366 TTTGACTATCGTTACATATGCGCGTTCGCGATAAATGATTCAATTCATCAAGGAAGC 425
QY 552 AspGluAspTyrArgValGlyAspLleValHisThrLeuThrAsnArgArgTrpSerGlu 571
Db 426 GATGAGAGTTGGAGATGGTAAATATGTGCACACACTAACAAATAGAAGGTGGTGGAA 485
QY 572 LysCysValSerTyrAlaGluSerHisAspGlnAlaLeuValGlyAspLysThrIleAla 591
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QY 592 PheTrpLeuMetAspLysAspMetTyrAspPheMetAlaLeuAspArgProSerThrSer 611
Db 546 TTTCTGGTTGATGCACAAAGATATGATGATTTTCATGGCTCTGAACGACCTTCGACACCT 605
QY 612 LeuLeuAspArgGlyLleAlaLeuHisLysMetIleArgLeuValThrMetGlyLeuGly 631
Db 606 AATATGATCGCGGAATAGCACTGATAAATGATTAGACTATACCAATGGCTNTAGGA 665
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QY 652 ProArg 653
Db 726 CCAAGA 731
RESULT 14
BU005876
LOCUS
DEFINITION QG99F08.717 bp mRNA linear EST 22-AUG-2002
QG99F08.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
BU005876
ACCESSION QG99F08, mRNA sequence.
VERSION BU005876.1 GI:22440271
KEYWORDS EST.
SOURCE Lactuca sativa.
ORGANISM Lactuca sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.
1 (bases 1 to 717)
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
Belongs to contig QG_CA_Contig6851, see <http://cgdb.ucdavis.edu/>
for details.
Plate: QGG9 row: F column: 08.
FEATURES
source
1. .717
/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"
/clone="QG99F08"
/lab_host="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"

/note="Vector: pBRCDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
TAG LIB=QG_EFGH lettuce serriola
TAG TISSUE=germinating seeds
TAG_SEQ=CTGTGCGG

PHASE COUNT	233 a	122 c	155 g	206 t	1 others
ORIGIN					
Alignment Scores:					
Pred. No.:	8.56e-106	Length:	717		
Score:	989.50	Matches:	183		
Percent Similarity:	82.56%	Conservative:	30		
Best Local Similarity:	70.93%	Mismatches:	26		
Query Match:	22.16%	Indels:	20		
DB:	14	Gaps:	1		
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QY	102	LysThrLeuAsnThrSerGluGluThrIleLeuAspGluSerAspArgIleArgGluArg	121		
DB	41	-----GAAAGTGAAGAAATAGAAAAATTA	64		
QY	122	GlyIleProProGlyLeuGlyGlnLysIleTyrGluLeuAspProLeuLeuThrAsn	141		
DB	65	TCGATTCCTCTCTGCGAAAGGAGAGATATGAAATGATGATCCTTTTAAGCAAT	124		
QY	142	TyrArgGlnHisLeuAspTyrArgTyrSerGlnTyrLysLysLeuArgGluAlaLeuAsp	161		
DB	125	CATCGTGAACATCTTGATAGATATTCACATACAGAAGATACGTGAAGCAATTCAC	184		
QY	162	LysTyrGluGlyLeuGluAlaPheSerArgGlyTyrGluLysMetGlyPheThrArg	181		
DB	185	AAATATGAAGTGGTTTGGAGCGTTTTCACGTGGTTATGAAAAATTAGTTTTCACCTCGA	244		
QY	182	SerAlaThrGlyIleThrTyrArgGluTyrPalaLeuGlyAlaGlnSerAlaLeuLeu	201		
DB	245	AGCAAAACAGGTATCACTTATAGAGAATGGCACCTGGGCAAGTCTGCTTCATTTAT	304		
QY	202	GlyAspPheAsnAsnThrPalaAsnAlaAspIleMetThrArgAsnGluPheGlyVal	221		
DB	305	GGAGATTCAACAACCTGGAATCCAAATGCTGATGTTATGACCCGGAATGAAATTTGGTGTG	364		
QY	222	TyrGluIlePheLeuProAsnAsnValAspGlySerProAlaIleProHisGlySerArg	241		
DB	365	TGGGAGATCTTTTGGCAACAAGTTGATGATCTTCACCTATTCCTCATGGTCTCGA	424		
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DB	425	GTAAGATTCTGATGGATACCCATCTGGCATTAAGACTCGATTCCCTGGATCAAG	484		
QY	262	TyrSerLeuGlnLeuProAspGluIleProTyrAsnGlyIleHisTyrAspProGluGlu	281		
DB	485	TTTTTCAGTACAGCAACCTGGTGGATTCCTTATATGAATATATATGATCCCAACAA	544		
QY	282	GluGluArgTyrIlePheGlnHisProArgProLysLysProLysSerLeuArgIleTyr	301		
DB	545	GAGGAATAATACGTGTTTCAACATCCAGACCAAGAGAGCGAATCTCTTANGATTTAT	604		
QY	302	GluSerHisIleGlyMetSerSerProGluProLysIleAsnSerTyrValAsnPheArg	321		
DB	605	GAGGCACATGTTGGGAATGAGTAGTACGGAACCAATGGATCACAGTATGCTAACTTTAGA	664		
QY	322	AspGluValLeuProArgIleLysLysLeuGlyTyrAsnAlaLeuGlnIleMet	339		
DB	665	GACGATGTTCTCCCTCGCATTAAGAA-CTCGGTTACATGATGATTCATCATG	717		
RESULT 15					

AW065909	639 bp	mrna	linear	EST 30-MAR-2000		
LOCUS	687002609.y1	687	- Early embryo	from Delaware Zea mays cDNA, mRNA		
DEFINITION	sequence.					
ACCESSION	AW065909					
VERSION	AW065909.1	GI:6020981				
KEYWORDS	EST.					
SOURCE	Zea mays.					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	1. (bases 1 to 639)					
AUTHORS	Walbot,V.					
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 687002 row: G column: 09.					
FEATURES	Location/Qualifiers					
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BASE COUNT	200 a	118 c	151 g	170 t		
ORIGIN						
Alignment Scores:						
Pred. No.:	2.76e-104	Length:	639			
Score:	976.00	Matches:	174			
Percent Similarity:	91.94%	Conservative:	20			
Best Local Similarity:	82.46%	Mismatches:	17			
Query Match:	21.86%	Indels:	0			
DB:	10	Gaps:	0			
US-10-056-454A-15_COPY_49_882 (1-834) x AW065909 (1-639)						
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DB	5	TTCTCCCGTAGTTATGAGAAGTTTGATTTATCCGCGGAGGTATCACATATCGA		64		
QY	190	GluTrpAlaLeuGlyAlaGlnSerAlaAlaLeuIleGlyAspPheAsnTrpAspAla		209		
DB	65	GAATGGGCTCCGAGCATTTTCTGCAGCATTTGGTGGTCACTCAACAACCTGGATCCA		124		
QY	210	AsnAlaAspIleMetThrArgAsnGluPheGlyValTrpGluIlePheLeuProAsnAsn		229		
DB	125	AATGCAGATCGTATGAGCAAAATGAGTTTGTTGGTGTGTTTTCGCCCAACAAT		184		
QY	230	ValAspGlySerProAlaIleProHisGlySerArgValLysIleArgMetAspThrPro		249		
DB	185	GCAGATGGTACATCACCTTATCTCATGATCTCGTGAAGGTGAGATGATGATCTCCA		244		


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QY 250 SerGlyValLysAspSerIleProAlaTrpIleAsnTyrSerLeuGlnLeuProAspGlu 269
Db 245 TCAGGGATAAAGGATTCAATCCAGCTGGATCAAGTACTCAGTCAGGCCGCCAGAGAA 304
QY 270 IleProTyrAsnGlyIleHisTyrAspProGluGluArgTyrIlePheGlnHis 289
Db 305 ATACCATATGATGGGATTATATATCATCTCTGAAAGAGGTAAAGTATGTCTTCAGGCAT 364
QY 290 ProArgProLysLysProLysSerLeuArgIleTyrGluSerHisIleGlyMetSerSer 309
Db 365 GCGCAACCTAACACCAACAAATCATTCGGATATATGAACACACATGTCGGAATCAGTAGC 424
QY 310 ProGluProLysIleAsnSerTyrValAsnPheArgAspGluValLeuProArgIleLys 329
Db 425 CCGGAACCGAAGATAAACAACATATGTAACCTTTAGGGATGAAGTCTCTCCCAAGATATAAA 484
QY 330 LysLeuGlyTyrAsnAlaLeuGlnIleMetAlaIleGlnGluHisSerTyrTyrAlaSer 349
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Db 545 TTTGGATACCATGTAACTAATTTTTTGGCCCAAGTAGTCGTTTGGTACCCCAAGAGAT 604
QY 370 LeuLysSerLeuIleAspLysAlaHisGluLeu 380
Db 605 TTGAAGTCCTTTGATTGATGAGACACATGAGCTT 637
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Job time : 2970 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:12:47 ; Search time 8049.92 Seconds
(without alignments)
11409.857 Million cell updates/sec

Title: US-10-056-454a-18_COPY_45_3200

Perfect score: 3156

Sequence: 1 AAAAACTCTCTCACTCACTG.....TGCTGATCTAATGATGTTT 3156

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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11: gb_sts.*

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27: em_sts.*

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33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rnd.*

36: em_htg_rnd.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2955.2	93.6	3074	6 AR123355	AR123355 Sequence
3	2849.6	90.3	2982	8 STU011888	STU011888 Solanum t
4	2847.4	90.2	3033	6 A58164	A58164 Solanum t
5	2846.4	90.2	2992	8 STU011890	STU011890 Solanum t
6	2838	89.9	3003	6 A58162	A58162 Sequence 12
7	2733.2	86.6	2955	8 STU011885	STU011885 Solanum t
8	2707.6	85.8	2975	6 A58163	A58163 Sequence 13
9	2485.8	78.8	2563	6 AX256072	AX256072 Sequence
10	2474.4	78.4	2529	6 A58167	A58167 Sequence 17
11	2446.6	77.5	2523	8 STU011889	STU011889 Solanum t
12	2445	77.5	2578	6 A58169	A58169 Sequence 19
13	2436.6	77.2	2493	8 SISREI1	SISREI1 Solanum t
14	2431	77.0	2576	6 A58166	A58166 Sequence 16
15	1717.6	54.4	3123	8 AB071286	AB071286 Ipomoea b
16	1511.8	47.9	2517	8 AB042937	AB042937 Ipomoea b
17	1479.4	46.9	1481	8 STU011891	STU011891 Solanum t
18	1442.8	45.7	3090	6 A92164	A92164 Sequence 30
19	1429.8	45.3	3360	8 AB029548	AB029548 Phaseolus
20	1390.2	44.0	3549	8 PSSREIGEN	PSSREIGEN P.sativum m
21	1377.8	43.7	2913	6 A92162	A92162 Sequence 28
22	1372.2	43.5	1393	6 AR123356	AR123356 Sequence
23	1323	41.9	2542	8 ATU22428	ATU22428 Arabidopsis
24	1296	41.1	2577	6 AX412751	AX412751 Sequence
25	1296	41.1	2577	6 AX412752	AX412752 Sequence
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27	1275.6	40.4	3015	6 E14723	E14723 Rice mRNA f
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29	1274.4	40.4	2364	6 E14724	E14724 Rice mRNA f
30	1272	40.3	2554	8 AF064560	AF064560 Hordeum v
31	1260.4	39.9	2918	6 R1CBCE3	R1CBCE3 Rice mRNA f
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ALIGNMENTS

RESULT 1
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LOCUS A58168 3231 bp DNA linear PAT 05-MAR-1998
DEFINITION Sequence 18 from Patent WO9634968.
ACCESSION A58168
VERSION A58168.1 GI:3713893
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE
AUTHORS
1 (bases 1 to 3231)
Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
TITLE
JOURNAL
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
Patent: WO 9634968-A 18 07-NOV-1996;

NAT STARCH CHEM INVEST (US)
 Other publication AU 5509996 961121.
 COMMENT
 FEATURES Location/Qualifiers
 source 1. .3231

FEATURES

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1. .3231
/organism="unidentified"
/db xref="taxon:32644"
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BASE COUNT	960 a	577 c	739 q	947 t	8 others

Query Match	99.9%;	Score 3154.2;	DB 6;	Length 3231;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 3156;	Conservative	0;	Mismatches	0;
			Indels	0;
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[illegible]

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1005	Db	GACATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCAAAATTAATGTGGAT	1064
1021	QY	GGTTCCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGATGGACATTCATCAGGT	1080
1065	Db	GGTTCCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACGATGGACATTCATCAGGT	1124
1081	QY	GTTAAGGATTCGAATTCCTGCTTGGATCAACTACTCTTTACAGCTTCCTGATGAATTCGA	1140
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1185	Db	TATAATGGAAATATATTATGATCCACCGAGAGGAGAGGATGTCGTTCCAAACCCACCG	1244
1201	QY	CCAAAGAAACCAAGTCGCTGAGAAATATGAATCTCAATTCGAAATGAGTAGTCCGGAG	1260
1245	Db	CCAAAGAAACCAAGTCGCTGAGAAATATGAATCTCAATTCGAAATGAGTAGTCCGGAG	1304
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1305	Db	CCTAAAATTAACTCATACGTGAATTTTGGAGATGGAATTCCTTCGCAATAAAAAACCTT	1364
1321	QY	GGGTACAAATGGGTGCAAAATATGGCTATTCAAGAGCATTCCTTATTATGCTAGTTTGGT	1380
1365	Db	GGGTACAAATGGGTGCAAAATATGGCTATTCAAGAGCATTCCTTATTATGCTAGTTTGGT	1424
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1425	Db	TATCATGTCACAAAATTTTTTGCACCAAGCAGCGGTTTTGGAACGCCGCCAGCACCTTAAG	1484
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1665	Db	AACGTGGAGGTACTTAGGTATCTTCTCAAAATCGAGATGGTGGTTGGATGAGTGCAAA	1724
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1725	Db	TTTGTGTGATTTAGATTTGATGGTGTGCATCAATGATGTATCTACCCAGGATTAATCG	1784
1741	QY	GTGGGATTCATCGGAACTACAGGAATPACTTTGGACTCGCAACTGATGTGATGCTGCC	1800
1785	Db	GTGGGATTCATCGGAACTACAGGAATPACTTTGGACTCGCAACTGATGTGATGCTGCC	1844
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1845	Db	GTGTATCTGATGCTGGCCAAAGATCTTATTCATGGGCTTTTCCAGATGCAATTAACCAT	1904
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1905	Db	GGTGAAGATGTTAGCGGAATGCCGACATTTTGATTCGCGHTCAAGATGGGGTGTTGGC	1964
1921	QY	TTTGTACTATCGGCTGCATATGCAATTCCTGATAAATGGATTTGAGTTGCTCAAGAAACGG	1980
1965	Db	TTTGTACTATCGGCTGCATATGCAATTCCTGATAAATGGATTTGAGTTGCTCAAGAAACGG	2024
1981	QY	GATGAGGATTTGGAGAGTGGGTGCATATTTGTTTCATACCTGCACAAATAGAGAAGTTCGGAA	2040

Db	2025	GATGAGGATGGAGAGTGGGTGATATGTTTCATACACTGCACAAATAGAAGATGGTCCGAA	2084
QY	2041	AAGTGTGTTTCATACGCTGAAGTCATGATCAAGCTCTAGTCGGTGATAAACTATAGCA	2100
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QY	2101	TTCTGGCTGATGGCAAGGATATGATGATTTTATGGCTTTGGATAGACCGTCAACATCA	2160
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Db	2205	TTAATAGATCGTGGGATAGCAATGTCACAAGATGATTAGGCTTGTAACTATGGGATAGGA	2264
QY	2221	GGAGAAGGATACCTAAATTTTCATGGGAAATGAATTCGGCCACCCCTGAGTGGATTGTTTC	2280
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QY	2281	CCTAGGCTGCAACACACCCCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTAT	2340
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QY	2341	GATAAATGCACACGGAGATTGACCTGGGAGATGCAGAAATATTAGATACCGTGGGTTG	2400
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QY	2401	CAAGAAATTTGACCGGGCTATGCAGTATCTTTGAAGATAAATATGAGTTTATGACTTCAGAA	2460
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Db	2625	CTGAGCCTGGAAAAATACAAGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTTC	2684
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Db	2745	CGTTCAATATGTTGATGACCTAGTATAGAACAGCAGTGGTCTATGACTAGTACAGAA	2804
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QY	2821	AACTTGTGATCGGTTGAAGATTTGAACCGCTACATAGAGCTCTTGTGAGTATCTGGCAA	2880
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QY	3001	TTTATGTCGAATGCTGGGACGGCTTCACGAGGTTTTCCTTAGTCAGTCTGTAATGT	3060
Db	3045	TTTATGTCGAATGCTGGGACGGCTTCACGAGGTTTTCCTTAGTCAGTCTGTAATGT	3104
QY	3061	CAPTCTTTTANATGTACGCCCACTAGAAATCAATATGTGACAGCTAAAAACAAATAC	3120

Db 3105 CATCICITTTTANATGTACAGCCCACTGAAATCAATTATGTGAGACCTAAAAACAATAAAC 3164

QY 3121 CATAAANTGGAAATAGTGCGATCTAATGAATGTTTT 3156
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Db 3165 CATAAANTGGAAATAGTGCTGATCTAATGAATGTTTT 3200
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RESULT 2
~~ARL23355~~

LOCUS ARL23355 3074 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169226.
ACCESSION ARL23355
VERSION ARL23355.1 GI:14108321
KEYWORDS see jcaas3, r
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3074)
AUTHORS Ek,B., Khosnoodi,J., Larsson,C.-T., Larsson,H. and Rask,L.
TITLE Starch branching enzyme II of potato
JOURNAL Patent: US 6169226-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
 1..3074
 /organism="unknown"
BASE COUNT 902 a 558 c 712 g 896 t 6 others
ORIGIN

Query Match 93.6%; Score 2955.2; DB 6; Length 3074;
Best Local Similarity 98.1%; Pred. No. 0;
Matches 3019; Conservative 2; Mismatches 41; Indels 14; Gaps 3;

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RESULT 3
LOCUS STU011888
DEFINITION Solanum tuberosum mRNA for starch branching enzyme II, sequence SBE A-4.
ACCESSION AJ011888
VERSION AJ011888.1 GI:4584508
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2982)
Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M.,
Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2982)
Jobling, S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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RESULT 4
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DEFINITION Sequence 14 from Patent WO9634968.
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VERSION A58164.1 GI:3713889
KEYWORDS
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ORGANISM
REFERENCE
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Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,
Sidebottom, Christopher,M. and Westcott,R.J.
IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION
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Query Match 90.28; Score 2847.4; DB 6; Length 3033;
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RESULT 7
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DEFINITION A-1.
ACCESSION AJ011885
VERSION AJ011885.1 GI:4584502
KEYWORDS SBEII gene; starch branching enzyme II.
SOURCE Solanum tuberosum.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 2955)
Jobling, S.A., Schwall, G.P., Westcott, R.J., Sidebottom, C.M.,
Debet, M., Gidley, M.J., Jeffcoat, R. and Safford, R.
A minor form of starch branching enzyme in potato (Solanum
tuberosum L.) tubers has a major effect on starch structure;
cloning and characterisation of multiple forms of SBE II
Unpublished
2 (bases 1 to 2955)
Jobling, S.A.
Direct Submission
Submitted (07-OCT-1998) Jobling S.A., Plant Science Unit, Unilever
Research, Colworth House, Sharnbrook, Bedford, MK44 1LQ, UK
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QY	1485	GGACATGTTTACAGCCATGATCAATAATACATTTAGATGAGTGCATGTTGACGG	1544
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AX256072
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DEFINITION Sequence 1 from Patent WO0170942.
ACCESSION AX256072
VERSION AX256072.1 GI:16075112
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 2563).
AUTHORS Poulson, P. and s Rensen, I.S.
TITLE Enzyme
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ORIGIN

Query Match 78.8%; Score 2485.8; DB 6; Length 2563;
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Db	121	TTGACGATCGGGAAAGTCCTTGTGCTTGGAAACCCAGAGTGATAGCTCCTCATCTCAA	180
QY	428	CAGACCAATTTGAGTTCACCTGAGACAGCTCCAGAAAATTCGCCAGCATCAACTGATGTGG	487
Db	181	CAGACCAATTTGAGTTCACCTGAGACATCTCCAGAAAATTCGCCAGCATCAACTGATGTAG	240
QY	488	ATAGTTCAACATGGAACAGCTGAGCAGATTAATACTGAGAACGATGAGCTTGAGCGGT	547
Db	241	ATAGTTCAACATGGAACAGCTGAGCAGATTAATACTGAGAACGATGAGCTTGAGCGGT	300
QY	548	CAAGTGATCTTACAGGAAGTGTGAAGAGTGTGATTTTGTTCATCACTACAACTACAAG	607
Db	301	CAAGTGATCTTACAGGAAGTGTGAAGAGTGTGATTTTGTTCATCACTACAACTACAAG	360
QY	608	AGGTGGTAAACTGGAGGAGCTTAACACATTAATFACCTCTGAGAGACAAATTAATGATG	667
Db	361	AGGTGGTAAACTGGAGGAGCTTAACACATTAATFACCTCTGAGAGACAAATTAATGATG	420
QY	668	AATCTGATAGGATCAGAGAGGGGCACTCCCTCCACCTGGACCTGGTTCAGAAAGATTTATG	727
Db	421	AATCTGATAGGATCAGAGAGGGGCACTCCCTCCACCTGGACCTGGTTCAGAAAGATTTATG	480
QY	728	AAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTCAGAGTATTCACAGTACA	787
Db	481	AAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTCAGAGTATTCACAGTACA	540
QY	788	AGAAATGAGGAGGCAATTCACAAGTATGAGGTGGTGTGGAGCTTTTCTCGTGT	847
Db	541	AGAAATGAGGAGGCAATTCACAAGTATGAGGTGGTGTGGAGCTTTTCTCGTGT	600
QY	848	ATGAAAAATGGGTTTCACCTGATGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG	907
Db	601	ATGAAAAATGGGTTTCACCTGATGCTACAGGTATCACTTACCGTGAGTGGGCTCCTG	660
QY	908	GTGCCAGTCAGCTGCTCATTTGGAGATTTCAACAATGGGAGCGAAAATGCTCAACATTA	967
Db	661	GTGCCAGTCAGCTGCTCATTTGGAGATTTCAACAATGGGAGCGAAAATGCTCAACATTA	720
QY	968	TGACTCGGAATGAATTTGGTCTCGGAGATTTTTCGCCAAATAAATGATGATGCTC	1027
Db	721	TGACTCGGAATGAATTTGGTCTCGGAGATTTTTCGCCAAATAAATGATGATGCTC	780
QY	1028	CTGCAATTCCTCATGCTGCTGAGTGAAGATPACGATGGACACATTCACGCTGTTAAGG	1087
Db	781	CTGCAATTCCTCATGCTGCTGAGTGAAGATPACGATGGACACATTCACGCTGTTAAGG	840
QY	1088	ATTCATTCCTGCTGATCAACTACTCTTTACAGCTTCCTGATGCAATTCATATATATG	1147
Db	841	ATTCATTCCTGCTGATCAACTACTCTTTACAGCTTCCTGATGCAATTCATATATATG	900
QY	1148	GAATATATATGATCCACCCCAAGAGGAGGTATGCTTCCACACCCAGCGGCAAGA	1207
Db	901	GGATATATATGATCCACCCCAAGAGGAGGTATATCTTCCACACCCAGCGGCAAGA	960
QY	1208	AACCAAGCTCGTGAGANATATGAATCTCATTTGGAATGAGTAGTCCGGAGCCTAAAA	1267
Db	961	AACCAAGCTCGTGAGANATATGAATCTCATTTGGAATGAGTAGTCCGGAACTAAAA	1020
QY	1268	TTAACTCATAGTGAATTTAGAGATGAAGTCTTCCGATATAAAACCTTGGGTACA	1327
Db	1021	TTAACTCATAGTGAATTTAGAGATGAAGTCTTCCGATATAAAACCTTGGGTAGG	1080
QY	1328	ATGGGTCAAAATATGCTATTCAGAGCATTCCTTATATGCTAGTGTGGTATCATG	1387
Db	1081	ATGGGTCAAAATATGCTATTCAGAGCATTCCTTATATGCTAGTGTGGTATCATG	1140
QY	1388	TCACAAATTTTTCACCAAGCAGCCGTTTGGAAACCCCGAGACCTTTAGTCTTTGA	1447
Db	1141	TCACAAATTTTTCACCAAGCAGCCGTTTGGAACTCCCGACGACCTTAAAGTCTTTGA	1200
QY	1448	TGATAAAGCTCATGAGTGAAGTGTGTTCTCATGAGCATTTGTCACAGCCCATGCAT	1507
Db	1201	TTGATAAAGCTCATGAGTGAAGTGTGTTCTCATGAGCATTTGTCACAGCCCATGCAT	1260
QY	1508	CAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTGTGTACTTCACT	1567
Db	1261	CAATAATACTTTAGATGGACTGAACATGTTTGACGGCACAGATAGTGTGTACTTCACT	1320
QY	1568	CTGAGACTCGTGGTTATCATTTGGATGGGATCCCGCTCTTTAACTATGGAACACTGGG	1627
Db	1321	CTGAGACTCGTGGTTATCATTTGGATGGGATCCCGCTCTTTAACTATGGAACACTGGG	1380
QY	1528	AGGTACTAGTATCTCTCAAAATCGAGATGGTGGTGGATGAGTGAACAAATTTGRTG	1687
Db	1381	AGGTACTAGTATCTCTCAAAATCGAGATGGTGGTGGATGAGTGAACAAATTTGRTG	1440
QY	1688	GATTTAGATTTGATGGTGTGCACATPCAAATGATATCTACACACCGATATPCGGTGGAT	1747
Db	1441	GATTTAGATTTGATGGTGTGCACATPCAAATGATATCTACACACCGATATPCGGTGGAT	1500
QY	1748	TCAGTGGAACTAGAGGAATACATTTGGACTCGCAACTGATGTGCTGCTCCCTGATC	1807
Db	1501	TCAGTGGAACTAGAGGAATACATTTGGACTCGCAACTGATGTGCTGCTCCCTGATC	1560
QY	1808	TGATGCTGGCCCAACGATCTTATTCATGGGCTTTTCCAGATGCAATTTACCATTTGCTGAAG	1867
Db	1561	TGATGCTGGCCCAACGATCTTATTCATGGGCTTTTCCAGATGCAATTTACCATTTGCTGAAG	1620
QY	1868	ATGTTAGCGGAATCCGACATTTTGTATTTCCCGTTCAAGATGGGGGTTGCTGTGACT	1927
Db	1621	ATGTTAGCGGAATCCGACATTTTGTATTTCCCGTTCAAGATGGGGGTTGCTGTGACT	1680
QY	1928	ATCCGCTGCATATGGCAATTTGCTGATTAATGATGCTGCTCAAGAAACGGGATGAGG	1987
Db	1681	ATCCGCTGCATATGGCAATTTGCTGATTAATGATGCTGCTCAAGAAACGGGATGAGG	1740
QY	1988	ATTTGAGAGTGGGTGATATTTGCTATACACTCACAAATAGAGATGGTCGGAAGAGTGTG	2047
Db	1741	ATTTGAGAGTGGGTGATATTTGCTATACACTCACAAATAGAGATGGTCGGAAGAGTGTG	1800
QY	2048	TTTCATACGCTGAAAGTCAATGATCAAGCTCTAGTGGTGTGAATAAATATAGCATCTGCG	2107
Db	1801	TTTCATACGCTGAAAGTCAATGATCAAGCTCTAGTGGTGTGAATAAATATAGCATCTGCG	1860
QY	2108	TGATGCAACAGATATGATGATTTTATGGCTTTTGGATAGACCGTCAACATCATTAATAG	2167
Db	1861	TGATGCAACAGATATGATGATTTTATGGCTTTTGGATAGACCGTCAACATCATTAATAG	1920
QY	2168	ATCGTGGATAGCATTCGACAAAGATGATTTAGGCTTTGTAAGTATGGATTTAGGAGAGAG	2227
Db	1921	ATCGTGGATAGCATTCGACAAAGATGATTTAGGCTTTGTAAGTATGGATTTAGGAGAGAG	1980
QY	2228	GGTACCTAAATTCATGGGAATGAATTCGGCCACCTCAGTGGATTTGATTTCCCTAGG	2287
Db	1981	GGTACCTAAATTCATGGGAATGAATTCGGCCACCTCAGTGGATTTGATTTCCCTAGG	2040
QY	2288	CTGAACACACCTCTCTGATGGCTCAGTAATTTCCGGGAAACCAATTCAGTTATGATAAT	2347
Db	2041	CTGAACACACCTCTCTGATGGCTCAGTAATTTCCGGGAAACCAATTCAGTTATGATAAT	2100
QY	2348	GCAGACGGAGATTTGACCTGGGAGATGCAAGATATTTAAGTACCGTGGGTTGCAAGAT	2407
Db	2101	GCAGACGGAGATTTGACCTGGGAGATGCAAGATATTTAAGTACCGTGGGTTGCAAGAT	2160
QY	2408	TTGACCGGCTATGAGATCTTTGAGATAAATATGAGTTTATGACTTCAGACACACCTAG	2467
Db	2161	TTGACCGGCTATGAGATCTTTGAGATAAATATGAGTTTATGACTTCAGACACACCTAG	2220
QY	2468	TCATATCAGAAAGATGAAGGATGATGATGATTTTATTTGAAAAAGAAACCTAGTTT	2527
Db	2221	TCATATCAGAAAGATGAAGGATGATGATGATTTTATTTGAAAAAGAAACCTAGTTT	2280
QY	2528	TTGCTCTTTAAATTTTCACTGGACAAAAGCTATTCAGACTATCGACTGCTGGCTGAAGC	2587
Db	2281	TTGCTCTTTAAATTTTCACTGGACAAAAGCTATTCAGACTATCGACTGCTGGCTGAAGC	2340

Db	1501	CTTTGGACGCGCACTGATGCTGATGCTGTTGATGATGCTGGTCAACGATCTAT	1560
QY	1830	TCATGGGCTTTTCCAGATGCAATACCAATGCTGAGATGTTAGCGGAATGCCGACAT	1889
Db	1561	TCACGGGCTTTTCCAGATGCAATACCAATGCTGAGATGTTAGCGGAATGCCGACAT	1620
QY	1890	TTGATATCCGTTCAAGATGGGGTGTGGCTTGGCTGCTATCGCTGCATATGCAATGC	1949
Db	1621	TTGATATCCGTTCAAGATGGGGTGTGGCTTGGCTGCTATCGCTGCATATGCAATGC	1680
QY	1950	TGATAAATGATTGAGTTGCTCAAGAACGGGATGAGGATGGAGATGGGTTGATATGT	2009
Db	1681	TGATAAATGATTGAGTTGCTCAAGAACGGGATGAGGATGGGTTGATATGT	1740
QY	2010	TCATACACTGACAAATAGAGATGGTCGGAAGAGTGTGTTTCATACCTGAAAGTATGA	2069
Db	1741	TCATACACTGACAAATAGAGATGGTCGGAAGAGTGTGTTTCATACCTGAAAGTATGA	1800
QY	2070	TCAGCTCTAGTCGGTGATAAACTATAGCAATCTGGCTGATGACAGGATATGATGA	2129
Db	1801	TCAGCTCTAGTCGGTGATAAACTATAGCAATCTGGCTGATGACAGGATATGATGA	1860
QY	2130	TTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATGCACAA	2189
Db	1861	TTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCGTGGGATAGCATGCACAA	1920
QY	2190	GATGATTAGGCTTTGATCTACTATGAGGATAGAGGAGAGGGTACCTAAATTCATGGGAA	2249
Db	1921	GATGATTAGGCTTTGATCTACTATGAGGATAGAGGAGAGGGTACCTAAATTCATGGGAA	1980
QY	2250	TGAATTCGGCACCTCGATGATGATGATGATGATGATGATGATGATGATGATGATG	2309
Db	1981	TGAATTCGGCACCTCGATGATGATGATGATGATGATGATGATGATGATGATGATG	2040
QY	2310	CTCAGTAATTCGGGAAACCAATTCAGTTATGATGATGATGATGATGATGATGATG	2369
Db	2041	CTCAGTAATTCGGGAAACCAATTCAGTTATGATGATGATGATGATGATGATGATG	2100
QY	2370	AGATGCGAGATATTTAGATACCTGGTTCGACAGATTTGACCGGGCTATGCGATCT	2429
Db	2101	AGATGCGAGATATTTAGATACCTGGTTCGACAGATTTGACCGGGCTATGCGATCT	2160
QY	2430	TGAAGATAAATATGAGTTTATGACTTCAGAACACAGTTCATATCAGCAAGAGTGAAG	2489
Db	2161	TGAAGATAAATATGAGTTTATGACTTCAGAACACAGTTCATATCAGCAAGAGTGAAG	2220
QY	2490	AGATAGGATGATTTGATTTGAAAAAGGAAACCTAGTTTGTCTTTTAAATTTTCACTGGAC	2549
Db	2221	AGATAGGATGATTTGATTTGAAAAAGGAAACCTAGTTTGTCTTTTAAATTTTCACTGGAC	2280
QY	2550	AAAAAGCTATTCAGACTATCCATAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTG	2609
Db	2281	AAAAAGCTATTCAGACTATCCATAGCTGCTGAGCTGAGCTGAGCTGAGCTGAGCTG	2340
QY	2610	GGACTCAGATGATCCACTTTTGGTGGCTTGGGAGAAATGATCATATATGCGGAATGTT	2669
Db	2341	GGACTCAGATGATCCACTTTTGGTGGCTTGGGAGAAATGATCATATATGCGGAATGTT	2400
QY	2670	CACCTTTGAAGATGGATGATGATGATGATGATGATGATGATGATGATGATGATG	2729
Db	2401	CACCTTTGAAGATGGATGATGATGATGATGATGATGATGATGATGATGATGATG	2460
QY	2730	AACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2789
Db	2461	AACAGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	2520
QY	2790	AGAAGAAT 2798	
Db	2521	NGAAGAAT 2529	
RESULT 11			

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Query Match

Best Local Similarity

Matches 2493; Conservative

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ORIGIN

Query Match

Best Local Similarity

Matches 2493; Conservative

QY

Db

QY

Db 61 GGGGAAAGTCCTTGTGCTGGAAACCCAGAGTAGCTCTCATCTCAACAAACCAATT 120
QY 438 TGAGTTCACTGAGACAGCTCCAGAAAATCCCAGCATCAACTGATGTGGATAGTCAAC 497
Db 121 TGAGTTCACTGAGACATCCAGAAAATCCCAGCATCAACTGATGTGGATAGTCAAC 180
QY 498 AATGGAACAGCTAGCCGATTAATACTGAGAACGATGACGTTGAGCCGTCAGTGTATCT 557
Db 181 AATGGAACAGCTAGCCGATTAATACTGAGAACGATGACGTTGAGCCGTCAGTGTATCT 240
QY 558 TACAGGAAGTGTGAAGAGTTCGGATTTTCCTCATCACTACAACTACAAAGAGTGTAA 617
Db 241 TACAGGAAGTGTGAAGAGTTCGGATTTTCCTCATCACTACAACTACAAAGAGTGTAA 300
QY 618 ACTGGAGGAGTCTAAACATTAATACTCTCAAGAGACAAATTAATGATGAATCTGATAG 677
Db 301 ACTGGAGGAGTCTAAACATTAATACTCTCAAGAGACAAATTAATGATGAATCTGATAG 360
QY 678 GATCAGAGAGAGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAATAGACCC 737
Db 361 GATCAGAGAGAGGGCATCCCTCCACCTGGACTTGGTCAGAAGATTTATGAATAGACCC 420
QY 738 CTTTGTGACAACTATCTGTCACACCTTCATTCAGAGTATTCACAGTACAGAAATGAG 797
Db 421 CTTTGTGACAACTATCTGTCACACCTTCATTCAGAGTATTCACAGTACAGAAATGAG 480
QY 798 GGAGGCAATGACAAGTATGAGGTTGGTGAAGCTTTTCTCGTGGTTATGAAGAAAT 857
Db 481 GGAGGCAATGACAAGTATGAGGTTGGTGAAGCTTTTCTCGTGGTTATGAAGAAAT 540
QY 858 GGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTAGTGGTCTGTCGCCAGTC 917
Db 541 GGGTTTCACTCGTAGTGTACAGGTATCACTTACCGTAGTGGTCTGTCGCCAGTC 600
QY 918 AGCTGCTCTCATTTGGAGATTTCAACAAATGGAGCGCAATGCTGACATTAATGACTCGGAA 977
Db 601 AGCTGCTCTCATTTGGAGATTTCAACAAATGGAGCGCAATGCTGACATTAATGACTCGGAA 660
QY 978 TGAATTTGGTCTGGAGATTTTCTGCCAAATAATGTTGGATGTTCTCTCGTGAATGCC 1037
Db 661 TGAATTTGGTCTGGAGATTTTCTGCCAAATAATGTTGGATGTTCTCTCGTGAATGCC 720
QY 1038 TCATGGTCCAGAGTGAAGATACCGATCGGACATTCATCAGGTGTTAAGGATTCATTC 1097
Db 721 TCATGGTCCAGAGTGAAGATACCGATCGGACATTCATCAGGTGTTAAGGATTCATTC 780
QY 1098 TGCTTGGATCAACTACTCTTACAGCTTCTGATGAATTCATATCCATATATGGAATATTA 1157
Db 781 TGCTTGGATCAACTACTCTTACAGCTTCTGATGAATTCATATATGGAATATTA 840
QY 1158 TGATCCACCGGAGAGAGGTATGTCCTCCACACCCACGGCCAAAGAAACCAAGTC 1217
Db 841 TGATCCACCGGAGAGAGGTATGTCCTCCACACCCACGGCCAAAGAAACCAAGTC 900
QY 1218 GCTGAGAATATGAATCTCATATGGAATGAGTAGTCCGGAGCTTAAATTAATCTCAT 1277
Db 901 GCTGAGAATATGAATCTCATATGGAATGAGTAGTCCGGAGCTTAAATTAATCTCAT 960
QY 1278 CGTGAATTTTAGAGATGAAGTCTCTCGCATAAAAAACCCTTGGGTACAAATCGGTGCA 1337
Db 961 CGTGAATTTTAGAGATGAAGTCTCTCGCATAAAAAACCCTTGGGTACAAATCGGTGCA 1020
QY 1338 AATTATGCTATTCAGAGCAATTCCTTATATGCTAGTTTGGTTATCATGTCACAAATTT 1397
Db 1021 AATTATGCTATTCAGAGCAATTCCTTATATGCTAGTTTGGTTATCATGTCACAAATTT 1080
QY 1398 TTTTGCACCAAGCAGCGTTTGGACGCCGACGACCTTAAGTCTTTGATGATAAGC 1457
Db 1081 TTTTGCACCAAGCAGCGTTTGGACGCCGACGACCTTAAGTCTTTGATGATAAGC 1140
QY 1458 TCATGAGCTAGGAATTTGTTCTCATGGACATGTTTCAGCCATGCATCAATATATAC 1517
Db 1517 TTTTGCACCAAGCAGCGTTTGGACGCCGACGACCTTAAGTCTTTGATGATAAGC 1140

Db 1141 TCATGAGCTAGGAATTTGTTCTCATGAGCATTTGTTACAGCCATGCATCAATAATAC 1200
QY 1518 TTTAGATGGACTGAACATGTTTGACGGCAGACAGTAGTTGTACTTTTCACTCTGAGGTG 1577
Db 1201 TTTAGATGGACTGAACATGTTTGACGGCAGACAGTAGTTGTACTTTTCACTCTGAGGTG 1260
QY 1578 TGTTTATCATGATGATGGGATTTCCGCCCTCTTTAACTATGGAACCTGGGAGGTACTTAG 1637
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QY 1638 GATCTTCTCTCAATTCGAGATGGTGGTGGATGAGTGCATAATTTGRTGGATTTAGATT 1697
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QY 1698 TGATGTGTGACATCAATGATGATATCACTCACCACGGATATCGTGGGATTCCTGGGAA 1757
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QY 1878 AATGCGCAATTTGATTTCCCGTTCACAGATGGGGTGTGGCTTGTGACTATCGGTGCA 1937
Db 1561 AATGCGCAATTTGATTTCCCGTTCACAGATGGGGTGTGGCTTGTGACTATCGGTGCA 1620
QY 1938 TATGCAATTTGCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1997
Db 1621 TATGCAATTTGCTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
QY 1998 GGGTGATATTTGTTACACTGACAAATAGAGATGGTGGGAAAGTGTGTTTCAACGC 2057
Db 1681 GGGTGATATTTGTTACACTGACAAATAGAGATGGTGGGAAAGTGTGTTTCAACGC 1740
QY 2058 TGAAGTCAATGATCAAGCTTAGTGGTCAATAAACTATAGCATTTCTGGCTGATGACAA 2117
Db 1741 TGAAGTCAATGATCAAGCTTAGTGGTCAATAAACTATAGCATTTCTGGCTGATGACAA 1800
QY 2118 GGATATGATGATTTTATGGCTTTGGATGATGATGATGATGATGATGATGATGATGATG 2177
Db 1801 GGATATGATGATTTTATGGCTTTGGATGATGATGATGATGATGATGATGATGATGATG 1860
QY 2178 AGCATTCACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2237
Db 1861 AGCATTCACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1920
QY 2238 TTTTATGGGAATGAATTCGGCCACCTTGATGATGATGATGATGATGATGATGATGATGATG 2297
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QY 2298 CCTCTGATGGCTCAGTAAATTCGGGAAACCAATTCAGTATGATGATGATGATGATGATGATG 2357
Db 1981 CCTCTGATGGCTCAGTAAATTCGGGAAACCAATTCAGTATGATGATGATGATGATGATGATG 2040
QY 2358 ATTTGACCTGGGAGATGAGAAATTTAAAGATACCGTGGTGGTGAAGAAATTTGACCGG 2417
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QY 2418 TATGCGATGCTTGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2477
Db 2101 TATGCGATGCTTGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
QY 2478 AAAGGATGAGGAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2537
Db 2161 AAAGGATGAGGAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 2220
QY 2538 TTTTCACTGGACAAAAGCTTATTCAGATATCGCATAGGCTGGCTGAGGCTGGGAAATA 2597
Db 2221 TTTTCACTGGACAAAAGCTTATTCAGATATCGCATAGGCTGGCTGAGGCTGGGAAATA 2280

QY	2598	CAAGGTTGCCTTGGACTCAGATCCACTTTTGGTGGCTTCGGGAGAAATTCATCAATAA	2657	QY	678	GATCAGAGAGAGGGGCAATCCCTCCACTGCACTTGGTCAGAAGATTTATGAAATAGACCC	737
Db	2281	CAAGGTTGCCTTGGACTCAGATCCACTTTTGGTGGCTTCGGGAGAAATTCATCAATAA	2340	Db	416	GATCAGAGAGAGGGGCAATCCCTCCACTGCACTTGGTCAGAAGATTTATGAAATAGACCC	475
QY	2658	TGCCGAATGTTTCACTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTTATGGTGTA	2717	QY	738	CCCTTTGCACAAACTATCGTCAACACCTTTGATTCACAGTATTCACAGTACAGAAATAGAG	797
Db	2341	TGCCGAATTTTCACTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTTATGGTGTA	2400	Db	476	CCCTTTGCACAAACTATCGTCAACACCTTTGATTCACAGTATTCACAGTACAGAAATAGAG	535
QY	2718	TGCACCTAGTAGAACAGCAGTGGTCTATGACACTAGTAGACA-----AGAAGA	2765	QY	798	GGAGGCAATTCAGCAAGTATGAGGTGGTGGTGGAGCTTTTCTCGTGGTTATGAAAAAT	857
Db	2401	TGCACCTAGTAGAACAGCAGTGGTCTATGACACTAGTAGACA-----AGAAGA	2460	Db	536	GGAGGCAATTCAGCAAGTATGAGGTGGTGGTGGAGCTTTTCTCGTGGTTATGAAAAAT	595
QY	2766	AGNAGAGAGAGTAGCAGTATGAGAGAGTAGTAGAGAGAGAGAGAGAGAGAGAGAG	2825	QY	858	GGGTTTCACCTCGTAGTCTCAGATATCATTACCTGAGTGGGCTCCTGGTCCAGTC	917
Db	2461	AGAAGAAGAGAGTAGCAGTATGAGAGAGTAGTAGAGAGAGAGAGAGAGAGAGAG	2520	Db	596	GGGTTTCACCTCGTAGTCTCAGATATCATTACCTGAGTGGGCTCCTGGTCCAGTC	655
QY	2826	GTG 2828		QY	918	AGCTGCTCATTTGGAGATTTCAACAATTTGGAGCGCAAAATGCTCAGATTTATGACTCGGAA	977
Db	2521	GTG 2523		Db	656	AGCTGCTCATTTGGAGATTTCAACAATTTGGAGCGCAAAATGCTCAGATTTATGACTCGGAA	715
RESULT 12				QY	978	TGAATTTGGTCTCTGGAGATTTTCTGCCAAATTAATGTGGATGGTCTCTCGCAATTC	1037
LOCUS	A58169	2578 bp	DNA	linear	PAT 05-MAR-1998		
DEFINITION	Sequence 19 from Patent WO9634968.			Db	716	TGAATTTGGTCTCTGGAGATTTTCTGCCAAATTAATGTGGATGGTCTCTCGCAATTC	775
ACCESSION	A58169			QY	1038	TCATGGGTCCAGAGTGAAGATACGATGGACACTTCATCAGGTGTTAAGGATTCATTC	1097
VERSION	A58169.1	GI:3713894		Db	776	TCATGGGTCCAGAGTGAAGATACGATGGACACTTCATCAGGTGTTAAGGATTCATTC	835
KEYWORDS	unidentified.			QY	1098	TGCTTGGATCAACTACTCTTTACAGTTCCTGATGAAATTCATATATATATATATATTA	1157
SOURCE	unclassified.			Db	836	TGCTTGGATCAACTACTCTTTACAGTTCCTGATGAAATTCATATATATATATATATTA	895
ORGANISM	unclassified.			QY	1158	TGATCCACCGAAGAGAGAGTATGCTTCCACACACCGCCGCAAGAACCAAGATTC	1217
REFERENCE	1 (bases 1 to 2578)			Db	896	TGATCCACCGAAGAGAGAGTATGCTTCCACACACCGCCGCAAGAACCAAGATTC	955
AUTHORS	Cooke,D., Debet,M., Gidley,M.J., Jobling,S.A., Safford,R.,			QY	1218	GCTGAGATATATGAAATCTCATATTTGGAATGAGTAGTCGGAGCCCTAAATTAACCTCATA	1277
TITLE	Sidebottom, Christopher,M. and Westcott,R.J.			Db	956	GCTGAGATATATGAAATCTCATATTTGGAATGAGTAGTCGGAGCCCTAAATTAACCTCATA	1015
JOURNAL	IMPROVEMENTS IN OR RELATING TO PLANT STARCH COMPOSITION			QY	1278	CGTGAATTTAGAGATGAAGTTCCTTCCTCGCATATAAAACCTTGGGTACAAATTCGCTGCA	1337
COMMENT	Patent: WO 9634968-A 19 07-NOV-1996;			Db	1016	CGTGAATTTAGAGATGAAGTTCCTTCCTCGCATATAAAACCTTGGGTACAAATTCGCTGCA	1075
FEATURES	NAT STARCH CHEM INVEST (US)			QY	1338	AAATATGGCTATTCAGAGCAATTCATTTATGCTAGTTTGGTATATCATGTACAAATTT	1397
	Other publication AU 550996 961121.			Db	1076	AAATATGGCTATTCAGAGCAATTCATTTATGCTAGTTTGGTATATCATGTACAAATTT	1135
	Location/Qualifiers			QY	1398	TTTTGCACCAACGACCGCTTTTGGACCGCCGACGACCTTAAAGTCTTTGATGATAAAGC	1457
	1. .2578			Db	1136	TTTTGCACCAACGACCGCTTTTGGACCGCCGACGACCTTAAAGTCTTTGATGATAAAGC	1195
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	770 a 462 c 616 g 730 t			Db	1196	TCATGAGCTAGGAAATTTGTTCTCATGGACATTTTCACAGCCATGCATCAATAATAC	1255
BASE COUNT	770 a 462 c 616 g 730 t			QY	1518	TTTATGATGACTGAACATTTTACAGCGCACAGATGTTGTTTACTTCTACTCTGGAGCTCG	1577
ORIGIN				Db	1256	TTTATGATGACTGAACATTTTACAGCGCACAGATGTTGTTTACTTCTACTCTGGAGCTCG	1315
Query Match	77.5%; Score 2445; DB 6; Length 2578;			QY	1578	TGGTTATCATTTGGAATGCGGCTTTTAACTATGGAACCTGGAGAGTACTTAG	1637
Best Local Similarity	98.4%; Pred. No. 0;			Db	1316	TGGTTATCATTTGGAATGCGGCTTTTAACTATGGAACCTGGAGAGTACTTAG	1375
Matches 2482; Conservative	2; Mismatches 27; Indels 12; Gaps 1;			QY	1638	GTATCTTCTCAAATTCGAGATGGTGGTTGGATGAGTGCATAATTTGRTGGATTTAGATT	1697
QY	318	GATCTTGCTGAAGTCTTCTTACGATTCGGAATCCGACCTTCTACAGTTGACGATC	377	Db	1376	GTATCTTCTCAAATTCGAGATGGTGGTTGGATGAGTGCATAATTTGATGATTAGATT	1435
Db	56	GATCTTGCTGAAGTCTTCTTACAAATTCGGAATCCGACCTTCTACAGTTGACGATC	115	QY	1698	TGATGGTGTGACATCAATGATGATATCTCACACCGGATTTATCGTGGGATTCACCTGGGA	1757
QY	378	GGGAAAGTCTTGTACCTGGAATCCAGAGTGAATAGCTCCCTCATCTCAACAGACCAATT	437	Db	1436	TGATGGTGTGACATCAATGATGATATCTCACACCGGATTTATCGTGGGATTCACCTGGGA	1495
Db	116	GGGAAAGTCTTGTGCTCGAATCCGACCTGAGTATAGTCTTATCCCTCAACAAACCAATT	175				
QY	438	TGAGTTCACTGAGACAGCTCCAGAAAATTCGCCAGCATCACTGATGAGTACTCAAC	497				
Db	176	TCAGTTCACTGAGACATCTCCAGAAAATTCGCCAGCATCACTGATGAGTACTCAAC	235				
QY	498	AATGGAACACGCTAGCCAGATTAACACTGAGACCATGACGTTGAGCCGTCAAGTACT	557				
Db	236	AATGGAACACGCTAGCCAGATTAACACTGAGACCATGACGTTGAGCCGTCAAGTACT	295				
QY	558	TACAGGAAGTGTGAAGAGTGGATTTGCTTTCATCCTACACTACAACTACAGAGAGGGTAA	617				
Db	296	TACAGGAAGTGTGAAGAGTGGATTTGCTTTCATCCTACACTACAACTACAGAGAGGGTAA	355				
QY	618	ACTGAGGAGTCTAAACATTAATTAATCTCTGAGAGACAAATTTATGATGAATCTGATAG	677				
Db	356	ACTGAGGAGTCTAAACATTAATTAATCTCTGAGAGACAAATTTATGATGAATCTGATAG	415				

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Db 2576 GTG 2578

RESULT 13

STSBEII

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

FEATURES

source

Location/Qualifiers

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BASE COUNT 742 a 445 c 595 g 711 t

ORIGIN

mat_peptide

Query Match

Best local similarity

Matches 2454; Conservative

77.2%; Score 2436.6; DB 8; Length 2493;

98.7%; Pred. No. 0;

2; Mismatches 31; Indels 0; Gaps 0;

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Db	1	GAAGAATCTTCTTACCAATCCGAAATCCGACCTTCTACAGTTCAGCATCGGGGAAGTC	60		1468	GGATTTCTTCTCATGGACATTTTCACAGCCATGCATCAATAATACTATTAGATGGA	1527
QY	388	CTTGTACCTGGAATCCAGAGTATAGTCTCTCATCTCTCAACAGACCAAAATTTAGTTCACT	447		1141	GGAATTTGTGTTCTCAATGGACATTTTCACAGCCATGCATCAATAATACTATTAGATGGA	1200
Db	61	CTTGTGCGGGAACCCAGAGTATAGTCTCTCATCTCTCAACAGACCAAAATTTAGTTCACT	120		1528	CTGAACATGTTTGGCGCACAGATAGTTGTTTACTCTCTCTGAGAGCTGCTGGTTATCAT	1587
QY	448	GAGACAGCTCCAGAAATTCGCCAGCATCAACTGATGTTGATGTTCAACAATGGAACAC	507		1201	CTGACATGTTTGGCGCACAGATAGTTGTTTACTCTCTCTGAGAGCTGCTGGTTATCAT	1260
Db	121	GAGACATCTCCAGAAATTCGCCAGCATCAACTGATGTTGATGTTCAACAATGGAACAC	180		1588	TGATGTTGGGATTCGCCCTCTTTAACTATGGAACCTGGGAGTACTTAGTATCTTCTC	1647
QY	508	GCTAGCCAGATTTAAACTGAGACGATGAGTTCAGCCCTCAAGTATCTTACAGGAAGT	567		1261	TGGATGTTGGATTCGCCCTCTTTAACTATGGAACCTGGGAGTACTTAGTATCTTCTC	1320
Db	181	GCTAGCCAGATTTAAACTGAGACGATGAGTTCAGCCCTCAAGTATCTTACAGGAAGT	240		1648	TCAATGCGAGATGTTGGTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGGTGTG	1707
QY	568	GTTGAACAGTTGGATTTGTTTCTCATCTCACTCAACTACAAGAGTGTAACTCGAGGAG	627		1321	TCAATGCGAGATGTTGGTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGGTGTG	1380
Db	241	GTTGAACAGTGGATTTGTTTCTCATCTCACTCAACTACAAGAGTGTAACTCGAGGAG	300		1708	ACATCAATGATTTACTCACACGGATTTACGGTGGGATTCACCTGGGAACCTACAGGAA	1767
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QY	688	AGGGCATCCCTCCACCTGGACTTGGTCAGAGATTTATGAAATAGACCCCTTTTGACA	747		1441	TACTTTGACTCGCAACTGATGTTGTTGTTATCTGATGCTCGGATCTGATGCTGCGCAACGATCTT	1500
Db	361	AGGGCATCCCTCCACCTGGACTTGGTCAGAGATTTATGAAATAGACCCCTTTTGACA	420		1828	ATTCATGGCTTTTCCAGATGCAATTTACCAATGCTGGAAGATTTGAGCGGAATCCGACA	1887
QY	748	AACATATGCTCAACACCTTGATTTACAGTATTTACAGTACAAGAAATGAGGAGGCAAT	807		1501	ATTCATGGCTTTTCCAGATGCAATTTACCAATGCTGGAAGATTTGAGCGGAATCCGACA	1560
Db	421	AACATATGCTCAACACCTTGATTTACAGTATTTACAGTACAAGAAATGAGGAGGCAAT	480		1888	TTTTGATTTCCCGTTCAAGATGGGGTGTGGCTTGACTATCGCTGCATATGCCAAT	1947
QY	808	GACAGATGAGGGTGGTTTGGAGCTTTTCTCGTGGTATGAAATGTTTCTACT	867		1561	TTTTGATTTCCCGTTCAAGATGGGGTGTGGCTTGACTATCGCTGCATATGCCAAT	1620
Db	481	GACAGATGAGGGTGGTTTGGAGCTTTTCTCGTGGTATGAAATGTTTCTACT	540		1948	GCTGATAATGATTTGAGTTGCTCAAGAACGGGATGAGATTTGAGAGTGGGTGATAT	2007
QY	868	CGTAGTGTACAGTATACATTTACGTTGAGTGGCTCTGTTGCTGCTGCTGCTGCTC	927		1621	GCTGATAATGATTTGAGTTGCTCAAGAACGGGATGAGATTTGAGAGTGGGTGATAT	1680
Db	541	CGTAGTGTACAGTATACATTTACGTTGAGTGGCTCTGTTGCTGCTGCTGCTGCTC	600		2008	GTTTCATACACTCACAATAAGAGTGGTCGGAAGTGTGTTTCTATACCTGAAAGTCAAT	2067
QY	928	ATTGAGATTTCAACAATTTGGAGCCAAATGCTGACATTTATGACATCGGAATTTGGT	987		1681	GTTTCATACACTCACAATAAGAGTGGTCGGAAGTGTGTTTCTATACCTGAAAGTCAAT	1740
Db	601	ATTGAGATTTCAACAATTTGGAGCCAAATGCTGACATTTATGACATCGGAATTTGGT	660		2068	GATCAAGCTCTAGTGGTGTATTAACATATAGCAATTTGCTGCTGATGACAGAGATATGAT	2127
QY	988	GTCGGGAGATTTTCTGCCAAATATGTTGATGTTCTCTGCAATTCCTCATGGTCC	1047		1741	GATCAAGCTCTAGTGGTGTATTAACATATAGCAATTTGCTGCTGATGACAGAGATATGAT	1800
Db	661	GTCGGGAGATTTTCTGCCAAATATGTTGATGTTCTCTGCAATTCCTCATGGTCC	720		2128	GATTTTATGGCTTTGGATAGACCTCAACATCATTAATAGATCGTGGGATAGCATTCAC	2187
QY	1048	AGAGTGAAGATACGATGAGACATTTATCAGGTGTTAAGGATTTCCATTCCTGCTGGATC	1107		1801	GATTTTATGGCTTTGGATAGACCTCAACATCATTAATAGATCGTGGGATAGCATTCAC	1860
Db	721	AGAGTGAAGATACGATGAGACATTTATCAGGTGTTAAGGATTTCCATTCCTGCTGGATC	780		2188	AAGATGATTAGGCTTAACTATGAGGATAGGAGAGAGGTTACCTAAATTTTCATGGGA	2247
QY	1108	AACTACTCTTACAGCTTCTGATGAATTCATATATGGAATATATATATCATCAACC	1167		1861	AAGATGATTAGGCTTAACTATGAGGATAGGAGAGAGGTTACCTAAATTTTCATGGGA	1920
Db	781	AACTACTCTTACAGCTTCTGATGAATTCATATATGGAATATATATATCATCAACC	840		2248	AATGAATTCGGCCACCTTCTGATGATTTCCCTAGGCTCAACAACACCTCTCTGAT	2307
QY	1168	GAGAGGAGATGATGTTCTCCACACCCCGCCCAAGAAACCAAGTCTGAGAATA	1227		1921	AATGAATTCGGCCACCTTCTGATGATTTCCCTAGGCTCAACAACACCTCTCTGAT	1980
Db	841	GAGAGGAGATGATGTTCTCCACACCCCGCCCAAGAAACCAAGTCTGAGAATA	900		2308	GGCTCAGTAAATTCGGGAACCAATTCAGTTATGATTAATGACAGCGGATTTGACCTG	2367
QY	1228	TATGAATCTCATATTTGGAATGATAGTCCGAGCCCTPAAATTAACATCACTGGAATTT	1287		1981	GGCTCAGTAAATTCGGGAACCAATTCAGTTATGATTAATGACAGCGGATTTGACCTG	2040
Db	901	TATGAATCTCATATTTGGAATGATAGTCCGAGCCCTPAAATTAACATCACTGGAATTT	960		2368	GGAGATGCAGAAATTTAAGATACCGTGGTTCGAGAAATTTGACCCGGGTATGCGAGTAT	2427
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Db	961	AGAGATGAAGTTCTTCTCGCATAAAACCTTGGTACAAATCGGTGCAAAATTTAGGCT	1020		2428	CTTGAAGATAAATGATGATTTATGACTTCAGAACACCTTCATATCACGAAAGGATGAA	2487
QY	1348	ATTCAAGACATCTTATTTATGCTAGTTTGGTTATCATGCTCAAAATTTTTCACCA	1407		2101	CTTGAAGATAAATGATGATTTATGACTTCAGAACACCTTCATATCACGAAAGGATGAA	2160
Db	1021	ATTCAAGACATCTTATTTATGCTAGTTTGGTTATCATGCTCAAAATTTTTCACCA	1080		2488	GGAGATGAGTATGATTTGATTTGAAAAAGGAACCTAGTTTTCCTTAAATTTTCACCTG	2547
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[illegible]

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Db	249	GATCTTTGCCAGAAATACTTCCCTATGAATCCGAACCCCTCTCTTTTAGAGTTGCAGCATC	308
QY	378	GGGAAAAGTCCTTGTAACCTGGATCCAGAGTGATAGCTCCTCATCCTCAACACACAATAAT	437
Db	309	AGAGAAGGTCCTTTGGTTGGTGGCGAGGGCGAGGATCATGGTTTCCAACATGATCAGTT	368
QY	438	TGAGTTCACTGAGACAGCTCCAGAAAATTTCCCAGCATCAACTGATGTGGATAGTTCAAC	497
Db	369	AGAGGTTGCTIGAGGCATTAATCAGAGATACCCAAAGTATCGGCTGACGTGGATTAATGTGAA	428
QY	498	AATGGAACAGCTGACCGAGATTAAAACTGAGAACGATGACGTTGAGCCCTCAAGTGATCT	557
Db	429	GATGGAAGAGAACAGCAACAGTGAAAGCAATGTGGATTTCGTAAGTAGCAAGTGATTC	488
QY	558	JACAGGAAGTGTGAAGAGTTGGATTTTTCATCACTACAACATACAAGAGSTGTGTA	617
Db	489	TAAAGAAACGTTCAAGACAGGATCACAGCTCTTCACTACAATTTGAAGAATGTGTA	548
QY	618	ACTGGAGGAGTCTAAAAACATTAATTAACTTCTCGAAGAGACAATTTATGATGATCTGATAG	677
Db	549	TGTGGAAGTTTCCAAAAACAGACACTTTGGATGA---CATCAGTGTGTAATCTGAAAT	605
QY	678	GATCAGAGAGGGGCGATCCCTCCACCTGGACTTGGTCAGAGAGATTATGAAATAGACCC	737
Db	606	GGTGAAGAAGGGGCGATTCTCCACCTGGACTTGGTCAGAGGATCATGAGATAGACCC	665
QY	738	CCTTTTGAACAACATACTCAACACCTTGATTACAGGTATTCACAGTACAAGAAATAG	797
Db	666	TCCTTTGAAAATTTCTGTGACCATCTTGATTATAGGTTTTTCGCACTATAGGAAAATCCG	725
QY	798	GGAGGCAATTGACAAGTATAGGGTGGTTTGGAAAGCTTTTCTCGTGGTTATGAAAAAT	857
Db	726	GGAAGCAATTAAACAGTATAGGGTGGCTTGGAAAGTATCTCTCGTGGCTATGAGAAAT	785
QY	858	GGTTTTCACGTAGTGTCTACAGTATCACTTACCCTGAGTGGGCTCCTGGTCCCACTC	917
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Db	846	GGCAACACTCATTTGGAGATTTCACAATTTGGAATCCAAATTCGATGCTGATGATCGGAA	905
QY	978	TGAATTTGGTCTGGGAGATTTTTCGCCAAATTAATGTGATGGTCTCCTGCAATTC	1037
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QY	1278	CGTGAATTTTAGAGATGAAGTTCTTCTCCTCGCATAAAAACCTTGGGTACANTGCGGTGCA	1337
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QY	1338	AAATTATGGCTATTCAAGAGCATCTTTATTATGCTAGTTTGGTGTATCATGTCACAAATTT	1397
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QY	1398	TTTTGGACCAAGAGCCGTTTGGAAAGCCGCGACGACCTTAAGTCTTTGATTGATAAAGC	1457
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QY	1638	GTATCTTCTCAAAATCGAGATGGTGTGGATGAGTGCAAAATTTGRTGGATTTAGATT	1697
Db	1566	GTATCTGCTCAAAACGCAAGATGGTGTGGATGAGTACAAGTTTGTATGGCTTCAGATT	1625
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Db	1866	TATGGCAATTCCTGATTAATGGAATGAGATTTCTCAAGAGAAGAGATGAGGATTTGCAAT	1925
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QY	2358	ATTGACCTGGGAGATGCAGAAATTTTAAGATACCGTGGGTTTGAAGAATTTTCAACCGGC	2417
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QY	2418	TAAGCAGTATCTTGAGATAAATAGAGTTTAAGACTTCAAGAACCACTTCATATCAGG	2477

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 12:28:17 ; Search time 657.636 Seconds
(without alignments)
10807.357 Million cell updates/sec

Title: US-10-056-454A-18_COPY_45_3200

Perfect score: 3156

Sequence: 1 AAAAACCTCCCACTAGT.....TGCATGCTAATGATGTTT 3156

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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23:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24:	/SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3154.2	99.9	3231	17	AA142632
2	2958.4	93.7	3074	18	AA169587
3	2847.4	90.2	3033	17	AA142630
4	2838	89.9	3003	17	AA142634
5	2706	85.7	2975	17	AA142635
6	2485.8	78.8	2563	23	ABK50301
7	2474	78.4	2531	17	AA171267
8	2471.2	78.3	2529	17	AA142637
9	2445	77.5	2578	17	AA142631

10	2427.8	76.9	2576	17	AA142636	Class A starch bra
11	1442.8	45.7	3090	19	AAV38720	Full length cassav
12	1377.8	43.7	2913	19	AAV38719	Full length cassav
13	1296	41.1	2715	21	AA142639	Arabidopsis thalia
14	1275.6	40.4	3015	19	AAV05939	Rice type IV starch
15	1260.4	39.9	2919	15	AAQ73750	Rice starch branch
16	1257.6	39.8	2726	22	AAH78337	Nucleotide sequenc
17	1203.6	38.1	2640	19	AAV70961	DNA encoding maize
18	1200.4	38.0	2665	18	AA169729	Plasmid pBE240 ins
19	1200.4	38.0	2725	19	AAV29757	Zea mays starch br
20	1185.6	37.6	3039	24	ABK15494	Wheat starch bran
21	1182.4	37.5	2968	22	AAH78342	Nucleotide sequenc
22	1059.8	33.6	2307	21	AA299938	DNA encoding part
23	1049.8	33.3	2087	18	AA169737	Corn starch branch
24	1048.2	33.2	2165	18	AA169736	Corn starch branch
25	963.2	30.5	1919	19	AAV38722	CDNA encoding star
26	730	23.1	1452	21	AA169577	Arabidopsis thalia
27	663.8	21.0	770	23	ABK50302	Potato starch bran
28	642.8	20.4	4563	22	AA169744	Wheat starch bran
29	637.4	20.2	3128	16	AA169774	Potato starch bran
30	632.4	20.0	2487	18	AA169747	Corn starch branch
31	632.4	20.0	2565	18	AA169752	Corn starch branch
32	632.4	20.0	2763	19	AAV29758	Zea mays starch br
33	632.4	20.0	2771	13	AAQ24257	Branching enzyme D
34	632.4	20.0	2772	18	AA169740	Plasmid pBE65 inse
35	623.2	19.7	2909	13	AAQ27778	Potato amylose-amy
36	618.8	19.6	2687	20	AA169746	WBE 1-D4 CDNA seq
37	611.8	19.4	2733	15	AAQ54674	Rice starch branch
38	611.8	19.4	2733	15	AAQ62135	Rice starch branch
39	598.2	19.0	3075	24	AA169880	Human DNA sequence
40	596.6	18.9	2899	22	AAH02926	Human shear stress
41	596.6	18.9	2955	24	ABN95650	Gene #2148 used to
42	593	18.8	2713	19	AAV70962	DNA encoding maize
43	585.2	18.5	728	23	ABK50303	Potato starch bran
44	546	17.3	1809	18	AA169753	Corn starch branch
45	546	17.3	1865	18	AA169748	Corn starch branch

ALIGNMENTS

RESULT 1
AA142632
ID AA142632 standard; DNA; 3231 BP.
XX
ID AA142632;
XX
AC
XX
25-FEB-1997 (first entry)
XX
DE Class A starch branching enzyme (psbe2con.seq).
XX
KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
FH Key Location/Qualifiers
FT misc_RNA 45..3200
FT FT /*tag= a
FT FT /note= "Claim 34"
FT CDS 228..2855
FT FT /*tag= c

WO9634968-A2.

07-NOV-1996.

03-MAY-1996; 96WO-GB01075.

10-APR-1996; 96GB-0007409.

05-MAY-1995; 95GB-0009229.

(NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

Db 1845 GTGATATCATGCTGGCCACGATCTTATCAAGGGCTTTTCCAGATGCAATTACCAATT 1904
QY 1861 GGTGAAGATGTTAGCGGAATCCGACATTTTGTATTCGGTTTCAAGATGGGGTGTGGC 1920
Db 1905 GGTGAAGATGTTAGCGGAATCCGACATTTTGTATTCGGTTTCAAGATGGGGTGTGGC 1964
QY 1921 TTTGACTATCGGCTGCATATGGCAATGCTGATAAATGATGTTGCTCAAGAAACGG 1980
Db 1965 TTTGACTATCGGCTGCATATGGCAATGCTGATAAATGATGTTGCTCAAGAAACGG 2024
QY 1981 GATGAGGATTTGGAGATGGGTGATATTTTTCATACACACACAAATAGAGATGGTCGAA 2040
Db 2025 GATGAGGATTTGGAGATGGGTGATATTTTTCATACACACACAAATAGAGATGGTCGAA 2084
QY 2041 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAACATATAGCA 2100
Db 2085 AAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAACATATAGCA 2144
QY 2101 TTCTGGCTGATGGACAGGATATGATGATTTTATGCTTTGGATAGACCCGTCACATCA 2160
Db 2145 TTCTGGCTGATGGACAGGATATGATGATTTTATGCTTTGGATAGACCCGTCACATCA 2204
QY 2161 TTAATAGATCGTGGATAGCATTCACAAAGATGATTAGGCTTTGAATATGGGATAGGA 2220
Db 2205 TTAATAGATCGTGGATAGCATTCACAAAGATGATTAGGCTTTGAATATGGGATAGGA 2264
QY 2221 GGAGAGGCTACCTTAATTTTCATGGGAAATGAATTCGGCCACCCCTGAGTGATGATTC 2280
Db 2265 GGAGAGGCTACCTTAATTTTCATGGGAAATGAATTCGGCCACCCCTGAGTGATGATTC 2324
QY 2281 CCTAGGGCTCAACACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTAT 2340
Db 2325 CCTAGGGCTCAACACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTAT 2384
QY 2341 GATAAATTCAGACGAGATTTGACCTGGGAGATGCACAAATTTAAGATACCGTGGTTG 2400
Db 2385 GATAAATTCAGACGAGATTTGACCTGGGAGATGCACAAATTTAAGATACCGTGGTTG 2444
QY 2401 CAGAAATTTGACCGGCTATGCAATATCTTTGAAGATAAATATGATGATGATTCAGAA 2460
Db 2445 CAGAAATTTGACCGGCTATGCAATATCTTTGAAGATAAATATGATGATGATTCAGAA 2504
QY 2461 CACGAGTTCATACAGAAAGATGAGGATAGGATGATGATGATGATGATGATGATGATGAT 2520
Db 2505 CACGAGTTCATACAGAAAGATGAGGATAGGATGATGATGATGATGATGATGATGATGAT 2564
QY 2521 CTAGTTTTTGTCTTTAATTTTCACTGGACAAAGCTATTCACAGATTCGCATAGGCTGG 2580
Db 2565 CTAGTTTTTGTCTTTAATTTTCACTGGACAAAGCTATTCACAGATTCGCATAGGCTGG 2624
QY 2581 CTGAGACCTGGAAATACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTTC 2640
Db 2625 CTGAGACCTGGAAATACAGGTTGCTTGGACTCAGATGATCCACTTTTGGTGGCTTC 2684
QY 2641 GGGAGAAATGATCAATATCCCAATGTTTCACCTTTGAAGGATGGTATGATGATGATGAT 2700
Db 2685 GGGAGAAATGATCAATATCCCAATGTTTCACCTTTGAAGGATGGTATGATGATGATGAT 2744
QY 2701 CTTCAATTTAGTGTATGCACTAGTAGAAGACAGAGTGTCTATGCCACTAGTAGACAA 2760
Db 2745 CTTCAATTTAGTGTATGCACTAGTAGAAGACAGAGTGTCTATGCCACTAGTAGACAA 2804
QY 2761 GAAGAAGAGAGAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2820
Db 2805 GAAGAAGAGAGAGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2864
QY 2821 AACTTGTGATCGGTTGAAGATTTGAAGCTTACATAGAGCTTCTTGACGATCTGGCAA 2880
Db 2865 AACTTGTGATCGGTTGAAGATTTGAAGCTTACATAGAGCTTCTTGACGATCTGGCAA 2924
QY 2881 TATTGCACTAGTCTTTGGCGGAATTTTCATGTCACAAAGGTTTGAATCTTTCCACTATT 2940
Db 2925 TATTGCACTAGTCTTTGGCGGAATTTTCATGTCACAAAGGTTTGAATCTTTCCACTATT 2984

QY 2941 AGTAGTGCAACGATATACGAGAGATGAAGTGTGTAACAAACATATGTAATTCGATGA 3000
Db 2985 AGTAGTGCAACGATATACGAGAGATGAAGTGTGTAACAAACATATGTAATTCGATGA 3044
QY 3001 TTTATGTGCAATGCTGGGACGGGCTTCACAGGTTTGGCTTAGTGAATTTCTGTAATTT 3060
Db 3045 TTTATGTGCAATGCTGGGACGGGCTTCACAGGTTTGGCTTAGTGAATTTCTGTAATTT 3104
QY 3061 CATCTCTTTANATGTACAGCCACACACAGTAATCAATTTATGTGAGACCTTAAACATAAC 3120
Db 3105 CATCTCTTTANATGTACAGCCACACACAGTAATCAATTTATGTGAGACCTTAAACATAAC 3164
QY 3121 CATAAAATGGAAATAGTGTGATCTAATGATGATGATGATGATGATGATGATGATGAT 3156
Db 3165 CATAAAATGGAAATAGTGTGATCTAATGATGATGATGATGATGATGATGATGATGAT 3200

RESULT 2

AAT69587

ID AAT69587 standard; cDNA; 3074 BP.

XX AAT69587;

XX 26-AUG-1997 (first entry)

XX Potato starch branching enzyme II gene (beII).

DE Starch branching enzyme II; beII gene; potato; transgenic plant;

XX amylopectin; amylose; starch; ss.

KW Solanum tuberosum.

XX Key

FH 189..2825 Location/Qualifiers

FT CDS

FT sig_peptide

FT mat_peptide

XX WO9720040-A1.

XX 05-JUN-1997.

XX 28-NOV-1996; 96WO-SE01558.

XX 19-APR-1996; 96SE-0001506.

XX 29-NOV-1995; 95SE-0004272.

XX (EKBB/) EK B.

XX (KHOS/) KHOSNOODI J.

XX (LARS/) LARSSON C.

XX (RASK/) RASK L.

XX (AMYL-) AMYLOGENE HB.

XX Ek B, Khosnoodi J, Larsson C, Larsson H, Rask L;

XX WPI; 1997-310596/28.

XX P-PSDB; AAW19113.

XX Isolated potato starch branching enzyme II - useful for altering

XX degree of amylopectin branching and amylopectin/amylose ratio in

XX potato starch

XX Claim 4; Page 12-15; 24pp; English.

XX A cDNA clone (AAT69587) codes for potato starch branching enzyme II

XX (BEII) (AAW19113). It was isolated from potato tuber cDNA by PCR

XX amplification using primers (AAT69588-89) based on tryptic peptides

XX of isolated BEII; the 5' and 3' ends of the sequence were detd. by

XX RACE. A vector comprising the whole or a functional active part of

1979	DB	GAACCGGATGAGGATGCGAGAGTGGGTGATATTGTTTCATACACTGACAAATAGAGATG	2030
2034	QY	GTGCGAAAGTGTGTTTTCATACGCTCAAAAGTCATGATCAAGCTCTAGTCGGTGATAAAC	2093
2039	DB	GTGCGAAAGTGTGTTTTCATACGCTGAAAAGTCATGATCAAGCTCTAGTCGGTGATAAAC	2098
2094	QY	TATAGCATCTGGCTGATGGCAAGGATATGTATGATTTTATGGCTTTGGATAGACCGTC	2153
2099	DB	TATAGCATCTGGCTGATGGCAAGGATATGTATGATTTTATGGCTCTGGATAGACCNIC	2158
2154	QY	AACATCATTAATAGATCTGGGATAGCATTCACAAGATGATTAAGCTTTGTAAGTATGGG	2213
2159	DB	AACATCATTAATAGATCTGGGATAGCATTCACAAGATGATTAAGCTTTGTAAGTATGGG	2218
2214	QY	ATTAGGAGGAAAGGTACCTAAATTTTCATGGGAATGAAATTCGGCCACCCTGAGTGGAT	2273
2219	DB	ATTAGGAGGAAAGGTACCTAAATTTTCATGGGAATGAAATTCGGCCACCCTGAGTGGAT	2278
2274	QY	TGATTTCCCTAGGCTGAAACACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAAT	2333
2279	DB	TGATTTCCCTAGGCTGAAACACACCTCTCTGATGGCTCAGTAAATCCCGGAAACCAAT	2338
2334	QY	CAGTTATGATAAATCCAGACCGAGATTTGACCTGGGAGATGAGAAATATTTAAGTACCG	2393
2339	DB	CAGTTATGATAAATCCAGACCGAGATTTGACCTGGGAGATGAGAAATATTTAAGTACCG	2398
2394	QY	TGGGTTGCAAGAAATTCACCGGGCTATGSCAGTACTTCAAGATAAATAGTATTATGAC	2453
2399	DB	TGGGTTGCAAGAAATTCACCGGGCTATGSCAGTACTTCAAGATAAATAGTATTATGAC	2458
2454	QY	TTCAGAACACCGATTTCATATCACGAAAGGATGAAGGATAGGATGATGATTTGAAA	2513
2459	DB	TTCAGAACACCGATTTCATATCACGAAAGGATGAAGGATAGGATGATGATTTGAAA	2518
2514	QY	AGGAAACCTAGTTTGTCTTTTAAATTTTCACTGGCAAAAAGCTATTCCAGACTATCGAT	2573
2519	DB	AGGAAACCTAGTTTGTCTTTTAAATTTTCACTGGCAAAAAGCTATTCCAGACTATCGAT	2578
2574	QY	AGGCTGGCTGAAGCCTGGAATAACAGGTTGCCTTGGACTCAGATGATCCACTTTTGG	2633
2579	DB	AGGCTGGCTGAAGCCTGGAATAACAGGTTGCCTTGGACTCAGATGATCCACTTTTGG	2638
2634	QY	TGGCTTCGGGAGAAATGATCATTAATGCCGAATGTTTCACCTTTCAAGGATGATATGA	2693
2639	DB	TGGCTTCGGGAGAAATGATCATTAATGCCGAATGTTTCACCTTTCAAGGATGATATGA	2698
2694	QY	TCGTCTCTGTTCAATTTATGGTGTATGCACCTAGTAGAACAGCACTGTGTATGCAC	2753
2699	DB	TCGTCTCTGTTCAATTTATGGTGTATGCACCTAGTAGAACAGCACTGTGTATGCAC	2758
2754	QY	AGACA---AAGAAGAAAGAAAGAAAGTATGACAGTAGTAGAAGCACTATAGTAGAAGA	2810
2759	DB	AGACAAGAAAGAAAGAAAGAAAGTATGACAGTAGTAGAAGCACTATAGTAGAAGA	2818
2811	QY	AGAATGAAGCACTGTGTATGATCGGTTTGAAGATTTGAACGCTACATAGAGCTTCTT	2870
2819	DB	AGAATGAAGCACTGTGTATGATCGGTTTGAAGATTTGAACGCTACATAGAGCTTCTT	2878
2871	QY	TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTATGTGACAAAGGTTTGCATTTCT	2930
2879	DB	TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTATGTGACAAAGGTTTGCATTTCT	2938
2931	QY	TTCCACTATTAGTAGTGAACGATATACGACAGATCAAGTCTGACAAACATATGTAA	2990
2939	DB	TTCCACTATTAGTAGTGAACGATATACGACAGATCAAGTCTGACAAACATATGTAA	2998
2991	QY	AATCGATGAATTTATGTCGAATGCTGGGACGGCTTCAGCAGGTTTGTCTAGTGGATC	3050
2999	DB	AATCGATGAATTTATGTCGAATGCTGGGACGGCTTCAGCAGGTTTGTCTAGTGGATC	3058
3051	QY	TGTAATTTGTCATCTC 3066	
3059	DB	TGTAATTTGTCATCTC 3074	

QY	284	CTGTATCTTGAAAGCACTCTCTTTACGGAAGATCTTGCTGAAAGTCTTCTTACG	343	QY	1364	ATTATGCTAGTTTGGTTATCATGTGCACAAATTTTTCACCAACAGCAGCCGTTTGGAA	1423
Db	245	CTGTATCTTGAAAGCACTCTCTTTACGGAAGATCTTGCTGAAAGTCTTCTTACA	304	Db	1325	ATTACGCTAGTTTGGTTATCATGTGCACAAATTTTTCACCAACAGCAGCCGTTTGGAA	1384
QY	344	ATTCCGAATCCGACCTTCTACAGTTGCAAGTTCGGGAAAGTCTTGTACCTGGAATCC	403	QY	1424	CGCCCAACGACCTTAAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTCTCA	1483
Db	305	ATTCCGAATCCGACCTTCTACAGTTGCAAGTTCGGGAAAGTCTTGTGCTGGAAACC	364	Db	1385	CGCCCAACGACCTTAAAGTCTTTGATTGATAAAGCTCATGAGCTAGGAATTTGTTCTCA	1444
QY	404	AGAGTGATAGCTCCTCATCTCAACAGACCAATTTAGTTCACAGAGCTCCAGAAA	463	QY	1484	TGGACATTTGTTACAGCCATGCATCAAAATATCTTTAGTAGGACTGAACATGTTGACG	1543
Db	365	AGAGTGATAGCTCCTCATCTCAACAGACCAATTTAGTTCACAGAGCTCCAGAAA	424	Db	1445	TGGACATTTGTTACAGCCATGCATCAAAATATCTTTAGTAGGACTGAACATGTTGACT	1504
QY	464	ATTCCCAACGATCACTGATGTGGATAGTTCAACATGGAACAGCTAGCCAGATAAA	523	QY	1544	GCACAGATAGTTTACTTTTCACTCTGGAGCTCGTGGTTATCATGAGCTGGGATCCC	1603
Db	425	ATTCCCAACGATCACTGATGTGGATAGTTCAACATGGAACAGCTAGCCAGATAAA	484	Db	1505	GCACAGATAGTTTACTTTTCACTCTGGAGCTCGTGGTTATCATGAGCTGGGATCCC	1564
QY	524	CTGAGAACGATGAGCTTGAAGCTCAAGTATCTTACAGCAAGTGTGAAGATTTGGATT	583	QY	1604	GCCTCTTAACTATGGAACCTGGAGGTAAGTATCTTCTCTCAAAATGCGAGATGGT	1663
Db	485	CTGAGAACGATGAGCTTGAAGCTCAAGTATCTTACAGCAAGTGTGAAGATTTGGATT	544	Db	1565	GCCTCTTAACTATGGAACCTGGAGGTAAGTATCTTCTCTCAAAATGCGAGATGGT	1624
QY	584	TTGCTTCACTACATCACTACAGAGGTTGATGATGATGATGATGATGATGATGATGAT	643	QY	1664	GGTGGATAGTGCACAAATTTGRTGGATTTAGATTTGATGGTGGTGCACATCAATGATATA	1723
Db	545	TTGCTTCACTACATCACTACAGAGGTTGATGATGATGATGATGATGATGATGATGAT	604	Db	1625	GGTGGATAGTGCACAAATTTGRTGGATTTAGATTTGATGGTGGTGCACATCAATGATATA	1684
QY	644	CTTCTCAAGAGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	703	QY	1724	CTCACCAGGATATTCGGTGGGATTCACCTGGGAACTACGAGGAATCTTTGGACTCGCAA	1783
Db	605	CTTCTCAAGAGCAATTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT	664	Db	1685	CTCACCAGGATATTCGGTGGGATTCACCTGGGAACTACGAGGAATCTTTGGACTCGCAA	1744
QY	704	CTGAGCTTGGTCAAGAGATTTATGAAATAGACCCCTTTTACAAAATCTATCGTCAACACC	763	QY	1784	CTGATGTGATGCTGCGGTGTATCTGATGCTGGCAACGATCTTTATTCATGGGCTTTTCC	1843
Db	665	CTGAGCTTGGTCAAGAGATTTATGAAATAGACCCCTTTTACAAAATCTATCGTCAACACC	724	Db	1745	CTGATGTGATGCTGCGGTGTATCTGATGCTGGTCAACGATCTTTATTCATGGGCTTTTCC	1804
QY	764	TTGATTACAGGATTTACAGTACAGAAAATGAGGAGGCAATTTGACAAATCTACAGGTTG	823	QY	1844	CAGATGCAATTTACCAATTTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTGTC	1903
Db	725	TTGATTACAGGATTTACAGTACAGAAAATGAGGAGGCAATTTGACAAATCTACAGGTTG	784	Db	1805	CAGATGCAATTTACCAATTTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATTCCTGTC	1864
QY	824	GTGTTGAAGCTTTTCTCGTGGTTATGAAAAATGGTTCCTACCTCGTAGTGCACAGGTA	883	QY	1904	AAGATGGGCTTGGCTTCTGACTATCGCTGCATATGCGCAATGCTGATAAATGGATTG	1963
Db	785	GTGTTGAAGCTTTTCTCGTGGTTATGAAAAATGGTTCCTACCTCGTAGTGCACAGGTA	844	Db	1865	AAGATGGGCTTGGCTTCTGACTATCGCTGCATATGCGCTGCATATGCGCAATGCGGATG	1924
QY	884	TCATTTACCGTGGTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	943	QY	1964	AGTTGCTCAAGAAACGGGATGAGGATGAGGAGTGGGTTGATTTGTTTATACATGACAA	2023
Db	845	TCATTTACCGTGGTGGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	904	Db	1925	AGTTGCTCAAGAAACGGGATGAGGATGAGGAGTGGGTTGATTTTATACATGACAA	1984
QY	944	ATTGGGACGAAATGCTGACATTTATGCTGGAATGATTTGGTGTCTGGAGATTTTTC	1003	QY	2024	ATAGAATGCTGGGAAAGTGTGTTTCTATACGCTGAAAGTGCATCAAGCTCAGTCG	2083
Db	905	ATTGGGACGAAATGCTGACATTTATGCTGGAATGATTTGGTGTCTGGAGATTTTTC	964	Db	1985	ATAGAATGCTGGGAAAGTGTGTTTCTATACGCTGAAAGTGCATCAAGCTCAGTCG	2044
QY	1004	TGCCAAATATGTTGGATGTTCTCTGCAATTCCTCATGGTCCAGAGTGAAGTACGCA	1063	QY	2084	GTGATAAATATAGCATTTCTGGCTGATGGCAAGGATATGATGATTTTATGCTTTGG	2143
Db	965	TGCCAAATATGTTGGATGTTCTCTGCAATTCCTCATGGTCCAGAGTGAAGTACGCA	1024	Db	2045	GTGATAAATATAGCATTTCTGGCTGATGGCAAGGATATGATGATTTTATGCTTTGG	2104
QY	1064	TGGACATTTATCAGGTTTAAAGATTTCCATTCCTGCTTGGATCAACTACTTCTTACAGC	1123	QY	2144	ATAGACCTTCACATCATTAATAGATTCGTTGGATAGCATTTGCACAAAGATGATGAGCTTG	2203
Db	1025	TGGACATTTATCAGGTTTAAAGATTTCCATTCCTGCTTGGATCAACTACTTCTTACAGC	1084	Db	2105	ATAGACCTTCACATCATTAATAGATTCGTTGGATAGCATTTGCACAAAGATGATGAGCTTG	2164
QY	1124	TTCCTGATGAATTTCCATATTAATGGAATATATGATCCACCGAAGAGGAGGATG	1183	QY	2204	TAACTATGGGATAGGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG	2263
Db	1085	TTCCTGATGAATTTCCATATTAATGGAATATATGATCCACCGAAGAGGAGGATG	1144	Db	2165	TAACTATGGGATAGGAGGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG	2224
QY	1184	TCTTCCACACCGGCAAGAAACCAAAAGTCTGCTGAGATATATGAAATCTCATATTG	1243	QY	2264	CTGAGTGGATTCATTTCCCTAGGCTGAAACACCTCTCTGATGGCTCAGTAAATTCGCG	2323
Db	1145	TCTTCCACACCGGCAAGAAACCAAAAGTCTGCTGAGATATATGAAATCTCATATTG	1204	Db	2225	CTGAGTGGATTCATTTCCCTAGGCTGAAACACCTCTCTGATGGCTCAGTAAATTCGCG	2284
QY	1244	GAATGAGTAGTCCGAGGCTTAAATTAATCACTGATGATGATGATGATGATGATGATGAT	1303	QY	2324	GAAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTGGGAGATGAGATATTT	2383
Db	1205	GAATGAGTAGTCCGAGGCTTAAATTAATCACTGATGATGATGATGATGATGATGATGAT	1264	Db	2285	GAAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTGGGAGATGAGATATTT	2344
QY	1304	CTCGATAAAAACCTTGGGTACATGCGGTCAAAATATGCTTATGCTTCAAGAGCATCTT	1363	QY	2384	TAAATACCGTGGGTTGAAAGATTTGACCGGCTTGCAGTATCTTGAAGATAAATATG	2443
Db	1265	CTCGATAAAAACCTTGGGTACATGCGGTCAAAATATGCTTATGCTTCAAGAGCATCTT	1324	Db	2345	TAAATACCGTGGGTTGAAAGATTTGACCGGCTTGCAGTATCTTGAAGATAAATATG	2404
				QY	2444	AGTTTATGACTTCAGAACACCCAGTTTCATATCAGAAAGGATGAAGAGATAGGATGATTG	2503

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Db 2405 AGTTTATGCTTCAGAACACCCAGTTCATAICGAAAGGATGAAGGAGATAGATGATG 2464
QY 2504 TATTTGAAAAGAAACCTAGTCTTTTGTCTTTAAATTTTTCACCTGGACAAAAGCTATTTCAG 2563
Db 2465 TATTTGAAAAGAAACCTAGTCTTTTGTCTTTAAATTTTTCACCTGGACAAAAGCTATTTCAG 2524
QY 2564 ACTATCGATAGGCTGGCTGAAGCTGGAAATACAAGTTGCCCTTGGACTCAGATGATC 2623
Db 2525 ACTATCGATAGGCTGGCTGAAGCTGGAAATACAAGTTGCCCTTGGACTCAGATGATC 2584
QY 2624 CACTTTTTTGGCTGGCTGGAGAAATGATCATAATGCGGAATGTTTCACCTTTGAAGGAT 2683
Db 2585 CACTTTTTTGGCTGGCTGGAGAAATGATCATAATGCGGAATGTTTCACCTTTGAAGGAT 2644
QY 2684 GGTATGATGATGCTGCTGCTTCAATTAATGGTGTATGTCACCTAGTAGAAGACGAGTGGTCT 2743
Db 2645 GGTATGATGATGCTGCTGCTTCAATTAATGGTGTATGTCACCTAGTAGAAGACGAGTGGTCT 2704
QY 2744 ATGCACTAGTAGACA-----AAGAAAGAAAGAAAGAAAGTAGCAGTAG 2788
Db 2705 ATGCACTAGTAGACAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAGCAGCAG 2764
QY 2789 TAGAAGAAAGTAGTAGTAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAGCAGCAG 2848
Db 2765 TAGAAGAAAGTAGTAGTAGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAGCAGCAG 2824
QY 2849 CGCTACATAGAGCTTCTTGAGCTATCTGGCAATATGTCACCTAGTGTGGCGGAATTTTCAT 2908
Db 2825 CGCTACATAGAGCTTCTTGAGCTATCTGGCAATATGTCACCTAGTGTGGCGGAATTTTCAT 2884
QY 2909 GTGACAAAGGTTTGCCTTCTTCCACTATTTAGTAGTCAACGATATAGCAGAGATGA 2968
Db 2885 GTGACAAAGGTTTGCCTTCTTCCACTATTTAGTAGTCAACGATATAGCAGAGATGA 2944
QY 2969 AGTCTGCAACAAACATATGTAATAATCGATGAATTTATGTCGAATGCTGGGAGC 3021
Db 2945 AGTCTGCAACAAACATATGTAATAATCGATGAATTTATGTCGAATGCTGGGAGC 2997

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RESULT 4

AA42634

ID AAT42634 standard; DNA; 3003 BP.

XX AC AAT42634;

XX AC AAT42634;

DT 03-MAR-1997 (first entry)

XX Class A starch branching enzyme (10con.seq).

DE Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;

KW amylose; viscosity; potato; ss.

XX Solanum tuberosum.

XX OS WO9634968-A2.

XX PN 07-NOV-1996.

XX PF 03-MAY-1996; 96WO-0801075.

XX PR 10-APR-1996; 96GB-0007409.

XX PR 05-MAY-1995; 95GB-0009229.

XX (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.

XX Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;

XX Sidebottom CM, Westcott RJ;

XX WPI; 1996-506170/50.

XX New potato plant starch having high amylose content - also class A

XX starch branching enzyme and corresp. DNA to alter the viscosity of

PT

PT starch; for use in food, biodegradable products, adhesives, etc.

XX Example 1; Page 38-39; 142pp; English.

XX Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.

XX Sequence 3003 BP; 895 A; 535 C; 706 G; 867 T; 0 other;

Query Match

Best Local Similarity 89.9%; Score 2838; DB 17; Length 3003;

Matches 2920; Conservative 2; Mismatches 47; Indels 15; Gaps 4;

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QY 53 TGGGCCCTTGAACCTCAGCAATTTGACACCTACCTAGTTAGTTACACTCTCTATCCTCATCAGAT 112
Db 3 TGGGCCCTTGAACCTCAGCAATTTGACACCTACCTAGTTAGTTACACTCTCTATCCTCATCAGAT 62
QY 113 CTCTATTTTCTCTTAATTCACCAAGGAATGAATTAAGAT-----TAGATT 163
Db 63 CTCTATTTTCTCTTAATTCACCAAGGAATGAATTAAGATGAATTTGTAAGAAC 122
QY 164 TGAAGCAGAGAGAAAGAAAGATGGTGTATACACTCTCTGGAGTTCTGTTTCTACTGTTTC 223
Db 123 CTAGGAGAGAGAAAGAAAGATGGTGTATACACTCTCTGGAGTTCTGTTTCTACTGTTTC 182
QY 224 CATCAGTGTACAAATCTAATGGATTCAGCAGTAAATGGTGTATGGAGGAATGCTATGTTT 283
Db 183 CATCAGTGTACAAATCTAATGGATTCAGCAGTAAATGGTGTATGGAGGAATGCTATGTTT 242
QY 284 CTGTATTTCTGAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACA 343
Db 243 CTGTATTTCTGAAAAGCACTCTCTTTCACGGAAGATCTTGGCTGAAAAGTCTTCTTACA 302
QY 344 ATTCGGAATCCGACCTTCTACAGTGTGAGCAATCGGGAAAGTCTTGTACTGGAATCC 403
Db 303 ATTCGGAATCCGACCTTCTACAGTGTGAGCAATCGGGAAAGTCTTGTACTGGAATCC 362
QY 404 AGAGTGTAGTCTCTCATCTCAACAGACCAATTTAGTTTCACAGCAGCAGCTCCAGAA 463
Db 363 AGAGTGTAGTCTCTCATCTCAACAGACCAATTTAGTTTCACAGCAGCAGCTCCAGAA 422
QY 464 ATTCCCGCAGCATCAACTGATGTGATAGTTCACAAATGGAACACGCTAGCAGATTAATA 523
Db 423 ATTCCCGCAGCATCAACTGATGTGATAGTTCACAAATGGAACACGCTAGCAGATTAATA 482
QY 524 CTGAGAACCATGAGCTTGAGCCGTCAAGTGTCTTACAGGAAGTGTGAGAGTGGATT 583
Db 483 CTGAGAACCATGAGCTTGAGCCGTCAAGTGTCTTACAGGAAGTGTGAGAGTGGATT 542
QY 584 TTGCTTCATCATCACTACAACTACAAGAGGTGTAACCTGGAAGAGTCTTAAACATTAATA 643
Db 543 TTGCTTCATCATCACTACAACTACAAGAGGTGTAACCTGGAAGAGTCTTAAACATTAATA 602
QY 644 CTCTCTGAGAGACAATTTATGATGATCTGATAGGATCAGAGAGGGGATCCCTCCAC 703
Db 603 CTCTCTGAGAGACAATTTATGATGATCTGATAGGATCAGAGAGGGGATCCCTCCAC 662
QY 704 CTGGACTTGTGAGAGATTTATGAATAGACCCCTTTTGACAAACTATCGTCAACACC 763
Db 663 CTGGACTTGTGAGAGATTTATGAATAGACCCCTTTTGACAAACTATCGTCAACACC 722
QY 764 TTGATTACAGGTATTTCACAGTACAAGAAATGAGGAGGCAATTCACAGTATGAGGGTG 823
Db 723 TTGATTACAGGTATTTCACAGTACAAGAACTGAGGAGGCAATTCACAGTATGAGGGTG 782
QY 824 GTTTCGAGAGCTTTTCTGCTGTTATGAAAAGTGGTTTTCACCTGCTAGTGTACAGGTA 883
Db 783 GTTTCGAGAGCTTTTCTGCTGTTATGAAAAGTGGTTTTCACCTGCTAGTGTACAGGTA 842
QY 884 TCACCTACCGTGTGAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 943
Db 843 TCACCTACCGTGTGAGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902

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QY	944	ATTGGGACGAAATCCTGACATATATGACTCGGAATGAATTTGGTCTGSGGAGATTTTC	1003	QY	2023	AATAGAAGATGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATCATCAAGCTCTAGTC	2082
Db	903	ATTGGGACGAAATCCTGACTTTATGACTCGGAATGAATTTGGTCTGAGAGATTTTC	962	Db	1983	AATAGAAGATGTCGGAAAAGTGTGTTTCATACGCTGAAAGTCATCATCAAGCTCTAGTC	2042
QY	1004	TGCCAAATAATCTGATGGTTCCTCCTGCAATCCCTCATGGGTCCAGAGTGAAGATCGCA	1063	QY	2083	GCTGATAAACHATAGCATTCCTGGCTGATGGACAAGATATGATATGATTTATGCTTTG	2142
Db	963	TGCCAAATAATCTGATGGTTCCTCCTGCAATCCCTCATGGGTCCAGAGTGAAGATCGTA	1022	Db	2043	GCTGATAAACHATAGCATTCCTGGCTGATGGACAAGATATGATATGATTTATGCTTTG	2102
QY	1064	TGGACACTTCATCAGTGTTAAGGATCCATTCCTGCTTGGATCAACTACTCTTTACAGC	1123	QY	2143	GATAGACCCCTCAACATCATTAATAGATCGTGGATAGCATTTGCACAGATGATAGCTT	2202
Db	1023	TGGACACTTCATCAGTGTTAAGGATCCATTCCTGCTTGGATCAACTACTCTTTACAGC	1082	Db	2103	GATAGACCCCTCAACATCATTAATAGATCGTGGATAGCATTTGCACAGATGATAGCTT	2162
QY	1124	TTTCTGATGAATTCATATATATGATCCACCCGGAAGAGGAGGTATG	1183	QY	2203	GTAACATATGGGATAGGAGAGAGGTACCTAAATTTTCATGGAAATGAATTCGGCCAC	2262
Db	1083	TTTCTGATGAATTCATATATATGATCCACCCGGAAGAGGAGGTATG	1142	Db	2163	GTAACATATGGGATAGGAGAGAGGTACCTAAATTTTCATGGAAATGAATTCGGCCAC	2222
QY	1184	TCTTCCACACCCGCGCAAGAAACCAAGTCGCTGAGATATATGATTCATATTTG	1243	QY	2263	CCTCAGTGGATTCATTTCCCTAGGCTGAAACACACCTCTCTGATGCTCAGTAATTC	2322
Db	1143	TCTTCCACACCCGCGCAAGAAACCAAGTCGCTGAGATATATGATTCATATTTG	1202	Db	2223	CCTCAGTGGATTCATTTCCCTAGGCTGAAACACACCTCTCTGATGCTCAGTAATTC	2282
QY	1244	GAATGATAGTCCGGAGCCTAAATTAACATACATGCTGAATTTTAGAGATGAAGTCTTC	1303	QY	2323	GGAACCAATTCAGTTATGATAATGCAGACCGAGATTTGACCTGGGAGATGCGAATAT	2382
Db	1203	GAATGATAGTCCGGAGCCTAAATTAACATACATGCTGAATTTTAGAGATGAAGTCTTC	1262	Db	2283	AGAACCAATTCAGTTATGATAATGCAGACCGAGATTTGACCTGGGAGATGCGAATAT	2342
QY	1304	CITCGCAT-AAAAAACCTTGGGTACATGCGGTGCAAAATATGCTATTCGAAGAGCATCT	1362	QY	2383	TTAAGATACCGTGGGTGCAAGATTTGACCGGGCTATGCAGATCTCTGAGATATAAT	2442
Db	1263	CITCGCAT-AAAAAACCTTGGGTACATGCGGTGCAAAATATGCTATTCGAAGAGCATCT	1322	Db	2343	TTAAGATACCGTGGGTGCAAGATTTGACCGGGCTATGCAGATCTCTGAGATATAAT	2402
QY	1363	TATTAATGCTAGTTTGGTTATCATGTCACAAATTTTTTTCACCAAGCAGCGGTTTGA	1422	QY	2443	GAGTTTATGACTTCAGAACACCCAGTTTCATATCAGAAAGGATGAAGAGATAGGATGAT	2502
Db	1323	TATTAATGCTAGTTTGGTTATCATGTCACAAATTTTTTTCACCAAGCAGCGGTTTGA	1382	Db	2403	GAGTTTATGACTTCAGAACACCCAGTTTCATATCAGAAAGGATGAAGAGATAGGATGAT	2462
QY	1423	ACGCCGACGACCTTAAGTCTTTGATGATGAAGTCAATGCTAGTAGGAATTTGTTCTC	1482	QY	2503	GTAATTTGAAAAAGGAAACCTAGTTTGTCTTTTAAATTTTCTACTGGACAAGAGCTATTC	2562
Db	1383	ACGCCGACGACCTTAAGTCTTTGATGATGAAGTCAATGCTAGTAGGAATTTGTTCTC	1442	Db	2463	GTAATTTGAAAAAGGAAACCTAGTTTGTCTTTTAAATTTTCTACTGGACAAGAGCTATTC	2522
QY	1483	ATGGACATCTTCACAGCCATGCATCAAAATTAATTTAGATGAGCTGAACATTTTGAC	1542	QY	2563	GACTATCCCATAGCTGGCTGAAGCTGGAATAACAGGTGCTTGGACTCAGATGAT	2622
Db	1443	ATGGACATCTTCACAGCCATGCATCAAAATTAATTTAGATGAGCTGAACATTTTGAC	1502	Db	2523	GACTATCCCATAGCTGGCTGAAGCTGGAATAACAGGTGCTTGGACTCAGATGAT	2582
QY	1543	GGCACAGATAGTTTACTTTCATCTGAGCTCGTGCTTATCAATGGATGGGATTC	1602	QY	2623	CCACTTTTGTGGCTTCGGGAGAAATGATCATATGCCGAATGTTTCCCTTTGAGGA	2682
Db	1503	GGCACAGATAGTTTACTTTCATCTGAGCTCGTGCTTATCAATGGATGGGATTC	1562	Db	2583	CCACTTTTGTGGCTTCGGGAGAAATGATCATATGCCGAATTTTCCCTTTGAGGA	2642
QY	1603	CGCCTCTTTAATGGAACCTGGGAGGTACTTAGGTATCTTCTCAAAATGCCAGATGG	1662	QY	2683	TGGTATGATGATCGCTCTCGTCAATTTATGTTGATGACCTAGTAGAACAGCTGGTC	2742
Db	1563	CGCCTCTTTAATGGAACCTGGGAGGTACTTAGGTATCTTCTCAAAATGCCAGATGG	1622	Db	2643	TGGTATGATGATCGCTCTCGTCAATTTATGTTGATGACCTAGTAGAACAGCTGGTC	2702
QY	1663	TGGTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGCTGACATCAATGATGAT	1722	QY	2743	TATGCACCTAGTAGACA---NAGAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTA	2799
Db	1623	TGGTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGCTGACATCAATGATGAT	1682	Db	2703	TATGCACCTAGTAGACA---NAGAGAAGAAGAAGAAGTAGCAGTAGTAGAAGAAGTA	2762
QY	1723	ACTCACACCGGATTTATCGGTGGGATTCACCTGGGAACCTACGAGGAATATTTGGACTCGCA	1782	QY	2800	GTAGTAGAAGAAGAATGAACGAACCTTGTGATCGCTTTGAAAGATTTGAACGCTACATAGA	2859
Db	1683	ACTCACACCGGATTTATCGGTGGGATTCACCTGGGAACCTACGAGGAATATTTGGACTCGCA	1742	Db	2763	GTAGTAGAAGAAGAATGAACGAACCTTGTGATCGCTTTGAAAGATTTGAACGCTACATAGA	2822
QY	1783	ACTGATGRTGATGCGCGTGTATGATGCTGCCAACGATCTTATTCATGGGCTTTTC	1842	QY	2860	GCTTCTTGACGTATCTGGCAATATGTCATGCTTGGCGGAATTTCAATGTCACAAAGG	2919
Db	1743	ACTGATGRTGATGCGCGTGTATGATGCTGCCAACGATCTTATTCATGGGCTTTTC	1802	Db	2823	GCTTCTTGACGTATCTGGCAATATGTCATGCTTGGCGGAATTTCAATGTCACAAAGG	2882
QY	1843	CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATCCCGTT	1902	QY	2920	TTTTCGAATTTCTTCCACTATTAGTAGTGCAACGATATACGAGAGATGAAGTCTGAAC-	2978
Db	1803	CCAGATGCAATTACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTGTATCCCGTT	1862	Db	2883	TTTTCGAATTTCTTCCACTATTAGTAGTGCAACGATATACGAGAGATGAAGTCTGAAC-	2942
QY	1903	CAAGATGGGGTGTGGTCTTGTACATCGCTGCAATGCGAATTTGCTGATTAATGGAT	1962	QY	2979	-AAACATATGTAATTCGAATGATTTATGCTCGAATGCTGGGACG	3021
Db	1863	CAAGATGGGGTGTGGTCTTGTACATCGCTGCAATGCGAATTTGCTGATTAATGGAT	1922	Db	2943	AAACATATGTAATTCGAATGATTTATGCTCGAATGCTGGGACG	2986
QY	1963	GAGTTGCTCAAGAACGGGATGAGGATTTGGAGGTGGGTGATTTGTTCAACACTGACA	2022	RESULT 5			
Db	1923	GAGTTGCTCAAGAACGGGATGAGGATTTGGAGGTGGGTGATTTGTTCAACACTGACA	1982	AAT42635			
				ID	AAT42635	standard; DNA; 2975 BP.	
				XX			

AC AAT42635;
 XX
 DT 03-MAR-1997 (first entry)
 XX
 DE Class A starch branching enzyme (11con.seq).
 XX
 KW Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
 XX
 KW amylose; viscosity; potato; ss.
 XX
 OS Solanum tuberosum.
 XX
 PN WO9634968-A2.
 XX
 PD 07-NOV-1996.
 XX
 PF 03-MAY-1996; 96WO-GB01075.
 XX
 PR 10-APR-1996; 96GB-0007409.
 PR 05-MAY-1995; 95GB-0009229.
 XX
 PA (NAT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
 XX
 PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
 PI Sidebottom CM, Westcott RJ;
 XX
 DR WPI: 1996-506170/50.
 XX
 PT New potato plant starch having high amylose content - also class A
 PT starch branching enzyme (SBE) has been obtained from
 PT potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.
 CC
 PS Example 1; Page 40-41; 142pp; English.
 XX
 CC Class A starch branching enzyme (SBE) has been obtained from
 CC potatoes. In class A SBE mols., a flexible N-terminal domain,
 CC is found, which is not found in class B mols.
 XX
 SQ Sequence 2975 BP; 871 A; 548 C; 693 G; 863 T; 0 other;
 Query Match 85.7%; Score 2706; DB 17; Length 2975;
 Best Local Similarity 95.8%; Pred. No. 0;
 Matches 2853; Conservative 2; Mismatches 87; Indels 36; Gaps 6;
 QY 55 GGGCCCTTGACCTCAGCAATTTGACACTCAGTTAGTTACACTCTCTATCCTCATCAGATCT 114
 DB 6 GGGCCCTTGACCTCAGCAATTTGACACTCAGTTAGTTACACTCTCTATCCTCATCAGATCT 65
 QY 115 CTATTTTCTCTTAATCCCAAGGAATGAATTAAGATTAGATTG----- 165
 DB 66 CTATTTTCTCTTAATCCCAAGGAATGAATTAAGATTAGATTG----- 165
 QY 166 -AAGGAGAGAAGAAGATGGTGTACACTCTCTGGAGTTGCGTTTCCCTACTCTCC 224
 DB 126 TAAGGAGAGAAGAAGATGGTGTATATCTCTCTGAGTTGCGTTTCCCTACTCTCC 185
 QY 225 ATCAGTGTACAATCTAATGGATTCAGCAGTAAATGGTGTACGAGAAATGCTAAATGTTTC 284
 DB 186 ATCAGTGTACAATCTAATGGATTCAGCAGTAAATGGTGTACGAGAAATGCTAAATGTTTC 245
 QY 285 TGTATTTCTTGAAGAACACTCTCTTTCACGGGAAGATCTGGCTGAAGAGTCTCTTACGA 344
 DB 246 TGTATTTCTTGAAGAACACTCTCTTTCACGGGAAGATCTGGCTGAAGAGTCTCTTACGA 305
 QY 345 TTCCGAATCCGACCTTCTACAGTTGCAATCGGGGAAGTCCCTGTACCTGGAAATCCA 404
 DB 306 TTCCGAATCCGACCTTCTACAGTTGCAATCGGGGAAGTCCCTGTACCTGGAAATCCA 365
 QY 405 GAGTGATAGCTCCCTCATCTCAACAGACCAATTTGAGTTCACTGACAGCTCCAGAAA 464
 DB 366 GAGTGATAGCTCCCTCATCTCAACAGACCAATTTGAGTTCACTGACAGCTCCAGAAA 425
 QY 465 TTCCCCAGCATCAACTGATGTGGATGTTTCAACATGGAACACCGTACCGAGATTAAAC 524
 DB 465 TTCCCCAGCATCAACTGATGTGGATGTTTCAACATGGAACACCGTACCGAGATTAAAC 524

Db 426 ATCCCGAGCATCAACTGATGTAGATAGTTCAACATGGAACACGCTAGCAGATTAAAC 485
 QY 525 TGAGAACGATGACGTTTGAGCCGTCAGTGTATTTACAGGAAGTGTGAGAGTTGATTT 584
 Db 486 TGAGAACGATGACGTTTGAGCCGTCAGTGTATTTACAGGAAGTGTGAGAGTTGATTT 545
 QY 585 TGCCTCATCACTACAACTACAAGAGTGTAACTGGAAGAGTGTAACTGGAAGAGTGTAACT 644
 Db 546 TGCCTCATCACTACAACTACAAGAGTGTAACTGGAAGAGTGTAACTGGAAGAGTGTAACT 605
 QY 645 TTCTGAAGAGACAATTTATGATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACC 704
 Db 606 TTCTGAAGAGACAATTTATGATGAATCTGATAGGATCAGAGAGAGGGGATCCCTCCACC 665
 QY 705 TGGACTTGGTCAGAAAGATTTATGAATAGACCCCTTTTGACAAACTATCTGTCACACCT 764
 Db 666 TGGACTTGGTCAGAAAGATTTATGAATAGACCCCTTTTGACAAACTATCTGTCACACCT 725
 QY 765 TGATTACAGGATTCACAGTACAGAAATAGAGGAGGCAATTTGACAACTATGAGGGTGG 824
 Db 726 TGATTACAGGATTCACAGTACAGAAATAGAGGAGGCAATTTGACAACTATGAGGGTGG 785
 QY 825 TTGGAAGCTTTTCTCGTGGTTATGAAAAAATGGGTTTCACTGCTAGTGTACAGGAT 884
 Db 786 TTGGAAGC-TTTTCTCGTGGTTATGAAAAAATGGGTTTCACTGCTAGTGTACAGGAT 844
 QY 885 CACTTACCGTGAAGTGGGCTCTGCTGAGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004
 Db 905 TTGGGAGCAAAATGCTGACATTTATGCTGCGAAATGAAATTTGGTCTGCTGCTGCTGCT 964
 QY 1005 GCCAAATAATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1054
 Db 965 GCCAAATAATGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1024
 QY 1065 GGACACTTCATCAGTGTAAAGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1124
 Db 1025 GGACACTTCATCAGTGTAAAGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
 QY 1125 TCCGTGATGAATTCATATATGGAATATATATGATATATATGATATATATGATATATAT 1184
 Db 1085 TCCGTGATGAATTCATATATGGAATATATATGATATATATGATATATATGATATATAT 1144
 QY 1185 CTTCACACACCCGCGCAAGAAACCAAGTCCGCTGAGAAATATGAAATCTCATATATG 1244
 Db 1145 CTTCACACACCCGCGCAAGAAACCAAGTCCGCTGAGAAATATGAAATCTCATATATG 1204
 QY 1245 AATGAGTAGTCCGAGCCTAAATTAACCTCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1304
 Db 1205 AATGAGTAGTCCGAGCCTAAATTAACCTCATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
 QY 1305 TGCATATAAAAGCTTTGGGTACAAATGCGGTGCAAAATATGCTGCTGCTGCTGCTGCTGCT 1364
 Db 1265 TGCATATAAAAGCTTTGGGTACAAATGCGGTGCAAAATATGCTGCTGCTGCTGCTGCTGCT 1324
 QY 1365 TTATGCTAGTGTGTTTATCATGCTACAAATTTTTTGGCAAGAGTCCGCTGCTGCTGCTGCT 1424
 Db 1325 TTATGCTAGTGTGTTTATCATGCTACAAATTTTTTGGCAAGAGTCCGCTGCTGCTGCTGCT 1384
 QY 1425 GCCGAGCAGCTTTAAGTCTTTGATTGATAAAGCTCATGAGTATGAGTATGTTGTTCTCAT 1484
 Db 1385 GCCGAGCAGCTTTAAGTCTTTGATTGATAAAGCTCATGAGTATGAGTATGTTGTTCTCAT 1444
 QY 1485 GGACATGTTTTCACAGCCTGATCAATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1544
 Db 1445 GGACATGTTTTCACAGCCTGATCAATAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1504
 QY 1545 CACAGATAGTGTGTTTACTTTCACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1604
 Db 1505 CACAGATAGTGTGTTTACTTTCACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1563

QY	1605	CCTCTTTAATGAACTGGAGTACTTAGGTATCTTCTCTCAAAATGCGAGATGGTG	1664	2685	GTATGATGATCGTCCCTGCTTCAATTTATGTTGATGACCTTAGTAAACAGCAGTGGTCTA	2744
Db	1564	CTCTCTTTAATGAACTGGAGTACTTAGGTATCTTCTCTCAAAATGCGAGATGGTG	1623	2644	GTATGATGATCGTCCCTGCTTCAATTTATGTTGATGACCTTAGTAAACAGCAGTGGTCTA	2703
QY	1665	GTGATGATGATCAAAATTTGRTGATTTAGATTTGATGTTGATGACATCAATGATGATAC	1724	2745	TGCACATAGTAGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2804
Db	1624	GTGATGATGATCAAAATTTGRTGATTTAGATTTGATGTTGATGACATCAATGATGATAC	1683	2704	TGCACATAGTAGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG	2745
QY	1725	TCACCAACGATTTATCGGTGGGATTCACCTGGGAACACAGAGAAATCTTTGGACTCCCAAC	1784	2805	AGAAGAAGAAATGAACAACTTTGTGATCGGCTTCAAAAGATTTGAACGCTACATAGAGCTTC	2864
Db	1684	TCACCAACGATTTATCGGTGGGATTCACCTGGGAACACAGAGAAATCTTTGGACTCCCAAC	1743	2746	CATTGAAGAATGAACAACTTTGTGATCGGCTTCAAAAGATTTGAACGCTACATAGAGCTTC	2803
QY	1785	TGATGTRGATGCTGCGCTGATCTGATGCTGCGCAACGATCTTATTCATGCGCTTTTCC	1844	2865	TTGACGTAATCTGCATATTTGCATGCTTTCGCGGAATTTTCATGTGACAA--AAGGTTTG	2923
Db	1744	TGATGTRGATGCTGCGCTGATCTGATGCTGCGCAACGATCTTATTCATGCGCTTTTCC	1803	2804	---CCACATAGAGCTTCTTGACATGCTTTCGCGGAATTTTCATGTGACAA--AAGGTTTG	2860
QY	1845	AGATGCAATTTACATTTGCTGAAGATTTAGCGGAATTCGCGACATTTTGTATTTCCCGTTCA	1904	2924	CAATTTCTTCCACTATTAGTAGTGAACGATATACGAGAGATGAAGTCTGACAAACA	2983
Db	1804	AGATGCAATTTACATTTGCTGAAGATTTAGCGGAATTCGCGACATTTTGTATTTCCCGTTCA	1863	2861	CAGTTCTTCCACTATTAGTAGTGAACGATATACGAGAGATGAAGTCTGACAAACA	2920
QY	1905	AGATGGGGGTGTTGGCTTTGACATCGCTGATGCGGATTTGATGATGATGATGATGATGAT	1964	2984	TATGTAATTCGATGAATTTATGTCGAATGCTGGGACG	3021
Db	1864	AGATGGGGGTGTTGGCTTTGACATCGCTGATGCGGATTTGATGATGATGATGATGATGAT	1923	2921	TATGTAATTCGATGAATTTATGTCGAATGCTGGGACG	2958
QY	1965	GTTCCTCAAGAAACGGATGAGGATTTGAGGAGTGGGATGATGATGATGATGATGATGATGAT	2024	RESULT 6		
Db	1924	GTTCCTCAAGAAACGGATGAGGATTTGAGGAGTGGGATGATGATGATGATGATGATGATGAT	1983	ABK50301	standard; cDNA; 2563 BP.	
QY	2025	TAGAAGATGCTGGGAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG	2084	XX	ABK50301;	
Db	1984	TAGAAGATGCTGGGAAAGTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGG	2043	XX	15-JUL-2002 (first entry)	
QY	2085	TGATAAATATGATCTGCTGATGGGACAGGATGATGATGATGATGATGATGATGATGATGATGAT	2144	DE	Potato cDNA encoding starch branching enzyme, SBE II.	
Db	2044	TGATAAATATGATCTGCTGATGGGACAGGATGATGATGATGATGATGATGATGATGATGATGAT	2103	XX	Potato; starch branching enzyme; SBE II; glucan branching enzyme;	
QY	2145	TAGACCTGACATCATTAATAGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT	2204	KW	GBE; ss; gene; plant; transgenic; antisense; food industry;	
Db	2104	TAGACCTGACATCATTAATAGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGAT	2163	KW	paper industry; chemical industry.	
QY	2205	AACTATGGGATTTAGGAGGAGAGGTTACCTAAATTTTCATGGGAATGAATTCGCGCACCC	2264	OS	Solanum tuberosum.	
Db	2164	AACTATGGGATTTAGGAGGAGAGGTTACCTAAATTTTCATGGGAATGAATTCGCGCACCC	2223	PH	Key	Location/Qualifiers
QY	2265	TGATGATGATTTTCCCTAGGCTGACACACCTCTCTGATGCTGATGATGATGATGATGATGATGAT	2324	FT	CDS	3, 2552
Db	2224	TGATGATGATTTTCCCTAGGCTGACACACCTCTCTGATGCTGATGATGATGATGATGATGATGAT	2283	FT	/*tag=	a
QY	2325	AAACCAATTCAGTTATGATAATGCAGACGAGATTTGACCTGGGAGATGACAGATATTTT	2384	FT	/product=	"SBE II"
Db	2284	AAACCAATTCAGTTATGATAATGCAGACGAGATTTGACCTGGGAGATGACAGATATTTT	2343	FT	/partial	
QY	2385	AAGATACCGTGGTGTGCAAGATTTGACCGGGCTATGATGATGATGATGATGATGATGATGATGATGAT	2444	FT	/note=	"No start codon shown"
Db	2344	AAGATACCGTGGTGTGCAAGATTTGACCGGGCTATGATGATGATGATGATGATGATGATGATGATGAT	2403	PN		
QY	2445	GTATATGATCTCAGAACACCGATTCATATCAGAAAGATGAAGGATAGGATGATGATGATGATGATGAT	2504	XX	GB2360521-A.	
Db	2404	GTATATGATCTCAGAACACCGATTCATATCAGAAAGATGAAGGATAGGATGATGATGATGATGATGAT	2463	XX	26-SEP-2001.	
QY	2505	ATTTGAAAAAGAAACCTAGTTTGTCTTTTAAATTTTTCATGAGCAAAAAGCTATTCAGA	2564	XX	20-MAR-2000; 2000GB-0006733.	
Db	2464	ATTTGAAAAAGAAACCTAGTTTGTCTTTTAAATTTTTCATGAGCAAAAAGCTATTCAGA	2523	PR	20-MAR-2000; 2000GB-0006733.	
QY	2565	CTATCGATAGCTGGCTGGAACCTGGGAAATACAGGTTGCTTGGACTCAGATGATCC	2624	PA	(DANI-) DANISCO AS.	
Db	2524	CTATCGATAGCTGGCTGGAACCTGGGAAATACAGGTTGCTTGGACTCAGATGATCC	2583	PI	Poulsen P, Sorensen IS;	
QY	2625	ACTTTTGGTGGCTTCGGGAGAAATTCATCATATGCGGATTTTTCACCTTTGAAGGATG	2684	DR	WPI: 2001-650142/75.	
Db	2584	ACTTTTGGTGGCTTCGGGAGAAATTCATCATATGCGGATTTTTCACCTTTGAAGGATG	2643	XX	P-PSDB; AAU80169.	

New transformed plants with reduced endogenous starch branching enzyme and heterologous glucan branching enzyme activities, useful for producing starch with improved properties, which is in the food, paper and chemical industries -

Example 1; Page 31-35; 61pp; English.

The invention relates to a transformed organism, preferably a transformed plant, having a reduced endogenous starch branching enzyme (SBE) activity, and having a heterologous glucan branching enzyme (GBE)

CC activity. The reduced SBE activity is effected via expression of a
CC nucleotide sequence that is antisense to at least part of a SBE exon.
CC Also included are a method of producing starch with altered
CC characteristics comprising (a) providing a plant having reduced
CC endogenous SBE activity, and having heterologous SBE activity
CC (b) propagating the plant of (a) and optionally (c) obtaining starch
CC from the plant; starch obtainable from the transformed plant; and
CC a nucleic acid construct system capable of directing the expression
CC of all or part of one or more antisense SBE exons and optionally one or
CC more heterologous SBE. The transformed plants are useful for producing
CC starch with modified and improved properties, which is an important raw
CC material and used in the food, paper and chemical industries. The
CC present sequence encodes potato SBE II, used to make transgenic plants of
CC the invention.

XX
SQ Sequence 2563 BP: 749 A; 462 C; 614 G; 738 T; 0 other;

Query Match	78.8%;	Score	2485.8;	DB	23;	Length	2563;
Best Local Similarity	98.4%;	Pred.	No. 0;				
Matches	2508;	Conservative	2;	Mismatches	39;	Indels	0;
Gaps	0;						

QY 248 TCACGAGTAATGGTATCGGAGGAAATGCTAATGTTCTGTTATCTTGGTAATCTTGAAGAAGCACTCTC 307
DB 1 TCACGAGTAATGGTATCGGAGGAAATGCTAATGTTCTGTTATCTTGGTAATCTTGAAGAAGCACTCTC 60

QY 308 TTTCACGAGAGATCTTGGCTGAAAGTCTTCTTACGATTCGGAATCCCGACCTTCTACAG 367
DB 61 TTTCACGAGAGATCTTGGCTGAAAGTCTTCTTACGATTCGGAATCCCGACCTTCTACAG 120

QY 368 TTGCAGCATCGGGAAGTCTTGTACTGGAATCCAGAGTATAGTCTTCATCTCCTCAA 427
DB 121 TTGCAGCATCGGGAAGTCTTGTGCTTGGACCCAGAGTATAGTCTTCATCTCCTCAA 180

QY 428 CAGACCAATTTGAGTCTCAGTACGAGAGTCTCAGAAAATTCGCCAGATCACTGATGCG 487
DB 181 CAGACCAATTTGAGTCTCAGTACGAGAGTCTCAGAAAATTCGCCAGATCACTGATGCG 240

QY 488 ATAGTTCAACAATGGACACGCTAGCCAGATTTAAACTGAGAAGTATGAGTCTGAGCGGT 547
DB 241 ATAGTTCAACAATGGACACGCTAGCCAGATTTAAACTGAGAAGTATGAGTCTGAGCGGT 300

QY 548 CAAGTGAICTTACAGGAAGTGTGAGAGTGTGATTTGCTTCACTACACTACACTCAAG 607
DB 301 CAAGTGAICTTACAGGAAGTGTGAGAGTGTGATTTGCTTCACTACACTACACTCAAG 360

QY 608 AAGGTGGTAACCTGAGGAGTCTAAACATTAATATCTCTGGAAGACAAATATTCATG 667
DB 361 AAGGTGGTAACCTGAGGAGTCTAAACATTAATATCTCTGGAAGACAAATATTCATG 420

QY 668 AATCTCATAGGATCAGAGAGAGGGGATCCCTCCACTGGACTTGGTTCAGAAGATTATG 727
DB 421 AATCTCATAGGATCAGAGAGAGGGGATCCCTCCACTGGACTTGGTTCAGAAGATTATG 480

QY 728 AAATAGACCCCTTTTGACAACTATCGTCACACCTTGTATTCAGAGTATTCACAGTACA 787
DB 481 AAATAGACCCCTTTTGACAACTATCGTCACACCTTGTATTCAGAGTATTCACAGTACA 540

QY 788 AGAAATAGGAGGACCAATTCAGAGTATGAGGAGTGTGGAAGCTTTTCTCGTGGTT 847
DB 541 AGAAATAGGAGGACCAATTCAGAGTATGAGGAGTGTGGAAGCTTTTCTCGTGGTT 600

QY 848 ATGAAAAATGGTTTCTACCTAGTGTACAGGTATTCATACCTGAGTGGGCTCCCTG 907
DB 601 ATGAAAAATGGTTTCTACCTAGTGTACAGGTATTCATACCTGAGTGGGCTCCCTG 660

QY 908 GTGCCAGTACGCTCTCTCATTTGGAGATTTCAACAATTTGGGACGCAATGCTGACATTA 967
DB 661 GTGCCAGTACGCTCTCTCATTTGGAGATTTCAACAATTTGGGACGCAATGCTGACATTA 720

QY 968 TGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAATTAATCTGGAATGTTCTC 1027
DB 721 TGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAATTAATCTGGAATGTTCTC 780

QY 1028 CTGCAATTCCTCATGGTCCAGAGTGAAGATAGCATGACACTTTCATCAGTGTAAAG 1087
DB 781 CTGCAATTCCTCATGGTCCAGAGTGAAGATAGCATGACACTTTCATCAGTGTAAAG 840

QY 1088 ATTCCATTCCTCTGTTGATCACTACTCTTTACAGTCTCTGATGAATTCATATAATG 1147
DB 841 ATTCCATTCCTCTGTTGATCACTACTCTTTACAGTCTCTGATGAATTCATATAATG 900

QY 1148 GAATATATATATGATCCACCCGAGAGAGAGTATGCTCTCAACACCCACGCCCAAGA 1207
DB 901 GGATATATATATGATCCACCCGAGAGAGAGTATATCTTCAACACCCACGCCCAAGA 960

QY 1208 AACCAAGTGGCTGAGATATATGAATCTCATATTTGGAATGAGTCTCGGAGCCCTAAA 1267
DB 961 AACCAAGTGGCTGAGATATATGAATCTCATATTTGGAATGAGTCTCGGAGCCCTAAA 1020

QY 1268 TTAACATCATAGTGAATTTAGAGATGAAGTCTTCTCCGCGATATAAAACCTTGGGTACA 1327
DB 1021 TTAACATCATAGTGAATTTAGAGATGAAGTCTTCTCCGCGATATAAAACCTTGGGTAGC 1080

QY 1328 ATGCGGTGCAAAATATGCTATTCAGAGCATCTTATATCTAGTCTTGGTTCATG 1387
DB 1081 ATGCGGTGCAAAATATGCTATTCAGAGCATCTTATATCTAGTCTTGGTTCATG 1140

QY 1388 TCACAAATTTTTCACCAAGAGCGCGTTTGGAAACCCGACGACCTTAAGTCTTTGA 1447
DB 1141 TCACAAATTTTTCACCAAGAGCGCGTTTGGAAACCCGACGACCTTAAGTCTTTGA 1200

QY 1448 TTGATAAAGCTCATGAGCTAGGAATGTTGTTCTCATGAGCATTTGTTACAGCCATGAT 1507
DB 1201 TTGATAAAGCTCATGAGCTAGGAATGTTGTTCTCATGAGCATTTGTTACAGCCATGAT 1260

QY 1508 CAAATAATPACFTTAGATGAGTGAACATGTTGACGGCACAGATAGTTGTTACTTTCACT 1567
DB 1261 CAAATAATPACFTTAGATGAGTGAACATGTTGACGGCACAGATAGTTGTTACTTTCACT 1320

QY 1568 CTGAGCTCGGGTATATCATTTGATGTTGGGATTCGCCCTCTTTAACTATGGAACCTGGG 1627
DB 1321 CTGAGCTCGGGTATATCATTTGATGTTGGGATTCGCCCTCTTTAACTATGGAACCTGGG 1380

QY 1628 AGGTACTTAGTATCTTCTCAAAATCGAGATGTTGGTGGATTCGAGTGAAGTGTGATG 1687
DB 1381 AGGTACTTAGTATCTTCTCAAAATCGAGATGTTGGTGGATTCGAGTGAAGTGTGATG 1440

QY 1588 GATTTAGATTTGATGTTGATGACATCAATGATGATCTACACGAGATTAATCGGTGGAT 1747
DB 1441 GATTTAGATTTGATGTTGATGACATCAATGATGATCTACACGAGATTAATCGGTGGAT 1500

QY 1748 TCACTGGGAATCAGGAGATACCTTTGAGTCTGCAACTGATGATGCTGCGGTGATC 1807
DB 1501 TCACTGGGAATCAGGAGATACCTTTGAGTCTGCAACTGATGATGCTGCGGTGATC 1560

QY 1808 TGATGCTGGCAACGATCTTATTCATGCGGTCTTCCAGATCAATTAACATTTGGTGAAG 1867
DB 1561 TGATGCTGGCAACGATCTTATTCATGCGGTCTTCCAGATCAATTAACATTTGGTGAAG 1620

QY 1868 ATCTTAGCGGAATCCGACATTTTATTCCTTCAAGATGGGGTGTGCTGCTTTGACT 1927
DB 1621 ATCTTAGCGGAATCCGACATTTTATTCCTTCAAGATGGGGTGTGCTGCTTTGACT 1680

QY 1928 ATCGGCTGATATGGAATTTGCTGATTAATTTGATGCTGCTCAAGAAACGGGATGAG 1987
DB 1681 ATCGGCTGATATGGAATTTGCTGATTAATTTGATGCTGCTCAAGAAACGGGATGAG 1740

QY 1988 ATTGAGACTGGGTGATATTTGTTATACACTGACAAATAGAGATGCTCGGAAAGTGTG 2047
DB 1741 ATTGAGACTGGGTGATATTTGTTATACACTGACAAATAGAGATGCTCGGAAAGTGTG 1800

QY 2048 TTTCATACCTGAAAGTCTATGATCAAGCTCTAGTCGCTGATATAAACTATAGCATTTCTGC 2107
DB 1801 TTTCATACCTGAAAGTCTATGATCAAGCTCTAGTCGCTGATATAAACTATAGCATTTCTGC 1860

QY 2108 TGATGGCAAGGATATGATGATTTTATGCTTTGGATAGACCGTCAACATCATTAATAG 2167

Db 661 TGGAGATTTCACAAATTGGGACCGCAAAATGCTGACATATGACTCGGAATGAATTTGGTGT 720
QY 990 CTGGGAGATTTTCTGCCAAATAATCTGGAATGTTCTCTCTGCAATTCCTCATGGGCCAG 1049
Db 721 CTGGGAGATTTTCTGCCAAATAATGATGATGTTCTCTCTGCAATTCCTCATGGGCCAG 780
QY 1050 AGTGAAGATACCGATGGACATTCATAGAGTTTAAAGGATTCATTCCTCTGGATCAA 1109
Db 781 AGTGAAGATACCGATGGACATTCATAGAGTTTAAAGGATTCATTCCTCTGGATCAA 840
QY 1110 CTACCTCTTACAGCTTCTCTGATGAATTCATATATGCAATATATATGATCCACCGCA 1169
Db 841 CTACCTCTTACAGCTTCTCTGATGAATTCATATATGCAATATATATGATCCACCGCA 900
QY 1170 AGAGGAGGATATGCTTCTCCACACCCAGCGCAAAAGAACCAAGTCTCAGAAATA 1229
Db 901 AGAGGAGGATATGCTTCTCCACACCCAGCGCAAAAGAACCAAGTCTCAGAAATA 960
QY 1230 TGAATCTCATATTTGAATGAGTAGTCCGGAGGCTAAATTAATCTCATAGCTGAATTTAG 1289
Db 961 TGAATCTCATATTTGAATGAGTAGTCCGGAGGCTAAATTAATCTCATAGCTGAATTTAG 1020
QY 1290 AGATGAAGTCTCTCTCCATATAAATAACCTTTGGGTACAAATGCGGTGCAAAATATGCGTAT 1349
Db 1021 AGATGAAGTCTCTCTCCATATAAATAACCTTTGGGTACAAATGCGGTGCAAAATATGCGTAT 1080
QY 1350 TCAGAGCAATCTTATATGCTAGTCTTTGGTTATCATGTCACAAATTTTTCACCAAG 1409
Db 1081 TCAAGAGCAATCTTATATGCTAGTCTTTGGTTATCATGTCACAAATTTTTCACCAAG 1140
QY 1410 CAGCGGTTTTCGACGCGCCGACGCTTAAGTCTTTGATGATGATAAGCTCATGAGCTAGG 1469
Db 1141 CAGCGGTTTTCGACGCGCCGACGCTTAAGTCTTTGATGATGATAAGCTCATGAGCTAGG 1200
QY 1470 AATTGTTGTTCTCATGACATGTTTCAGAGCATGCTCAATTAATCTTACTCTGAGCTCGTGTATCATTTG 1589
Db 1261 GAACATGTTTGACGGCACAGATGTTGTTACTTCTACTCTGAGCTCGTGTATCATTTG 1320
QY 1590 GATCTGGGATTCGCGCTCTTAACTATGGAACCTGGAGTACTTAAAGTATCTCTCTC 1649
Db 1321 GATCTGGGATTCGCGCTCTTAACTATGGAACCTGGAGTACTTAAAGTATCTCTCTC 1380
QY 1650 AAATCGAGATGTTGGTGGATGATGTCAAATTTGRTGGATTTAGATTTGATGTTGAC 1709
Db 1381 AAATCGAGATGTTGGTGGATGATGTCAAATTTGRTGGATTTAGATTTGATGTTGAC 1440
QY 1710 ATCAATGATGTATCTACTCACCACCGAATATCGGIGGATTCACCTGGGAATACGAGGAATA 1769
Db 1441 ATCAATGATGTATCTACTCACCACCGAATATCGGIGGATTCACCTGGGAATACGAGGAATA 1500
QY 1770 CTTTGGACTCGCACTGATGATGCTGCGGTGATCTGATGCTGCGCAACGATCTAT 1829
Db 1501 CTTTGGACTCGCACTGATGATGCTGCGGTGATCTGATGCTGCGCAACGATCTAT 1560
QY 1830 TCATGGGCTTTCCCGAGATGCAATTAACATTTGGTGAAGATTTAGCGGAATGCCGACAT 1889
Db 1561 TCACGGGCTTTCCCGAGATGCAATTAACATTTGGTGAAGATTTAGCGGAATGCCGACAT 1620
QY 1890 TTGTATCCGGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGCAATTCG 1949
Db 1621 TTGTATCCGGTTCAAGATGGGGGTGTTGGCTTTGACTATCGGCTGCATATGCAATTCG 1680
QY 1950 TGATAAATGATTTGATGCTCAAGAAACGGGATGAGGATGAGAGTGGGTGATATTTG 2009
Db 1681 TGATAAATGATTTGATGCTCAAGAAACGGGATGAGGATGAGAGTGGGTGATATTTG 1740
QY 2010 TCATACACTGACAAATAGAGATGTTGGAAGATGCTGTTTCATACGCTGAAAGTCAATGA 2069
Db 1741 TCATACACTGACAAATAGAGATGTTGGAAGATGCTGTTTCATACGCTGAAAGTCAATGA 1800

QY 2070 TCAAGCTCTAGTCGGTGAATAAACTATAGCAATTCCTGCTGATGCAAGGATATGATGA 2129
Db 1801 TCAAGCTCTAGTCGGTGAATAAACTATAGCAATTCCTGCTGATGCAAGGATATGATGA 1860
QY 2130 TTTTATGGCTTTGGATAGACCGTCAACATCATTAATAGATCTGGTGGATAGCATTCACAA 2189
Db 1861 TTTTATGGCTCTGGATAGACCGTCAACATCATTAATAGATCTGGTGGATAGCATTCACAA 1920
QY 2190 GATGATTAGGCTTTGAACATATGGGATAGGAGAGAGGTTACTAAATTTTCATGGGAAA 2249
Db 1921 GATGATTAGGCTTTGAACATATGGGATAGGAGAGAGGTTACTAAATTTTCATGGGAAA 1980
QY 2250 TGAATTCGGCCACCTTGAGTGGATGATTTCCCTAGGCTGAAACACACCTCTCTCATGG 2309
Db 1981 TGAATTCGGCCACCTTGAGTGGATGATTTCCCTAGGCTGAAACACACCTCTCTCATGG 2040
QY 2310 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTGG 2369
Db 2041 CTCAGTAATTCGGGAAACCAATTCAGTTATGATAAATGCAGACGAGATTTGACCTGG 2100
QY 2370 AGATCAGATAATTTAAGATACCTGGGTTGCAAGAAATTTGACCGGCTATGCAATCT 2429
Db 2101 AGATCAGATAATTTAAGATACCTGGGTTGCAAGAAATTTGACCGGCTATGCAATCT 2160
QY 2430 TGAAGATAAATAGATTTATGACTTCAGAACACCAAGTTTCATATCACGAAAGGATGAAG 2489
Db 2161 TGAAGATAAATAGATTTATGACTTCAGAACACCAAGTTTCATATCACGAAAGGATGAAG 2220
QY 2490 AGATAGGATGATTTGATTTGAAAAGGAAACCTAGTTTGTCTTTAAATTTTCACTGGAC 2549
Db 2221 AGATAGGATGATTTGATTTGAAAAGGAAACCTAGTTTGTCTTTAAATTTTCACTGGAC 2280
QY 2550 AAAAGCTATTACAGACTATCGCATAGGCTGAGGCTGAAAGCTGGAATAACAGGTTGCTT 2609
Db 2281 AAAAGCTATTACAGACTATCGCATAGGCTGAGGCTGGAATAACAGGTTGCTT 2340
QY 2610 GGACTCAGATGATTCACACTTTTGGTGGCTTCGGGAGAAATGATGATATGCGGAATGTTT 2669
Db 2341 GGACTCAGATGATTCACACTTTTGGTGGCTTCGGGAGAAATGATGATATGCGGAATGTTT 2400
QY 2670 CACCTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2729
Db 2401 CACCTCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
QY 2730 AACAGAGTGGTCTATGCACTAGTAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2789
Db 2461 AACAGAGTGGTCTATGCACTAGTAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
QY 2790 AGAAGAAGT 2798
Db 2521 NGAAGAATT 2529
RESULT 8
AAT42637
ID AAT42637 standard; DNA; 2529 BP.
XX AAT42637;
AC AC
XX XX
DT 03-MAR-1997 (first entry)
XX XX
DE Class A starch branching enzyme (pcrsbe2con.seq) cloned in QE32.
XX Starch branching enzyme; SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX Solanum tuberosum.
OS Solanum tuberosum.
XX WO9634968-A2.
PN WO9634968-A2.
XX XX
PD 07-NOV-1996.
XX XX

PF 03-MAY-1996; 96WO-GB01075.
XX
PR 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
PA (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
XX
PI Cooke D, Debet M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX
XX WPI; 1996-506170/50.
XX
XX New potato starch having high amylose content - also class A
XX starch branching enzyme and corresp. DNA to alter the viscosity of
XX starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 51-53; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
XX potatoes. In class A SBE mols., a flexible N-terminal domain,
XX is found, which is not found in class B mols.
XX
XX Sequence 2529 BP; 735 A; 459 C; 597 G; 723 T; 15 other;
XX
XX Query Match 78.3%; Score 2471.2; DB 17; Length 2529;
XX Best Local Similarity 98.1%; Pred. No. 0;
XX Matches 2482; Conservative 12; Mismatches 35; Indels 0; Gaps 0;
XX
QY 270 GAATGCTATGTTCTGATCTTGAAGAAGCACTCTCTTCACGGGAATCTTGGCTGA 329
DB 1 GGATGCTATGTTCTGATCTTGAAGAAGCACTCTCTTCACGGGAATCTTGGCTGA 60
QY 330 AATGCTCTCTACGATCCGAATCCGACCTTCTACAGTTTGCAGATCGGGGAAGTCCT 389
DB 61 AATGCTCTCTACGATCCGAATCCGACCTTCTACAGTTTGCAGATCGGGGAAGTCCT 120
QY 390 TGTACCTGGATCCAGATGATAGCTCTCATCTCAACAGACAAATTTGATTCACATGA 449
DB 121 TGTGCTGGAAACAGATGATAGCTCTCATCTCAACAGACAAATTTGATTCACATGA 180
QY 450 GACAGCTCCAGAAATTCACAGATCACTGATGATGATGATGATGATGATGATGATGAT 509
DB 181 GACATCTCCAGAAATTCACAGATCACTGATGATGATGATGATGATGATGATGATGAT 240
QY 510 TAGCCAGATTAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
DB 241 TAGCCAGATTAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
QY 570 TGAAGATGGATTTGCTTCACTACATCACTACAGATGATGATGATGATGATGATGATGAT 629
DB 301 TGAAGATGGATTTGCTTCACTACATCACTACAGATGATGATGATGATGATGATGATGAT 360
QY 630 TAAACATTAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 689
DB 361 TAAACATTAATTAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
QY 690 GGGATCCCTCCACCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 749
DB 421 GGGATCCCTCCACCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
QY 750 CTATCGTCAACACCTTGATTAACAGATTAACAGATTAACAGATTAACAGATTAACAGAT 809
DB 481 CTATCGTCAACACCTTGATTAACAGATTAACAGATTAACAGATTAACAGATTAACAGAT 540
QY 810 CAAGTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 869
DB 541 CAAGTATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 870 TAGTGCTACAGATTAACCTTACAGATTAACCTTACAGATTAACCTTACAGATTAACCTT 929
DB 601 TAGTGCTACAGATTAACCTTACAGATTAACCTTACAGATTAACCTTACAGATTAACCTT 660
QY 930 TGGAGATTTCAACATTCGGAGCAAAATGCTGACATTTAGCTCGGAATGAATTTGGTGT 989

661 TGGAGATTTCAACATTCGGAGCAAAATGCTGACATTTAGCTCGGAATGAATTTGGTGT 720
990 CTGGGAGATTTTCTGCGCAAAATTAATGATGGATGTTCTCTGCAATTCCTCATGGTCCAG 1049
721 CTGGGAGATTTTCTGCGCAAAATTAATGATGGATGTTCTCTGCAATTCCTCATGGTCCAG 780
1050 AGTGAAGATACGATGGACACTTCACAGATGTTAGGATTCATTCCTGCTTGGATCAA 1109
781 AGTGAAGATACGATGGACACTTCACAGATGTTAGGATTCATTCCTGCTTGGATCAA 840
1110 CTACTCTTTACAGCTTCTCTGATGAATTCATTAATGAATTAATTAATGATCAACCCGA 1169
841 CTACTCTTTACAGCTTCTCTGATGAATTCATTAATGAATTAATTAATGATCAACCCGA 900
1170 AGAGGAGAGGATGATGTTTCCACACCCACCGCCCAAGAAACCAAGTTCGTGAGAATATA 1229
901 AGAGGAGAGGATGATGTTTCCACACCCACCGCCCAAGAAACCAAGTTCGTGAGAATATA 960
1230 TGAATCTCATATTTGGAATGAGTAGTCCGGAGCCCTAAATTAATCACTACCTGAATTTTAG 1289
961 TGAATCTCATATTTGGAATGAGTAGTCCGGAGCCCTAAATTAATCACTACCTGAATTTTAG 1020
1290 AGATGAAGTTCTTCTCTGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1349
1021 AGATGAAGTTCTTCTCTGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1080
1350 TCAAGAGCATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1409
1081 TCAAGAGCATTTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
1410 CAGCCGTTTGGAAACCGCCGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1469
1141 CAGCCGTTTGGAAACCGCCGACGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
1470 AATGTTGTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1529
1201 AATGTTGTTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
1530 GAACATGTTTGCAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1589
1261 GAACATGTTTGCAGGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
1590 GATGTTGGATTCGCGCTCTTAACTATGGAACCTGGAGGATGATGATGATGATGATGATGAT 1649
1321 GATGTTGGATTCGCGCTCTTAACTATGGAACCTGGAGGATGATGATGATGATGATGATGAT 1380
1650 AAATGCGAGATGGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1709
1381 AAATGCGAGATGGTGGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
1710 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1769
1441 ATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
1770 CTTTGGATTCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1829
1501 CTTTGGATTCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
1830 TCATGGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATGTTAGCGGAATGCCACAT 1889
1561 TCACGGGCTTTTCCAGATGCAATTAACCATTTGGTGAAGATGTTAGCGGAATGCCACAT 1620
1890 TTGATTCCTGCTCAAGATGGGGGTTGGCTTTGACATTCGGCTGCAATGGCAATTCG 1949
1621 TTGATTCCTGCTCAAGATGGGGGTTGGCTTTGACATTCGGCTGCAATGGCAATTCG 1680
1950 TCATGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2009
1681 TGATAAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740
2010 TCATACATGCAAAATAGAAGATGGTTCGGAAGATGTTTTCATACGCTGGAAGTCATGA 2069

DE Class A starch branching enzyme (86con.seq) cloned in QE32.
XX
KW Starch branching enzyme: SBE; class A; class B; Solanum tuberosum;
KW amylose; viscosity; potato; ss.
XX
OS Solanum tuberosum.
XX
PN W09634968-A2.
XX
PD 07-NOV-1996.
XX
PF 03-MAY-1996; 96WO-GB01075.
XX
PP 10-APR-1996; 96GB-0007409.
PR 05-MAY-1995; 95GB-0009229.
XX
XX (NATT) NAT STARCH & CHEM INVESTMENT HOLDING COR.
PA
XX Cooke D, Dabert M, Gidley MJ, Jobling SA, Safford R;
PI Sidebottom CM, Westcott RJ;
XX WPI; 1996-506170/50.
XX
XX New potato plant starch having high amylose content - also class A
PT starch branching enzyme and corresp. DNA to alter the viscosity of
PT starch; for use in food, biodegradable products, adhesives, etc.
XX
XX Example 1; Page 49-51; 142pp; English.
XX
XX Class A starch branching enzyme (SBE) has been obtained from
CC potatoes. In class A SBE mols., a flexible N-terminal domain,
CC is found, which is not found in class B mols.
XX
XX Sequence 2576 BP; 770 A; 462 C; 615 G; 729 T; 0 other;
SQ

Query Match 76.9%; Score 2427.8; DB 17; Length 2576;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2478; Conservative 2; Mismatches 29; Indels 14; Gaps 2;

QY 318 GATCTGGCTGAAAGCTCTCTTACGATTCGGAAATCCGAACTTCACAGTTCCAGCATC 377
DB 56 GATCTGGCTGAAAGCTCTCTTACAAATTCGAAATTCGAACTTCACAGTTCCAGCATC 115

QY 378 GGGGAAGTCCCTGTACCTGGAAATCCAGAGTATAGTCTCTCATCTCAACAGACCAATT 437
DB 116 GGGGAAGTCCCTGTGCTGGAAATCCAGAGTATAGTCTCTCATCTCAACAAACCAATT 175

QY 438 TGAGTTCACTGAGACAGTCCAGAAATTCGCCAGCATCAACTGATGTGGATGTTCAAC 497
DB 176 TGAGTTCACTGAGACATCTCCAGAAATTCGCCAGCATCAACTGATGTAGATTCAAC 235

QY 498 AATGGAACACGCTAGCCAGATTAACCTCAGACGATGACGTTGAGCCGCTCAAGTGATCT 557
DB 236 AATGGAACACGCTAGCCAGATTAACCTCAGACGATGACGTTGAGCCGCTCAAGTGATCT 295

QY 558 TACAGGAAGTGTGAAGAGTGGATTTGCTTCATCACTACAACCTCAAGAGGTTGATAA 617
DB 296 TACAGGAAGTGTGAAGAGTGGATTTGCTTCATCACTACAACCTCAAGAGGTTGATAA 355

QY 618 ACTGAGGAGTCTAAACATTAATTAATCTCTGAAGAGCAATTAATGATGAATCTGATAG 677
DB 356 ACTGAGGAGTCTAAACATTAATTAATCTCTGAAGAGCAATTAATGATGAATCTGATAG 415

QY 678 GATCAGAGAGGGGATCCCTCCACCTGAGTGGTTCAGACGATTTATCAATAGACCC 737
DB 416 GATCAGAGAGGGGATCCCTCCACCTGAGTGGTTCAGACGATTTATCAATAGACCC 475

QY 738 CTTTTGACAACTATCGTCAACACCTTGATTACAGGATTCACAGTACAAGAAATGAG 797
DB 476 CTTTTGACAACTATCGTCAACACCTTGATTACAGGATTCACAGTACAAGAACTGAG 535

QY 798 GGAGGCAATTGACAGATGAGGGTGGTTTGAAGCTTTTCTCGTGGTTATCAAAAAT 857
DB

DB 536 GGAGGCAATTGACAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCGTGTATGAAAAAT 595
QY 858 GGGTTTCACTCGTAGTGTACAGGTATACCTTACCGTGGAGGGCTCTCGTGTGCCAGTC 917
DB 596 GGGTTTCACTCGTAGTGTACAGGTATACCTTACCGTGGAGGGCTCTCGTGTGCCAGTC 655
QY 918 AGCTGCTCTCANTGGAGATTCAACAATGGAGCGAAATGCTGACATTAATGACTCGAA 977
DB 656 AGCTGCTCTCANTGGAGATTCAACAATGGAGCGAAATGCTGACATTAATGACTCGAA 715
QY 978 TGAATTTGGTCTCTGGAGATTTTCTGCCAAATTAATGCTGGATGGTCTCTCGCAATTC 1037
DB 716 TGAATTTGGTCTCTGGAGATTTTCTGCCAAATTAATGCTGGATGGTCTCTCGCAATTC 775
QY 1038 TCATGGTCCAGAGTGAAGATACGATGGACATTCATCAGTGTCTTAAGGATTCATTC 1097
DB 776 TCATGGTCCAGAGTGAAGATACGATGGACATTCATCAGTGTCTTAAGGATTCATTC 835
QY 1098 TGGTTGATCACTACTCTTTTACAGTCTCTGATGAAATTCATATAATGAATATATTA 1157
DB 836 TGGTTGATCACTACTCT--TACAGCTTCTCTGATGAAATTCATATAATGAATATATTA 893
QY 1158 TGATCCACCCGAGAGGAGGATGCTTCCACACCCGAGCGCCAGAAACCAAGTC 1217
DB 894 TGATCCACCCGAGAGGAGGATGCTTCCACACCCGAGCGCCAGAAACCAAGTC 953
QY 1218 GCTGAGAATATATGAATCTCATATTTGGAATCAGTAGTCCGAGGCTAAAATTAACATTA 1277
DB 954 GCTGAGAATATATGAATCTCATATTTGGAATCAGTAGTCCGAGGCTAAAATTAACATTA 1013
QY 1278 CGTGAATTTAGAGATGAAGTCTCTCTCGATTAATAAACTGGGGTACAATGGGGTGA 1337
DB 1014 CGTGAATTTAGAGATGAAGTCTCTCTCGATTAATAAACTGGGGTACAATGGGGTGA 1073
QY 1338 AATTATGGCTATTCAAGACGATTTTATATGCTAGTTTGGTTATCATGTCACAAATTT 1397
DB 1074 AATTATGGCTATTCAAGACGATTTTATATGCTAGTTTGGTTATCATGTCACAAATTT 1133
QY 1398 TTTTGCAACCAAGCAGCGTTTGGAAACGCCCGACGACCTTAAGTCTTTGATGATAAAGC 1457
DB 1134 TTTTGCAACCAAGCAGCGTTTGGAAACGCCCGACGACCTTAAGTCTTTGATGATAAAGC 1193
QY 1458 TCATGAGCTAGGAATTTGTTCTCATGGACATGTTTTCAGCCATGATGATCAATCAATATAC 1517
DB 1194 TCATGAGCTAGGAATTTGTTCTCATGGACATGTTTTCAGCCATGATGATCAATCAATATAC 1253
QY 1518 TTTAGATGGAATGGAATTTTCAGCGCACAGATGTTGTTTACTTTTCACTCTCGAGCTG 1577
DB 1254 TTTAGATGGAATGGAATTTTCAGCGCACAGATGTTGTTTACTTTTCACTCTCGAGCTG 1313
QY 1578 TGGTTATCANTGGATGGAATTTCCGCTCTTTAACTATGGAACCTGGAGGATCTAG 1637
DB 1314 TGGTTATCANTGGATGGAATTTCCGCTCTTTAACTATGGAACCTGGAGGATCTAG 1373
QY 1638 GATCTCTCTCAAAATGCGAGATGTTGGTGGATGATGAGTCAAAATTTGRTGGATTTAGATT 1697
DB 1374 GATCTCTCTCAAAATGCGAGATGTTGGTGGATGATGAGTCAAAATTTGRTGGATTTAGATT 1433
QY 1698 TGATGCTGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1757
DB 1434 TGATGCTGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
QY 1758 CTACGAGGAATTTTGGACTCGCAACTGATGATGATGATGATGATGATGATGATGATGAT 1817
DB 1494 CTACGAGGAATTTTGGACTCGCAACTGATGATGATGATGATGATGATGATGATGATGAT 1553
QY 1818 CAACGATCTTATTCATGCGCTTTTCCAGATGCAATTTACCAATTTGTTGAAGTGTGAGCG 1877
DB 1554 CAACGATCTTATTCATGCGCTTTTCCAGATGCAATTTACCAATTTGTTGAAGTGTGAGCG 1613
QY 1878 AATGCCGACATTTTGTATTCGCTTCAAGATGGGGTGTGGCTTTGACTATCGGCTGCA 1937
DB 1614 AATGCCGACATTTTGTATTCGCTTCAAGATGGGGTGTGGCTTTGACTATCGGCTGCA 1673

QY	537	CGTTGAGCGGTCAAGTGATCTTACAGGAAGTGTGAAGAGTTGGATTTTGCTTCATCACT	596	Db	1477	TGGAAGCTGGAGGTCCTAAGATTTCTTCTTCAAAATGCAAGATGGTGGTGGAGAGTA	1536
Db	490	AAAAAGATCG-----	499	QY	1677	CAAAATTTGRTGGATTTAGATTTGATGGTGTGACATCAATGATGATATCTACCCACGAGATT	1736
QY	597	ACAACTACAGAAGGTGGTAACACTGGAGGAGTCTAAACAAATTAATACHTTCTGAAGAGAC	656	Db	1537	CAGGTTTGATGGTTTTAGATTTGATGGGTGACTTCCATGATGATACACTCCCCATGGGTT	1596
Db	500	-----GTTCCCAATTGCATGAGAC	516	QY	1737	ATCGGTGGGATTCACCTGGGAACACAGAGGAATATTTGGACTCGCAACTGATSTGATGC	1796
QY	657	AATTATTGATGATCTGATAGGATCAGAGAGAGGGGCAATCCCTCCACCTGGACTTGGTCA	716	Db	1597	GCAGGTAGCTTTTACTGGCAACTACAATGAGTACTTTGGATATGCAACTGATGATGATGC	1656
Db	517	AATTACATTTGAAAAAGTGAATCTAAACCAAGGTCCTATCTCCACCTGGCAGTGGCA	576	QY	1797	TGCGGTGATCTGATGCTGCCACACGATCTTATTCATGCGGTCTTTCCCAAGTGCATATAC	1856
QY	717	GAGATTTTATGAATAGACCCCTTTTGTACAAAATCTGCTCAACACCTTGTGATACAGGTA	776	Db	1657	TGTGATTTATTTGATGCTTGTGAATGATATGATTCACGGTCTTTTCCCTGAGGCTGTATC	1716
Db	577	GAGAAATATGACATAGATCCAAAGCTTGGCAGGTTTCCGTCACGATCTTGACATACCGATA	636	QY	1857	CATTGTTGAAGATGTTAGCGGAATGCCGACATTTTGTATTTCCCTTCAAGATGGGGGTGT	1916
QY	777	TTACACAGTACAGAAAATGAGGAGGCAATGTACAAGTATGAGGGTGGTTTGAAGCTTT	836	Db	1717	CATTGGTGAAGATCTTAGCGGAAGCCACAATTTTGCATTTCCAGTGGGAAGATGTTGGTGT	1776
Db	637	TTACACAGTACAAAAGGCTCGTGAGGAAATTGACAAGTATGAAGTATGAAGTGGATSCAT	696	QY	1917	TGCTTTGATCTATCGGCTGCATATGGAATTTGCTGTGATTAATGGAATGAGTTGCTTCARAAA	1976
QY	837	TTCTCGTGTATGAAAAAATGGTTTCACTCGTAGTGTACAGGTATACATTACCGTGA	896	Db	1777	TGATTTGATTTACCGTCTCCACATGGCCATTTGCCGATAAATGGATTGAGATTCCTTAAGAA	1836
Db	697	CTCTCGTGAATTTGAAAAGTTTGGTTTCTTACAGAGTGAACAGGAATAACTATTATAGGA	756	QY	1977	ACGGATGAGSATTGGAGAGTGGGTGATTTTTCATACACTGACACTGACAAATGAGCATGGTC	2036
QY	897	GTGGGCTCTGTTGCCAGTCAAGCTCTCTCATTTGGAGATTTTCAACAATTTGGGACGAAA	956	Db	1837	GAGAGATGAGACTGGAAAATGGGTGACATTTGTGATACACTCACCACACAGAAAGTGGTT	1896
Db	757	ATGGGCACCTGGAGCTACGTGGGCTGCACITATTGGAGATTTCAACAATTTGGAATCCTAA	816	QY	2037	GGAAAAGTGTSTTTTCATACGCTGAAAGTCAATGATCAAGCTCTAGTCGGTGATATAAACTAT	2096
QY	957	TGCTGACATATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAAAATAGT	1016	Db	1897	GGAAAAGTGTSTTTTCATGCTGAAAGTCAATGATCAAGCTCTTTGTTGTCACAAAATCTAT	1956
Db	817	TCAGAGATGATGACTCGGAATGAGTTTGGTGTCTGGGAGATTTTCTGCGCAAAATAGC	876	QY	2097	AGCATTTCTGCTCATGGCAAGGATATGATGATTTTATGGCTTTGGATAGACCGTCAAC	2156
QY	1017	GGATGTTCTCTCTGCAATTCCTCATGCGTCCAGAGTGAAGATACGATGACACTTCATC	1076	Db	1957	TGCATTTTGGCTGATGGACAAGGACATGTACGACTTCATGGCTCGTGACAGACCATCTAC	2016
Db	877	AGATGTTTCAACCAATTCCTCATGCTTGGATCAAGTTCTCAGTTCAGGCACTGGTGAAT	936	QY	2157	ATCATTAATAGATCGTGGGATAGCATTTGCACAAGATGATGATTTTATGGCTTTGGATAGACCGTCAAC	2216
QY	1077	AGTGTGTTAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGCTTCTCTGATGAAAT	1136	Db	2017	TCTCTTTATAGATCGTGGATAGCATTTGCACAAATGATCAGGCTTATTTACCATGGGCTT	2076
Db	937	TGGCAATCAAGATTCATTCCTGCTGGATCAAGTTCTCAGTTCAGGCACTGGTGAAT	996	QY	2217	AGGAGAGAGGGTACCTAAATTTTCATGGAAATGAATTCGGCCACCTGAGTGGATTGA	2276
QY	1137	TCATATATGGAATATATGATCCACCCAGAGGAGAGATGATGCTTCCCAACACC	1196	Db	2077	AGCGGAGAAGGATTTTGAATTTTATGGGAAATGAATTTGGACATCTCTCAGTGGATTGA	2136
Db	997	CCCATACAATGGCATATGATGATCCACCAAGGAGGAGAGATGATGTTTCAACATCC	1056	QY	2277	TTTCCCTAGGCTGACACACACTCTCTGATGGCTCAGTAATTTCCCGGAAACCAATTCAG	2336
QY	1197	ACGGCCAAAGAAACCAAGTCGTGAGATATATGATCTCATTTATGGAAATGATGATCC	1256	Db	2137	TTTTCCAAAGAGGGATCGACATCTGCCCAATGTTAAAGTAAATTTCCAGGGAACCAACACAG	2196
Db	1057	TCAGCCAAAGACCAAAATCACTAGGATTTATGAACTCAATGTTGGGATGGATAGTAT	1116	QY	2337	TTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGACAGATATTTTAAGATACCTGG	2396
QY	1257	GGAGCCTAAATTAACATATATGAGATGAAGTCTTTCCCTCGCATAAAAA	1316	Db	2197	TTATGATAAATGACCTGCTGATGATTTGATCTAGGTGATGACAGACTATCTAAGATATCATGG	2256
Db	1117	GGAGCCAAATTAACACATATGCCAACTTTAGAGATGATATGCTTCTCGCATCAAAA	1176	QY	2397	GTTGCAAGAAATTTGACCGGCTATGCAATCTTTGAAGATATAATATAGTTTATGACTTC	2456
QY	1317	CCTTGGGTACATCGGTCGAATATGCTATTTCAAGAGATCTTATATGCTAGTTT	1376	Db	2257	AATGCAAGAGTTTGTATCAGGCAATGCAACATCTTTGAAGAAGCCCTATGTTTTCATGACTTC	2316
Db	1177	GCTTGGCTACAAGTGTTCAGATCATGSCATTTCAAGAGCATTTCCATTTATGCTAGTTT	1236	QY	2457	AGAACACCAGTTTCATATCAGCAAGGATGAGAGATGAGATGATTTGATTTGAAAAAGG	2516
QY	1377	TGTTTATCATGTCACAAAATTTTTCACCAACAGCAGCCGCTTTTGGAAACCCCGACCACT	1436	Db	2317	TGAGCACCAAGTATATATCAGGAAGGATGAAGGAGATCGGATCAITCTCTTTGAGAGGG	2376
Db	1237	TGSGTACCAATGTCACAACTTTTTCACCTAGCAGCCGATTTGGAATCTCTGATGATTT	1296	QY	2517	AAACCTTAGTTTGTCTTTAAATTTTTCACCTGGACAAAAGCTATTCAGACTATCGCATAGG	2576
QY	1437	TAAGTCTTTGATGATAAAGCTCATGAGCTAGGAATTTGTTTCTCATGAGCATTTGTCA	1496	Db	2377	AAACCTTTGTTTGTATTTCACTTTTCTTGGACTAACAGCTATTCAGATTAACGAGTTGG	2436
Db	1297	GAACTCTTTAATAGATAAAGCTCATGAGTTAGGCTGCTTGTCTCATGAGTATTTTCA	1356	QY	2577	CTGGCTGAAGCCTTGGAAAAATACAAGGTTGCCCTTGGACTCAGATGATCCACTTTTTTGGTGG	2636
QY	1497	CAGCCATGATCAATAATATCTTTAGATGGAATGAAATGTTTGAAGGACAGATAGTTG	1556	Db	2437	CTGCTTCAAGTCTCAGGAAAGTACAAGATTTGTTTGGACTCGGATGATGGCTTTTTCGAGG	2496
Db	1357	TAGCCATGCGTCAAAATAATACCTTGGATGGGCTGAACATGTTTGTATGATGATGATCA	1416	QY	2637	CTTTCGGGAAATGATCATTAATGCCGAATGTTTACCTTTGAAAGGATGATGATGATGATCG	2696
QY	1557	TTACTTTCACCTGAGGCTGCGGTTTATCATTTGATGAGTGGGATTTCCGCTCTTTAACTA	1616	Db	2497	CTTCAACAGGCTTAGTGCATGATGCCGAGCATTACCTTTTGGGGTGGTATGATGAACCG	2556
Db	1417	CTACTTCCACTCCGGATCACGGGGTCATCATTTGGTGGGACTCTCGGCTTTTCAACTA	1476	QY	2697	TCTCTCTCAATATGCTGTATGCACTTAGTACAGACAGCAGTGGTCTATGCTACTAGTAGA	2756
QY	1617	TGGAACCTGGGAGTACTTAGGTATCTTCTCTCAAAATGCGAGATGGTGTGGATGAGTG	1676				

QY	1932	GCTGCATATGGCAATTGCTGATAAATGGATTGAGTTGCTCAAGAAACCGGATGAGGATTG	1991
DB			
DB	1667	TCGCCACATGGCTGTTGCTGATAAATGGGTTGAGATTATTCAGAAGAGAGATGAAGATTG	1726
QY	1992	GAGAGTGGGTGANATTGTTCAATACACTGCACAAATAGAGAATGGTTCGGAAAGTGTGTTTC	2051
DB			
DB	1737	GAAATGGGTGACATTGTACATATGCTTGACCAACAGCGGTGGTTGGAAAGTGTGTTTC	1786
QY	2052	ATACGCTGAAGATCATGATCAAGCTCTAGTCGGTGATAAAACATATAGCATTCGGCTGAT	2111
DB			
DB	1787	TTATGCTGAAGAGTCATGACCAAGGCCCTTGTGGTGCACAAAACATATTGCATTTGGCTGAT	1846
QY	2112	GGACAAGGATATGATGATTATTATGGCTTTGGGATAGACCGTCAACATCATTAATAGATCG	2171
DB			
DB	1847	GGACAAGGATATGATGACTTCATGGCTCTTGACAGACCAATCTACTCCTCTCATAGATCG	1906
QY	2172	TGGGATAGCATTCGACAAGATGATTAGGCTTGTAACCTATGGGATTAGGAGGAGAAGGTA	2231
DB			
DB	1907	TGGAGTAGCATTCGACAAAATGATCAGGCTTATTACCATGGGATTAGCGCGAGAAGGATA	1966
QY	2232	CCATAATTTTCATGGGAATGAATTCGCCACCTCGAGTGGATTGATTTCCCTAGGGCTGA	2291
DB			
DB	1967	TTTGAAATTTATGGGAATGAATTTGACACCCCGAGTGGATTGATTTTCCAAGAGCTGA	2026
QY	2292	ACAACACCTCTGTATGGGCTCAGTAAATTCGCCGAAACCAATTCAGTTATGATAAATGCAG	2351
DB			
DB	2027	TCATACATCTTCCCAGTGGTAAATTTGTTCTCGGACCAATTCACGTTATGTAATAATGCCG	2086
QY	2352	ACGGAGATTTGACCTGGGAGATGCGAATAATTTAAGTACCGTGGGTTGCAAGAAATTTGA	2411
DB			
DB	2087	CGGTAGGTTTGATCTAGGCAATTTCAAGACATCTGAGATATCATGGAATCAAGAGTTTGA	2146
QY	2412	CCGGGCTATGCAGTATCTTCAAGATAAATAAGTTTATGACTTCAGACTCAGACACACCGTTCA	2471
DB			
DB	2147	TCAAGCAATTCAGCATCTTCAAGAGAGCTTAAGTTTCATGACTTCTGACGCCCAATACAT	2206
QY	2472	ATCAGAAAGGATGAAGGATAGGATGATTGTATTTGAAAGAGAAACCTAGTTTTCGT	2531
DB			
DB	2207	ATCAGGAAGGATGAAGGATCGGATCAITGCTTCGAGAGGGGAACCTCGTTTTCGT	2266
QY	2532	CTTTAATTTTCATGACACAAAGACTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGG	2591
DB			
DB	2267	ATTCAATTTTCATTTGGCATAGCAGCTATTCCGATTACCAGTTGGCTGCTTAAGCCAGG	2326
QY	2592	AAAATCAAGGTTGGCTTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAAATGA	2651
DB			
DB	2327	AAAGTACAGATAGTCTTGGATTCAAGATATCTTTGTTGGAGGCTTTGGCAGGCTTAG	2386
QY	2652	TCATATGCGGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCCTCGTTCAATTAT	2711
DB			
DB	2387	TCATATGACAGACATTCAGCTTTCAAGGGTGGTACGATAACCGGCCICGATCCTCAT	2446
QY	2712	GGGTATGACACCTAGTAGACACAGCTGGTCTATGCATAGTAGACAAAGAGAGAAGA	2771
DB			
DB	2447	GGGTACACACCAATGAGAACACAGCTGGTCTATGCTTTAGTGGAGGATGAAGTGGAGAA	2506
QY	2772	AGAAGAAGTAGCAGTAGTAGAAGAAGTACTAGTAGAAGAAGAAATGAACCAACTCTGTATC	2831
DB			
DB	2507	TGAATTTGGAACCTGTGCGCGGTTAGATATATCTTTAACCAACAGGTTCTGACAGCAATG	2566
QY	2832	CGGTT	2836
DB			
DB	2567	CCATT	2571

RESULT 13

AAC45939

ID AAC45939 standard; DNA; 2715 BP.

XX
AC
BACA
XX

AAC4:
AC
XX

XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 48320.
DE	Hybridisation assay; genetic mapping; gene expression control;
XX	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 990S-0121825.
PR	05-MAR-1999; 990S-0123180.
PR	09-MAR-1999; 990S-0123548.
PR	23-MAR-1999; 990S-0125788.
PR	25-MAR-1999; 990S-0126264.
PR	29-MAR-1999; 990S-0126785.
PR	01-APR-1999; 990S-0127462.
PR	06-APR-1999; 990S-0128234.
PR	08-APR-1999; 990S-0128714.
PR	16-APR-1999; 990S-0129845.
PR	19-APR-1999; 990S-0130077.
PR	21-APR-1999; 990S-0130449.
PR	23-APR-1999; 990S-0130510.
PR	23-APR-1999; 990S-0130891.
PR	28-APR-1999; 990S-0131449.
PR	30-APR-1999; 990S-0132048.
PR	30-APR-1999; 990S-0132407.
PR	04-MAY-1999; 990S-0132484.
PR	05-MAY-1999; 990S-0132485.
PR	06-MAY-1999; 990S-0132486.
PR	06-MAY-1999; 990S-0132487.
PR	07-MAY-1999; 990S-0132863.
PR	11-MAY-1999; 990S-0134256.
PR	14-MAY-1999; 990S-0134218.
PR	14-MAY-1999; 990S-0134219.
PR	14-MAY-1999; 990S-0134221.
PR	14-MAY-1999; 990S-0134370.
PR	18-MAY-1999; 990S-0134768.
PR	19-MAY-1999; 990S-0134941.
PR	20-MAY-1999; 990S-0135124.
PR	21-MAY-1999; 990S-0135353.
PR	24-MAY-1999; 990S-0135629.
PR	25-MAY-1999; 990S-0136021.
PR	27-MAY-1999; 990S-0136392.
PR	28-MAY-1999; 990S-0136782.
PR	01-JUN-1999; 990S-0137222.
PR	03-JUN-1999; 990S-0137528.
PR	04-JUN-1999; 990S-0137502.
PR	07-JUN-1999; 990S-0137724.
PR	08-JUN-1999; 990S-0138094.
PR	10-JUN-1999; 990S-0138540.
PR	10-JUN-1999; 990S-0138847.
PR	14-JUN-1999; 990S-0139119.
PR	16-JUN-1999; 990S-0139452.
PR	16-JUN-1999; 990S-0139453.
PR	17-JUN-1999; 990S-0139492.
PR	18-JUN-1999; 990S-0139454.
PR	18-JUN-1999; 990S-0139455.
PR	18-JUN-1999; 990S-0139456.
PR	18-JUN-1999; 990S-0139457.
PR	18-JUN-1999; 990S-0139458.
PR	18-JUN-1999; 990S-0139459.
PR	18-JUN-1999; 990S-0139460.
PR	18-JUN-1999; 990S-0139461.
PR	18-JUN-1999; 990S-0139462.
PR	18-JUN-1999; 990S-0139463.
PR	18-JUN-1999; 990S-0139750.
PR	18-JUN-1999; 990S-0139763.

PR	21-JUN-1999;	99US-0139817.	PR	27-AUG-1999;	99US-0151080.
PR	22-JUN-1999;	99US-0139899.	PR	30-AUG-1999;	99US-0151303.
PR	23-JUN-1999;	99US-0140353.	PR	31-AUG-1999;	99US-0151438.
PR	23-JUN-1999;	99US-0140354.	PR	01-SEP-1999;	99US-0151930.
PR	24-JUN-1999;	99US-0140695.	PR	07-SEP-1999;	99US-0152363.
PR	28-JUN-1999;	99US-0140823.	PR	10-SEP-1999;	99US-0153070.
PR	29-JUN-1999;	99US-0140991.	PR	13-SEP-1999;	99US-0153758.
PR	30-JUN-1999;	99US-0141287.	PR	15-SEP-1999;	99US-0154018.
PR	01-JUL-1999;	99US-0141842.	PR	16-SEP-1999;	99US-0154039.
PR	01-JUL-1999;	99US-0142154.	PR	20-SEP-1999;	99US-0154779.
PR	02-JUL-1999;	99US-0142055.	PR	22-SEP-1999;	99US-0155139.
PR	06-JUL-1999;	99US-0142390.	PR	23-SEP-1999;	99US-0155486.
PR	08-JUL-1999;	99US-0142803.	PR	24-SEP-1999;	99US-0155659.
PR	09-JUL-1999;	99US-0142920.	PR	28-SEP-1999;	99US-0156458.
PR	12-JUL-1999;	99US-0142977.	PR	29-SEP-1999;	99US-0156596.
PR	13-JUL-1999;	99US-0143542.	PR	04-OCT-1999;	99US-0157117.
PR	14-JUL-1999;	99US-0143624.	PR	05-OCT-1999;	99US-0157753.
PR	15-JUL-1999;	99US-0144005.	PR	08-OCT-1999;	99US-0157865.
PR	16-JUL-1999;	99US-0144085.	PR	07-OCT-1999;	99US-0158029.
PR	16-JUL-1999;	99US-0144086.	PR	08-OCT-1999;	99US-0158232.
PR	19-JUL-1999;	99US-0144325.	PR	12-OCT-1999;	99US-0158369.
PR	19-JUL-1999;	99US-0144331.	PR	13-OCT-1999;	99US-0159293.
PR	19-JUL-1999;	99US-0144332.	PR	13-OCT-1999;	99US-0159294.
PR	19-JUL-1999;	99US-0144333.	PR	13-OCT-1999;	99US-0159295.
PR	19-JUL-1999;	99US-0144334.	PR	14-OCT-1999;	99US-0159329.
PR	19-JUL-1999;	99US-0144335.	PR	14-OCT-1999;	99US-0159330.
PR	20-JUL-1999;	99US-0144352.	PR	14-OCT-1999;	99US-0159637.
PR	20-JUL-1999;	99US-0144632.	PR	14-OCT-1999;	99US-0159638.
PR	20-JUL-1999;	99US-0144884.	PR	18-OCT-1999;	99US-0159584.
PR	21-JUL-1999;	99US-0144814.	PR	21-OCT-1999;	99US-0160741.
PR	21-JUL-1999;	99US-0145086.	PR	21-OCT-1999;	99US-0160767.
PR	21-JUL-1999;	99US-0145088.	PR	21-OCT-1999;	99US-0160768.
PR	22-JUL-1999;	99US-0145085.	PR	21-OCT-1999;	99US-0160770.
PR	22-JUL-1999;	99US-0145087.	PR	21-OCT-1999;	99US-0160814.
PR	22-JUL-1999;	99US-0145089.	PR	21-OCT-1999;	99US-0160815.
PR	22-JUL-1999;	99US-0145192.	PR	22-OCT-1999;	99US-0160980.
PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160981.
PR	23-JUL-1999;	99US-0145218.	PR	22-OCT-1999;	99US-0160989.
PR	23-JUL-1999;	99US-0145224.	PR	25-OCT-1999;	99US-0161404.
PR	26-JUL-1999;	99US-0145276.	PR	25-OCT-1999;	99US-0161405.
PR	27-JUL-1999;	99US-0145913.	PR	25-OCT-1999;	99US-0161406.
PR	27-JUL-1999;	99US-0145918.	PR	26-OCT-1999;	99US-0161359.
PR	27-JUL-1999;	99US-0145919.	PR	26-OCT-1999;	99US-0161360.
PR	28-JUL-1999;	99US-0145951.	PR	26-OCT-1999;	99US-0161361.
PR	02-AUG-1999;	99US-0146386.	PR	28-OCT-1999;	99US-0161920.
PR	02-AUG-1999;	99US-0146388.	PR	28-OCT-1999;	99US-0161992.
PR	02-AUG-1999;	99US-0146389.	PR	28-OCT-1999;	99US-0161993.
PR	03-AUG-1999;	99US-0147038.	PR	29-OCT-1999;	99US-0162142.
PR	04-AUG-1999;	99US-0147204.			
PR	04-AUG-1999;	99US-0147302.			
PR	05-AUG-1999;	99US-0147192.			
PR	05-AUG-1999;	99US-0147260.			
PR	06-AUG-1999;	99US-0147303.			
PR	06-AUG-1999;	99US-0147416.			
PR	09-AUG-1999;	99US-0147493.			
PR	09-AUG-1999;	99US-0147935.			
PR	10-AUG-1999;	99US-0148171.			
PR	11-AUG-1999;	99US-0148319.			
PR	12-AUG-1999;	99US-0148341.			
PR	13-AUG-1999;	99US-0148565.			
PR	13-AUG-1999;	99US-0149368.			
PR	16-AUG-1999;	99US-0149175.			
PR	17-AUG-1999;	99US-0149426.			
PR	18-AUG-1999;	99US-0149722.			
PR	20-AUG-1999;	99US-0149723.			
PR	20-AUG-1999;	99US-0149929.			
PR	20-AUG-1999;	99US-0149902.			
PR	23-AUG-1999;	99US-0149930.			
PR	23-AUG-1999;	99US-0150566.			
PR	26-AUG-1999;	99US-0150884.			
PR	27-AUG-1999;	99US-0151065.			
PR	27-AUG-1999;	99US-0151066.			
<div> <div>Query Match</div> <div>41.1%;</div> <div>Score 1296;</div> <div>DB 21;</div> <div>Length 2715;</div> </div>					
<div> <div>Best Local Similarity</div> <div>76.2%;</div> <div>Pred. No. 0;</div> </div>					
<div> <div>Matches 1593;</div> <div>Conservative 1;</div> <div>Mismatches 456;</div> <div>Indels 0;</div> <div>Gaps 0;</div> </div>					
QY	686	AGAGGGGCATCCCTCCACCTTGGTTCAGAGATTTATGAATAGACCCCTTTTGA	745		
Db	443	AGAGGAAGATCCACCTCCCTGGAGATGGGAGAGATATATGACATTCATCCTATGTGA	502		
QY	746	CAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTACAAGAAATGAGGAGGCAA	805		
Db	503	ACAGTCATCGTATCATCTTGATTACCGATATGGGAGTACAGAAACTCGGTGAAGAA	562		
QY	806	TTGACAAAGTATGAGGGTGGTTGGAAGCTTTTCTCGTGGTATGAAAAATGGGTTTCA	865		
Db	563	TTGACAAAGTATGAGGGTGGTTGGAAGCTTTTCTCGTGGTATGAAAAATGGGTTTCA	622		
QY	866	CTCGTAGTGTACAGGTATCACTTACCGTGAGTGGGCTCTCGTGGTGGCCAGTCAGTCCTC	925		
Db	623	CTCGAGCGGCACCTGGTATCACTTACCGGGAATGGCAGCGGAGCTTAAGGACGATCAC	682		
QY	926	TCATTGGAGATTTCAACAATTTGGACGCAATGCTGACATTTACCTCGGAATGAATTTG	985		
Db	683	TGATCGGAGATTTTAACTGGAATGCGAAATCTGATGTTATGGCTCGGACGACTTG	742		

Qy	986	GTGCTCGGAGATTTTCTGCCAAATAATGTGGATGTTTCTCTGCGAATTCCTCATGGGT	1045
Db	743	GTGCTGGGAAATATTTCTGCCAAATAATGCTGATGGCTCACCAGCAATTCGCCCATGGCT	802
Qy	1046	CCAGAGTCAAGATACGCATGCACACTTCATCAGGTGTTAAGGATTCATTCCTGCTGGTGA	1105
Db	803	CCCGTGTGAAGATCCGCATGSGATACCCCATCTGGTATTAAAGACTCCATTCAGAGTTGGA	862
Qy	1106	TCACTACTCTTTACAGCTTCCTGATGAAATCCATATAATGGAATATATATATGATCCAC	1165
Db	863	TCAAGTATCTGTCCAGCCACCTGGCGAGATCCATATAATGGATATATATGACCCCTC	922
Qy	1166	CGGAAGGAGAGGTATGTCTTCCACACCCAGGCCAAAGAAACCAAGTCCGCTGAGAA	1225
Db	923	CTGAGGAGGATAAATATGCGCTTCAACATCTCTGTCCAAAGAAACCCACATCGCTGCGTA	982
Qy	1226	TATATGAATCTCATATTGGAATGAGTAGTCCGGAGCCTAAATTAATCTACATACGTGAAT	1285
Db	983	TATATGAATCACATGTTGGAAATGAGTAGTACGAAACCAAGATATAATACATATGCCAAT	1042
Qy	1286	TTAGAGATGAAGTCTTCCTCCGATAAAAACCTTGGGTACAAATGCGGTGCAAAATATATGG	1345
Db	1043	TTAGAGATGATGACTTCCCGGTATAAAAAAGCTAGGCTATAATGCTGTGCAGATAATGG	1102
Qy	1346	CTATTCAAGAGCATCTTATATATGCTAGTTTTGGTTATCAATGTACAAATTTTTTTGGCAC	1405
Db	1103	CCATTCAAGAGCATGCCCTACTATGCCAGCTTTGGGTATCATGTGACAAATTTTTTTGGCAC	1162
Qy	1406	CAAGACGCCGTTTTGAAACGCCGAGACCTTAAGTCTTTGATGTATAAGTCATCATGAGC	1465
Db	1163	CTAGCAGCCGCTTTGNAACACTGATGACCTTAATCTTTGATAGCAAGCTCATGAGC	1222
Qy	1466	TAGGAATGTTGTTCTCATGGACATTTGTTACAGCCATGCATCAAAATAATACTTTAGATG	1525
Db	1223	TAGGCTGGTGTGTTCTGATGGATATTGTGCACAGCCATGCATCAAAAAACACACTGGATG	1282
Qy	1526	GACTGAACATGTTGAGCGCACAGATAGTTGTACTTTTTCACCTCGAGCTCGTGGTTATC	1585
Db	1283	GCTTGACATGTTTGATGGTACTGATGGTCAATATTTCACCTCTGATCGCTGGTGTATC	1342
Qy	1586	ATTGGATGTGGGATTCOCGCTCTTAACTATUGAAACTGGGAGGTACTTAGTATCTTTC	1645
Db	1343	ATTGGATGTGGATTCCTCGTCTTTCAATACGGAAGCTGGGAAGTGTCTAGTATCTTTC	1402
Qy	1646	TCTCAAGCGGAGATGGTGGTGGATGAGTGCAGAAATTTGRTGGATTTAGATTTGATGGTG	1705
Db	1403	TTTCCAAACGGAGATGGTGGCTGGAAGATACAAGTTTGTATGGTTTCAGATTTGATGGTG	1462
Qy	1706	TGACATCAATGATGTATACTCACCACGGATATTCGGTGGGATTCCTCTGGAACTACGAGG	1765
Db	1463	TGACTTCCATGATGTACATCATCATCATGACTCGAGTCCGAATTTTACTGGGAATTACAATG	1522
Qy	1766	AATPACTTGGACTPCGCAACTGATGTGATGCTGCCGTGTATCTGATGCTGGCCACAGTATC	1825
Db	1523	AGTACTTTGGATATCTACTGATGTTGACGCTGTGCTCTATCTAATGCTGGTGAAGATTT	1582
Qy	1826	TTATTCATGGCTTTTCCAGATGCAATTACCATTTGGTGAAGAIGTGTAGCGGAATGCCGA	1885
Db	1583	TGATTCATGGCTATACCCCTGAGGCTATTGTTGTCGGCGAAGATGTTACGGGATGCCAG	1642
Qy	1886	CATTTTGTATTCGGTTCAGATGGGGTGTGGCTTTTGACTATACGGCTGCATATGGCAA	1945
Db	1643	CTTTTTTTCGCTCTCGTGAAGACGGTGTGCTGGGTTTTGACTACCGCTCTACACATGGCAG	1702
Qy	1946	TTGCTCATAAATGGATTTGCTCAAGAAACGGATCAGATTTGGAGAGTGGGTGATATA	2005
Db	1703	TGCGACATTAATGGATTGAGCTTCTTAAGAAGAGACGAGACTGGCAGGTTTGTGTATA	1762
Qy	2006	TTGTTTCATACCTTGACAAATAGAAGATGTCGGAAGGTCTGTTTCATACGCTGAAGTCT	2065
Db	1763	TAACTTTCAGCTTACCAACAGAGGTGGGGAGAAATAIGTGTGCTCTATGCAGAGATCT	1822

QY	2056	ATGATCAAGCTCTAGTCGGTGATAAAAAATATAGCATTTCTGGCTGATGGACAAGGATATGT	2122
Db	1823	ATGATCAAGCCCTTGTGTGGACAAAAACGATAGCTTTCTGGCTAATGGATAAGCAATGT	1882
QY	2126	ATGATTTTATGGCTTGGATAGACCCGTCAACATCATTAATAGATCGTGGGATAGCATTGC	2185
Db	1883	ATGATTTTATGGCCGTGTGATAGACAGGCCACTCCGCGTGTAGACCGTGGGATGCTTTTAC	1942
QY	2186	ACAAGATGATTAGGCTTGTAACATATGGGATTAGGAGGAGAGGCTACCTAAATTTCTATGG	2245
Db	1943	ACAAATGATCCGTCTCATTAAGATGGATGGGTGGGAGAAGGATACCTCAATTTTCATGG	2002
QY	2246	GAATGAATTCGGCCACCCCTGAGTGGATTTGATTTTCCCTAGGGCTGAACAACACTCTCTG	2305
Db	2003	GAACGAATTTGGACACCCAGATGGATCGACTTTCCCAAGGACCGACCGACTTCCCTG	2062
QY	2306	ATGGCTCAGTAATTTCCGGAAACCAATTCAGTTATGATAAATCGACACCGAGATTGGAOC	2365
Db	2063	ATGGCAGAGTCATCCCTGGGAATTAATGGTAGTTATGATAAATGATCCGACGTAGGTTGATC	2122
QY	2366	TGGGAGATGCAAGATATTTAAGATACCGTGGGTTTGCAGAAATTTGACCGGGCTATGCAGT	2425
Db	2123	TGGGAGATGCAAGATATCTTAGATACCATGGATTCAGACTACAGAGTTTGTATCGAGCAATGCAAA	2182
QY	2426	ATCTTGAGATATAATATGAGTTTATGACTTTCAGAAACCACTAGTTTCATATCAGAAAGGATG	2485
Db	2183	ATCTAGAGGAGACCTATGGTTTCATGACTTCAGAGCACCATAGATATCCGCAAGATG	2242
QY	2486	AAGGAGATAGGATTAATTTGAAAAGGAACCTAGTTTGTCTTAAATTTTCACT	2545
Db	2243	AAGGAGACAGATCAATTTGATTCGAGAGAGTAACTTGCTCTTCGTTTCAACTTCCACT	2302
QY	2546	GGACAAAAGCTATTTACAGACTATCGCATAGGCTGGCTGAAGCCCTGGAATATACAAGTTG	2605
Db	2303	GGACCAACAGTTACTCTGACTACCGTATCGTTGCTCTGTTCGGAAGATACAAAATCG	2362
QY	2606	CCTTGGACTCAGATGATCCACTTTTGGTGGCTTCGGGAGAATTGATCAATGCCGAAT	2665
Db	2363	TTTTGGACTGTGAATACTTTATTGGAGCCTTCAACCGCTAGATGACTCCGGGAGT	2422
QY	2666	GTTTACCTTTGAAGGATGATGATGATCGTCTCGTTCAATTATGGTGTATGCACTTA	2725
Db	2423	TTTTCACTCTGATGGAAGCAGCACATAGGCTTGTCTCCTTCATGGTATGCACCGT	2482
QY	2726	GTAGACAGCAGTGGTCTATGCACTACTACAAAGAGAGAGAGAGA	2775
Db	2483	GCAGAACCGTCTAGTTTACGTCGAGTAGATGATGATGATGAA	2532
RESULT 14			
AAV05639			
ID	AAV05639 standard; cDNA to mRNA; 3015 BP.		
AC	AAV05639;		
XX			
DT	01-MAY-1998 (first entry)		
XX			
DE	Rice type IV starch branching enzyme cDNA.		
XX			
KW	Rice; type IV starch branching enzyme; amylopectin synthesis; ds.		
XX			
OS	Oryza sativa.		
XX			
PH	Key	Location/Qualifiers	
FT	CDS	129..2654	
FT		/*tag= a	
FT	sig_peptide	129..287	
FT		/*tag= b	
FT	mat_peptide	288..2651	
FT		/*tag= c	
FT	/product= type_IV_starch_branching_enzyme		
PN	JF10004970-A.		

XX 13-JAN-1998.
 PD 24-JUN-1996; 96JP-0162983.
 PF 24-JUN-1996; 96JP-0162983.
 XX (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
 PA (MIK) MITSUI TOATSU CHEN INC.
 XX WPI; 1998-133625/13.
 DR P-PSDB; AAW41763.
 XX Rice starch branching enzyme gene - synthesises amylopectin to yield
 PT high quality starch
 PS Claim 4; Pages 5-8; 13pp; Japanese.
 XX The present sequence encodes the rice type IV starch branching
 CC enzyme, which has the ability to synthesise amylopectin. The
 CC quality of starch is improved by the use of the protein.
 XX Sequence 3015 BP; 796 A; 606 C; 819 G; 794 T; 0 other;
 SQ
 Query Match 40.4%; Score 1275.6; DB 19; Length 3015;
 Best Local Similarity 75.3%; Pred. No. 0;
 Matches 1587; Conservative 1; Mismatches 520; Indels 0; Gaps 0;
 QY 663 TGATGATCTGATAGATCAGAGAGAGGGGCGATCCCTCCACCTGGACTTGGTCAGAGAT 722
 DB 554 TGAACCAACTGTGGAGGATTAACACACGAGTTATCCACCACACAGAGATGGGAGAGAT 613
 QY 723 TTATGAATAGACCCCTTTTGACAAACTATGCTCAACACCTTGTATACAGGTATTACACA 782
 DB 614 ATACCAATATGACCAATGCTGGAAGGATTCGGAACCATCTTGATACCATGATACAGTGA 673
 QY 783 GTACAGAAATAGAGGAGGCAATTCACAAAGTATGAGGTGGTTTGGAACTTTTCTCG 842
 DB 674 ATACAGAGAAATGCGTGCAGCTATTGACCAACATGAAGTGGCTTGGATGCAATTTCTCG 733
 QY 843 TGGTATGAAAATAGGTTTCACTGCTAGTGTACAGGTATCAGTACCTACCTGAGTGGGC 902
 DB 734 TGGTTACGAAAGCTTGGATTTACCCGACGCTGAGGCAATTAACCTACCGAATGGGC 793
 QY 903 TCTGTGTCAGTACGCTGCTCTCAATGGAGATTTCAACAATTTGGAGCAAAATGCTGA 962
 DB 794 ACTGAGACACAGTCTGCAGCATTTAGTGTGACTTCAACAATTTGGAACCAATGCAGA 853
 QY 963 CATATGACTCGGAATGATTTGGTGTCTGGGAGATTTTCTGCCAAATATGATGGATGG 1022
 DB 854 TACTATGACAGAAATGATGTTGTTGGGAGATTTCCCTGCCTAACCAATGCTGATGG 913
 QY 1023 TTCTCTGCAATTCCTCATGGGTCAGAGTGAAGATACGATGAGCACTTCATCAGTGT 1082
 DB 914 ATCCCTGCTATTCCTCATGGCTCAGCTGTAAGATTTCCGATGATACACCATCTGGCGT 973
 QY 1083 TRAGATTCATTCCTGCTTGGATCACTACTCTTACAGCTTCCTGATGAATTCGATA 1142
 DB 974 AAGAGATCAATTCCTGCTGGATTAAGTTGCTGTGCGAGCTCCAGGTGAAATACOGTA 1033
 QY 1143 TRATGAATATATATGATCCACCCGAGAGAGAGATGATGCTTCCACACCCACCGGCC 1202
 DB 1034 CAACGATATATATGATCCACCTGAAGAAGAAATATGATTCACATCCTCAACC 1093
 QY 1203 AAAGAACCAAGTCTGAGATATATGAATCTCATATTGGAATGAGTAGTCCGGAGCC 1262
 DB 1094 TAACAGCAAAATTCCTGCGGATATATGATCAATATGGAATGAGTAGCCCGAACC 1153
 QY 1263 TAAATTAATCATGCTGAATTTTAGAGATGAAGTTCCTTCGCAATAAAACCTTGG 1322
 DB 1154 GAAGATAAACACATATGCTAAATTTTAGGATGAGGTGCTACCAAGAATTAAGAGCTTGG 1213
 QY 1323 GTACATGGGTGCAAAATATGCTATTACAGAGCATCTTATATGCTAGTTTGGTTA 1382

DB 1214 GTACAATGCTGTACAGATATGCAATCCAGGAGCACTCTTATTACCAAGCTTTGGSTA 1273
 QY 1383 TCATGTCACAAAATTTTTCACCAAGCAGCCGCTTTTGGACCCGCGACACCTTAAGTC 1442
 DB 1274 TCAITGTTAACTCTTTTCGCGCAAGTAGCCGTTTGGAAACCCGACAGACTGAATC 1333
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 DB 1334 TCTGATTTAAAGCTCACAGAGCTGTTTGTCTGCTTACTTATGATATTTTTCACAGTCA 1393
 QY 1503 TGCATCAAAATATCTTTTAGATGACACGACATGTTTTCAGCGGCACAGATAGTTTACTT 1562
 DB 1394 TGCATCAAAATATCTTTTAGATGACATGTTTTCAGCGGCACAGATAGTTTACTT 1453
 QY 1563 TCACCTGAGGCTGCTGTTTATCATTTGATGTTGGGATTTCCGCTCTTTTAACTATGAAA 1622
 DB 1454 CCATGTTGGACACAGGGGTCATCTGATGTTGGGATTTCTCGGCTGTTCAACTATGGGAG 1513
 QY 1623 CTGGAGGTACTTTAGGTATCTTCTCAAAATGCGAGATGTTTGGATGAGTGCAGAAAT 1682
 DB 1514 TTGGGAAGTTTAAAGATATTTACTGTCGAATGCAAGGTGCTGCTTGAAGAATACAGTT 1573
 QY 1683 TGTGATTTAGATTTGATGTTGATGATCAATGATGTTATCTACCTACCCACGATATCGGT 1742
 DB 1574 TGTGATGTTTCGATTTGATGGGTGACCTCCATGATGTTATCTCATCATGTTTACAGGT 1633
 QY 1743 GGATTCACCTGGGAATCTACGAGGAATTTTGTGACTCGCAACTGATGTRGATGCTGCGT 1802
 DB 1634 GGCATTTACCTGGCAACTATGCGGAATTTTGTGATTTGCTGCTGCTGCTGCTGCTGCTGCT 1693
 QY 1803 GTATCTGATCTGGCAACGATCTTATTCATGGGCTTTTCCAGAGCAATTAACCAATGG 1862
 DB 1694 TTACTTGTGCTGCTGCAAGCTATTAATTCATGGGCTTTATCTGAGGCTGTAGCATTGG 1753
 QY 1863 TGAAGATTTAGCGGAATGCGGACATTTTGTATTCGCTTCAGATGGGGTGTGCTT 1922
 DB 1754 TGAAGATGTCAGCGGATGCCCATTTTGTATTCCTGTTTCAAGATGGTGTGTTGTTT 1813
 QY 1923 TGACTATGCTGCTGCAATGCTGATTAATGATTAATGATTTGATGCTCAAGAAACGGGA 1982
 DB 1814 TGACTATGCTGCTGCAATGCTGATTAATGATTAATGATTTGATGCTCAAGAAACGGGA 1873
 QY 1983 TGAGGATTTAGAGTGGGTGATTTGTTATACACTGACAAATAGAGATGTTGCGGAAA 2042
 DB 1874 CGAATATGGAATGGGTGATATGCTGACACCTAACCAATAGAGTGGTCAGAGAA 1933
 QY 2043 GTGTTTTCATGCTGAAAGTCAATGATCAAGCTCTAGTCTGCTGATGATAAACTATAGCAT 2102
 DB 1934 GTGTTTTCATGCTGAAAGTCAATGATCAAGCTCTAGTCTGCTGATGATAAACTATAGCAT 1993
 QY 2103 CTGGCTGATGGAACAGGATATGATGATTTTATGGCTTTGATGATGATGATGATGATGAT 2162
 DB 1994 CTGGCTGATGGAACAGGATATGATGATTTTATGGCTTTGATGATGATGATGATGATGAT 2053
 QY 2163 AATGATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
 DB 2054 CATGATGCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2113
 QY 2223 AGAAGGCTACCTAAATTTTCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 2282
 DB 2114 CGAAGGCTACCTAAATTTTCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 2173
 QY 2283 TAGGGCTGAACAAACCTCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2342
 DB 2174 AAGAGGCTGAACAAACCTCTCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2233
 QY 2343 TAAATGACAGGAGATTTGACCTGGGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 2402
 DB 2234 TAAATGACAGGAGATTTGACCTGGGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGAT 2293
 QY 2403 AGAATTTGACCGGCTATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAT 2462

Db 2294 AGAGTTTGATCAGGCCATGCGATCTTGAGGAAAAATATGGATTCAATGACATCTGAGCA 2353
 QY 2463 CCAGTTTCATATCAGAAAGATCAAGGATAGATGATGATTTGAAAAAGAAACCT 2522
 Db 2354 CCAGTATATATCGCGAAACACAGAGAGGATAGGTGATCATCTTCGAGAGAGAGATTT 2413
 QY 2523 AGTTTGTCTTTAAATTTTACATCGACAAAAAGCTATTTCAGACTATCGCATAGCGTGGCT 2582
 Db 2414 GGTATTCGTCTCAACTTCCACTGGAGTATAGCTATTTTGATATCGCGTCGGTGT 2473
 QY 2583 GAAGCCTGGAATAATACAGGTTGCCCTTGACTCAGATGATGCCACTTTTGGTGGCTCGG 2642
 Db 2474 AAAGCCTGGAAGTACAAAGATTGTTGGACTCAGACGATGGCTCTTTGGTGGATTGAG 2533
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 QY 2703 TTCAATATTGGTGTATGACCTAGTAGAAGCAGTGGTCTATGCACTAGTACACAAAGA 2762
 Db 2594 TTCAATTCGGTGTACACCCCAAGCAGACCGCGTCTGTTATGCACTTACAGAGGACTA 2653
 QY 2763 AGAAGAG 2770
 Db 2654 ATGATCAG 2661

RESULT 15

ID AAQ3750 standard; cDNA to mRNA; 2919 BP.
 AC AAQ3750;

DT 05-JUL-1995 (first entry)
 DE Rice starch branching enzyme.

ST Starch branching enzyme; rice; starch content; ds.
 OS Oryza sativa.

Key Location/Qualifiers
 5'UTR 1..127
 FT /*tag= a
 FT transit_peptide 128..322
 FT /*tag= b
 FT mat_peptide 323..2606
 FT /*tag= c
 FT /product= branching_enzyme
 FT 2603..2919
 FT /*tag= d

JP06261767-A.

20-SEP-1994.

22-OCT-1993; 93JP-0265171.

29-OCT-1992; 92JP-0291719.

(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

WPI; 1994-337418/42.

P-PSDB; AAR60811.

New gene of branching enzyme of rice starch - useful for increasing starch yield of rice grains

Claim 1; Page 9-12; 13pp; Japanese.

The rice starch branching enzyme is encoded by the cDNA sequence AAQ3750. The starch content of rice grains can be increased by increasing the expression of branching enzyme in rice plants.

XX Sequence 2919 BP; 755 A; 590 C; 800 G; 774 T; 0 other;
 SQ Query Match 39.9%; Score 1260.4; DB 15; Length 2919;
 Best Local Similarity 74.6%; Pred. No. 0;
 Matches 1582; Conservative 1; Mismatches 537; Indels 0; Gaps 0;
 QY 659 TTATGTATGATCTGATAGATCATGAGAGAGGGGATCCCTCCACCTGGACTTGGTTCAGA 718
 Db 504 TTGAAGAATTAGTGTCTGACGAGAAACACAGAGTTGTCACCAACAGAGATGGGCAAA 563
 QY 719 AGATTATGAATAGACCCCTTTTGACAAACTATCTGCAACACTTCTGACACCTTGTATACAGGTA 778
 Db 564 AAATATCCAGATGGACTCTATGCTTAATGGCTATAAGTACCACTTTGAATATCGATATA 623
 QY 779 CACAGTACAAGAAATGAGGGAGGCAATTCACAAAGTATGAGGGTGGTGGTGGTGGTGGT 838
 Db 624 GCATATAGGAGACTCGCTTCAGACATTCATCAGTATGAGGAGGACTGGAACATTTT 683
 QY 839 CTGCTGGTTATGAAAAATGGGTTTCACTGCTAGTGTCTACAGTATCACTTACCGTGTAGT 898
 Db 684 CTCGGGTTATGAGAGTTTGGATTTAATCACAGTGTCTGAAGGTGTCACTTATCGAAT 743
 QY 899 GGGCTCCTGTGCCCCAGTCTCTCATTTGGAGATTTCAACAATTTGGAGCCAAATG 958
 Db 744 GGGCTCCCGGGGCACATTCGACGATTTAGTGTGACTTCAACAATTTGAATGCAATG 803
 QY 959 CTGACATTTACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATAATGTGG 1018
 Db 804 CAGACCGCATGAGCAAAAATGAGTTTGGTGTCTTTGGGAGATTTTCTGCCCTAACAACTG 863
 QY 1019 ATGGTTCTCTGCAATTCCTCATGGTCCAGAGTGAAGATACCGATGGAACACTTCATPAG 1078
 Db 864 ATGGCTCATCTCTATTCACATGGCTACGTAAAGTGTGCAATGAACTCCATCTG 923
 QY 1079 GTGTTAAGGATTCCTCTTGGATCAACTTCTTACAGTTCCTTCTGATGAATTC 1138
 Db 924 GTATAAGGATTTCTTCTGCTGATCAAGTACHTCTGTCAGCGCGGAGGAAATCC 983
 QY 1139 CATATAATGGAATATATTAATGATCCACCGAGAGGAGGTATGTTCTTCCAAACCCAC 1198
 Db 984 CATACAATGCAATATATATGATCTCTGACGAGGAGAGTACATATTCACGATCCTC 1043
 QY 1199 GGCCAAAGAAACCAAGTCTCTGAGATATATGAATCTCAATTTGGAATGAGTACGTCGG 1258
 Db 1044 AACCTAAAGAGCAAAAGTCAATTCGGGATATACGAAATCATGTTGGAATGAGTACGCG 1103
 QY 1259 AGCTAAATTAATCATACGTGAATTTTAGAGATGAAGTCTTCTCTCGCATAAAAACC 1318
 Db 1104 AGCCAAAGATCAACAGCTATGCAAACTTTAGGATGAGGTCTCCAAAGATCAAAAGC 1163
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 Db 1164 TTGGATACAAATGCGTGCAAAATATGCAAAATTCAGAGCATGATATATGGAAGCTTG 1223
 QY 1379 GTTATCATGTCACAAATTTTTCACCAAGAGCGGTTTGGACCGCCGAGACCTTA 1438
 Db 1224 GTTACCATGTCCCAATTTCTTTGACCAAGTATGCTTTGCGGACCCCAAGAGATTAA 1283
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 Db 1284 AGTCATTGATTAAGCTCATGAGCTTGGTTTGTGCTCATGAGTGTGTTTCA 1343
 QY 1499 GCCATGCATCAAAATATCTTTAGATGAGTGAACATGTTTACGCGCACAGATAGTGTG 1558
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 QY 1559 ACTTTCACCTGAGCTCGTGGTTATCATGATGGATGTGGGATTCGCCCTCTTTAATG 1618
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Db	1704	TCGGTGAAGATGTCAGTGAATGCCATCAATTTGCCCTTCTGTTCAAGATGGTGGGTTG	1763		
QY	1919	GCTTTGACTATCGGCTGCATATGGCAATTCGTATAAATGGATTTGATTTGCTCAAGAAAC	1978		
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QY	2099	CATTCTGGCTGATGGACAAAGGATATGATGATTTTATGCTTTGGATAGACCCGTCAACAT	2158		
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QY	2699	CTCGTTCAATTTATGTTGATGACACCTGATGAGACAGCACTGGTCTATGCACTAGTAGACA	2758		
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Search completed: July 5, 2003, 13:51:51
Job time : 674.636 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:31:27 ; Search time 137.619 Seconds
(without alignments)
7032.959 Million cell updates/sec

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Perfect score: 3156
Sequence: 1 AAAACCTCCCTCCACTCAGT.....TGCTGATCTAATGATGTTT 3156

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2955.2	93.6	3074	4	US-09-087-277-1 Sequence 1, Appli
2	2955.2	93.6	3074	4	US-09-087-277-1 Sequence 1, Appli
3	1372.2	43.5	1393	4	US-09-087-277-3 Sequence 3, Appli
4	1372.2	43.5	1393	4	US-09-087-277-3 Sequence 3, Appli
5	1200.4	38.0	2665	4	US-09-257-894-1 Sequence 1, Appli
6	1200.4	38.0	2725	3	US-08-941-445A-14 Sequence 14, Appli
7	1049.8	33.3	2087	4	US-09-257-894-9 Sequence 9, Appli
8	1048.2	33.2	2165	4	US-09-257-894-8 Sequence 8, Appli
9	637.4	20.2	3128	3	US-08-716-449-1 Sequence 1, Appli
10	632.4	20.0	2487	4	US-09-257-894-19 Sequence 19, Appli
11	632.4	20.0	2565	4	US-09-257-894-24 Sequence 24, Appli
12	632.4	20.0	2763	3	US-08-941-445A-16 Sequence 16, Appli
13	632.4	20.0	2772	4	US-09-257-894-12 Sequence 12, Appli
14	623.2	19.7	2909	4	US-08-104-158-1 Sequence 1, Appli
15	546	17.3	1809	4	US-09-257-894-25 Sequence 25, Appli
16	546	17.3	1865	4	US-09-257-894-20 Sequence 20, Appli
17	371.6	11.8	11478	3	US-08-981-803-29 Sequence 29, Appli
18	371.6	11.8	11478	4	US-08-983-440-29 Sequence 29, Appli
19	358.2	11.3	5402	4	US-09-221-017B-194 Sequence 194, App
20	107	3.4	414	4	US-09-257-894-2 Sequence 2, Appli
21	70.6	2.2	2426	4	US-08-528-0260-3 Sequence 3, Appli
22	63.2	2.0	4403765	4	US-09-103-840A-2 Sequence 2, Appli
23	63.2	2.0	4411529	4	US-09-103-840A-1 Sequence 1, Appli
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25	54.6	1.7	571	4	US-09-257-894-16 Sequence 16, Appli
26	53.8	1.7	16442	3	US-08-781-891-208 Sequence 208, App
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C 28	49.4	1.6	188	1	US-08-115-497-21	Sequence 21, Appli
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C 30	49.4	1.6	188	2	US-08-291-011-1	Sequence 1, Appli
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C 34	46.8	1.5	252	2	US-08-623-906A-1	Sequence 1, Appli
C 35	46.6	1.5	661	3	US-08-961-083-77	Sequence 77, Appli
C 36	46.6	1.5	11384	4	US-08-961-527-45	Sequence 45, Appli
C 37	46.4	1.5	6701	4	US-09-004-838-107	Sequence 107, App
C 38	46.4	1.5	43795	3	US-08-742-185-101	Sequence 101, App
C 39	45.8	1.5	2100	1	US-07-927-316A-1	Sequence 1, Appli
C 40	45.2	1.4	3211	2	US-08-574-959A-8	Sequence 8, Appli
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C 42	45.2	1.4	3901	2	US-08-574-959A-6	Sequence 6, Appli
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C 44	45	1.4	2691	4	US-09-298-924-5	Sequence 5, Appli
C 45	43.2	1.4	3337	1	US-08-072-610-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-087-277-1
Sequence 1, Application US/09087277B

Patent No. 6169226
GENERAL INFORMATION:
APPLICANT: EK, Bo
APPLICANT: KHOSNOODI, Jamshid
APPLICANT: LARSSON, Clas-Tomas
APPLICANT: LARSSON, Hakan
APPLICANT: RASK, Lars
TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
FILE REFERENCE: 003300-486
CURRENT APPLICATION NUMBER: US/09/087,277B
CURRENT FILING DATE: 1998-05-29
EARLIER APPLICATION NUMBER: PCT/SE96/01558
EARLIER FILING DATE: 1996-11-28
EARLIER APPLICATION NUMBER: SE 9504272-7
EARLIER FILING DATE: 1995-11-29
EARLIER APPLICATION NUMBER: SE 9601506-0
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1
LENGTH: 3074
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: bell gene
OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
OTHER INFORMATION: (potato)
FEATURE:
NAME/KEY: CDS
LOCATION: (189)..(2825)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (189)..(332)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (333)..(2825)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (92)..(2156)
OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
OTHER INFORMATION: n wherein n = A, C, G or T.
FEATURE:
NAME/KEY: misc_feature
LOCATION: (285)..(287)
OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
OTHER INFORMATION: or Phe.
FEATURE:

see sequence 3, ver1

note date

PO
LATE

; NAME/KEY: misc_feature		
; LOCATION: (1404)..(1406)		
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.		
; FEATURE:		
; NAME/KEY: misc_feature		
; LOCATION: (1428)..(1430)		
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.		
; FEATURE:		
; NAME/KEY: misc_feature		
; LOCATION: (1896)..(1898)		
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys		
; OTHER INFORMATION: or Phe.		
; FEATURE:		
; NAME/KEY: misc_feature		
; LOCATION: (2154)..(2156)		
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.		
; US-09-087-277-1		
Query Match 93.6%; Score 2955.2; DB 4; Length 3074;		
Best Local Similarity 98.1%; Pred. No 0;		
Matches 3019; Conservative 2; Mismatches 41; Indels 14; Gaps 3;		
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US-09-658-499-1
; Sequence 1, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:beii gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; NAME/KEY: misc_feature
; LOCATION: (92)..(2156)
; OTHER INFORMATION: Nucleotides 92, 285, 1406, 1430, 1897 and 2156 are
; OTHER INFORMATION: n wherein n = A, C, G or T.
; NAME/KEY: misc_feature
; LOCATION: (285)..(287)
; OTHER INFORMATION: Amino acid -16 is Xaa wherein Xaa = Ile, Leu, Val
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1404)..(1406)
; OTHER INFORMATION: Amino acid 358 is Xaa wherein Xaa = Leu or Phe.
; NAME/KEY: misc_feature
; LOCATION: (1428)..(1430)
; OTHER INFORMATION: Amino acid 366 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc_feature
; LOCATION: (1896)..(1898)
; OTHER INFORMATION: Amino acid 522 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc_feature
; LOCATION: (2154)..(2156)
; OTHER INFORMATION: Amino acid 608 is Xaa wherein Xaa = Pro.
US-09-658-499-1

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QY 2514 AGGAAACCTAGTTTGTCTTTAATTTTACCTGGACAAAAGCTATTCAGACTATCGCAT 2573
Db 2519 AGGAAACCTAGTTTGTCTTTAATTTTACCTGGACAAAAGCTATTCAGACTATCGCAT 2578
QY 2574 AGGCTGGCTGAAGCCTGGAATACAAAGTTTCCCTTGGACTCAGATGATCCACTTTTGG 2633
Db 2579 AGGCTGGCTGAAGCCTGGAATACAAAGTTTCCCTTGGACTCAGATGATCCACTTTTGG 2638
QY 2634 TGGCTTCGGGAGAAATGATCAATCCGAAATGTTTACCTTTGAAGGATGATGATGA 2693
Db 2639 TGGCTTCGGGAGAAATGATCAATCCGAAATGTTTACCTTTGAAGGATGATGATGA 2698
QY 2694 TCGTCTCGTTCAATATGTTGATGACCTAGTAGACAGCAGTGGCTATGCACTAGT 2753
Db 2699 TCGTCTCGTTCAATATGTTGATGACCTAGTAGACAGCAGTGGCTATGCACTAGT 2758
QY 2754 AGACA---AAGAAGAAGAGAGAGAGAGTAGTAGTAGAGAGAGTAGTAGTAGAAGA 2810
Db 2759 AGACAAGAGAGAGAGAGAGAGAGAGTAGTAGTAGTAGAGAGAGTAGTAGTAGAAGA 2818
QY 2811 AGAATGAACGAACTTGTGATCGGTTGAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
Db 2819 AGAATGAACGAACTTGTGATCGGTTGAAGATTTGAACGCTACATAGAGCTTCTTGACG 2878
QY 2871 TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTCATGTTGACAAAAGTTTGCATTTCT 2930
Db 2879 TATCTGGCAATATTCATCAGTCTTGGCGGAATTTTCATGTTGACAAAAGTTTGCATTTCT 2938
QY 2931 TTCCACTATTAGTAGTGAACCATATACGACAGATGAAGTGTGTAACAAACATATGTAA 2990
Db 2939 TTCCACTATTAGTAGTGAACCATATACGACAGATGAAGTGTGTAACAAACATATGTAA 2998
QY 2991 AATCGATGAATTTATGCGAATGCTGGGACGGCTTCAGCAGGTTTGTCTAGTAGGTTTC 3050
Db 2999 AATCGATGAATTTATGCGAATGCTGGGACGGCTTCAGCAGGTTTGTCTAGTAGGTTTC 3058
QY 3051 TGTAAATTCATCTC 3066
Db 3059 TGTAAATTCATCTC 3074
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RESULT 3

US-09-087-277-3

; Sequence 3, Application US/09087277B

; Patent No. 6169226

; GENERAL INFORMATION:

; APPLICANT: EK, BO

```
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Cids-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/087,277B
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: PCT/SE96/01558
; EARLIER FILING DATE: 1996-11-28
; EARLIER APPLICATION NUMBER: SE 9504272-7
; EARLIER FILING DATE: 1995-11-29
; EARLIER APPLICATION NUMBER: SE 9601506-0
; EARLIER FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
; US-09-087-277-3
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Query Match 43.5%; Score 1372.2; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 1002 TCTGCCAAATAATGTGGATGGTTCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 1061
Db 1 TCTGCCAAATAATGTGGATGGTTCTCTCTGCAATTCCTCATGGGTCCAGAGTGAAGATACG 60

QY 1062 CATGGACACTTCATCAGGTGTTAAGGATTCCTTCCTGATCCATTCCTGATCAACTACTCTTACA 1121
Db 61 TATGGACACTCCATCAGGTGTTAAGGATTCCTTCCTGATCAACTACTCTTACA 120

QY 1122 GCTTCCTGATGAATTCCTATATATGAATATATATATATATATATATATATATATATATATAT 1181
Db 121 GCTTCCTGATGAATTCCTATATATGAATATATATATATATATATATATATATATATATATAT 180

QY 1182 TGCTTTCCAAACCCACGGCCAAAGAAACCAAGTCGCTGAGAAATATATGAATCTCATAT 1241
Db 181 TATCTTCCAAACCCACGGCCAAAGAAACCAAGTCGCTGAGAAATATATGAATCTCATAT 240

QY 1242 TGGAAATGAGTAGTCCCGAGCCCTAAAATTAACCTACTACTAGTGAATTTTAGAGATGAAGTTCT 1301
Db 241 TGGAAATGAGTAGTCCCGAGCCCTAAAATTAACCTACTACTAGTGAATTTTAGAGATGAAGTTCT 300

QY 1302 TCTTCGCATAAAAAACCTTGGGTACAAATCGGTGCAAAATATATGCTTATTTCAACGAGCATTC 1361
Db 1302 TCTTCGCATAAAAAACCTTGGGTACAAATCGGTGCAAAATATATGCTTATTTCAACGAGCATTC 1361
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Db 301 TCTCGCATAAAAAGCTGGGTGACATCGGTGGCAAAATATATGGCTATTCAGAGCATTC 360
QY 1362 TTATTAIGTAGTGTGGTTATCATGTCAAAATTTTTTGGACCAAGCAGCGTTTGG 1421
Db 361 TTATTAIGTAGTGTGGTTATCATGTCAAAATTTTTTGGACCAAGCAGCGTTTGA 420
QY 1422 AACGCCGACGACCTTAAGTCTTTGATTAAGCTCATAGCTAGGCTAGGAATTTGTTCT 1481
Db 421 AACNCCGACGACCTTAAGTCTTTGATTAAGCTCATAGCTAGGCTAGGAATTTGTTCT 480
QY 1482 CATGGACATGTTTCAGACCATCATCAATTAATCTTAGATGGACTCAACATGTTGA 1541
Db 481 CATGCACATGTTTCAGACCATCATCAATTAATCTTAGATGGACTCAACATGTTGA 540
QY 1542 CGGCACAGATGTTTACTTTCACCTCGAGCTCGTGTATCATTTGATGGATGGGATTC 1601
Db 541 CGGCACAGATGTTTACTTTCACCTCGAGCTCGTGTATCATTTGATGGATGGGATTC 600
QY 1602 CGGCCTCTTAAGTATGGAACCTGGAGTACTTAGTATCTTCTCAATCGGAGATG 1661
Db 601 CGGCCTCTTAAGTATGGAACCTGGAGTACTTAGTATCTTCTCAATCGGAGATG 660
QY 1662 GTGGTTGGATGAGTCAAAATTTGRTGGATTTAGATTTGATGCTGACATCAATGATGA 1721
Db 661 GTGGTTGGATGAGTCAAAATTTGATTTAGATTTGATGCTGACATCAATGATGA 720
QY 1722 TACTCACACGAGTATCGGTGGGATTCACCTGGGAACCTACGAGGAATCTTTGGACTGC 1781
Db 721 TACTCACACGAGTATCGGTGGGATTCACCTGGGAACCTACGAGGAATCTTTGGACTGC 780
QY 1782 AACTGATGATGCTGCGGTGATCTGATGCTGCGCAACGATCTATTCATGGGCTTTT 1841
Db 781 AACTGATGATGCTGCGGTGATCTGATGCTGCGCAACGATCTATTCATGGGCTTTT 840
QY 1842 CCCAGATGCAATTTACATTTGTTGAGATGTTAGCGGAATGCGACATTTTGTATCCCGT 1901
Db 841 CCCAGATGCAATTTACATTTGTTGAGATGTTAGCGGAATGCGACATTTTGTATCCCGT 900
QY 1902 TCAAGATGGGTTGTGGCTTTGACTATCGGCTGCATATGGCAATTTGCTGATAATGGAT 1961
Db 901 TCAAGATGGGTTGTGGCTTTGACTATCGGCTGCATATGGCAATTTGCTGATAATGGAT 960
QY 1962 TGAGTTGCTCAAGAACGGGATGAGATGGAGATGGGTGATATGTTTCATACACTGAC 2021
Db 961 TGAGTTGCTCAAGAACGGGATGAGATGGAGATGGGTGATATGTTTCATACACTGAC 1020
QY 2022 AATAGAAGATGCTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAATGATCAAGCTCTAG 2081
Db 1021 AATAGAAGATGCTCGGAAAAGTGTGTTTCATACGCTGAAAGTCAATGATCAAGCTCTAG 1080
QY 2082 CGGTGATAAACTATAGCATTTCTGCTGATGGACAAGGATATGATGATTTTATGGCTTT 2141
Db 1081 CGGTGATAAACTATAGCATTTCTGCTGATGGACAAGGATATGATGATTTTATGGCTTT 1140
QY 2142 GGATAGACCGTCAACATCAATTAATAGATCGTGGGATAGCATTTGCCAAGATCATAGGCT 2201
Db 1141 GGATAGACCGTCAACATCAATTAATAGATCGTGGGATAGCATTTGCCAAGATCATAGGCT 1200
QY 2202 TGTAACTATGGATTAGGAGAGAAGGTACCTAAATTTTCATGGGAAATGAATTCGGCCA 2261
Db 1201 TGTAACTATGGATTAGGAGAGAAGGTACCTAAATTTTCATGGGAAATGAATTCGGCCA 1260
QY 2262 CCCGTAGTGGATTCATTTCCCTAGGCTGACACACACCTCTCTGATGCTCAGTAATTC 2321
Db 1261 CCCGTAGTGGATTCATTTCCCTAGGCTGACACACACCTCTCTGATGCTCAGTAATTC 1320
QY 2322 CGGAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGATA 2381
Db 1321 CGGAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATGCAGATA 1380
QY 2382 TTTAAGTACCGT 2394
Db 1381 TTTAAGTACCGT 1393

RESULT 4

US-09-658-499-3
; Sequence 3, Application US/09658499
; Patent No. 6469231
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/09/658,499
; CURRENT FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; NAME/KEY: misc.feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; NAME/KEY: misc.feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is Xaa wherein Xaa = Thr.
; NAME/KEY: misc.feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is Xaa wherein Xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; NAME/KEY: misc.feature
; LOCATION: (1148)..(1150)
; OTHER INFORMATION: Amino acid 383 is Xaa wherein Xaa = Pro.
US-09-658-499-3

Query Match 43.5%; Score 1372.2; DB 4; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 1002 TCTGCCAAATAATGTGGATGTTCTCCTGCAATTCCTCATGGTCCAGATGAAGATACG 1061
Db 1 TCTGCCAAATAATGTGGATGTTCTCCTGCAATTCCTCATGGTCCAGATGAAGATACG 60
QY 1062 CATGCACACTTCATCAGGTTGTAAGATTCCTGCTGGATCCATTCCTGCTGGATCACTCTTTACA 1121
Db 61 TATGGACATTCATCAGTGTGTAAGATTCCTGCTGGATTCCTGCTGGATCACTCTTTACA 120
QY 1122 GCTTCCTGATGAAATTCATATAATGGAATATATGATCCACCGAGAGAGAGTA 1181
Db 121 GCTTCCTGATGAAATTCATATAATGGAATATATGATCCACCGAGAGAGAGTA 180
QY 1182 TGTCTTCCACACCCACCGCCAAAGTCCGTGAGATATATGATATCATAT 1241
Db 181 TATCTTCCACACCCACCGCCAAAGTCCGTGAGATATATGATATCATAT 240
QY 1242 TGGATGAGTAGTCGCGGAGCCTAAATTAACCTACATACGTGATTTTAGATGAAGTCTCT 1301


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Db      241  TGGAAATGAGTACGCGAGCCTAAATTAACATCATACGGAATTTTAGAGATGAAGTTCT 300
QY      1302  TCCTCGCAATAAAACCTTGGGTACAAATCGCGTGCAGAAATATGGCTATTCAAGAGCATTC 1361
Db      301  TCCTCGCAATAAAAGCTTGGGTACAAATCGCGTGCAGAAATATGGCTATTCAAGAGCATTC 360
QY      1362  TTATTATGCTAGTTTGGTTATCATGTGCACAAATTTTTTTTGCACCAAGCAGCGTTTGG 1421
Db      361  TTATTATGCTAGTTTGGTTATCATGTGCACAAATTTTTTTTGCACCAAGCAGCGTTTGA 420
QY      1422  AACGCCGACGACCTTAAGTCTTTGATGATAAGCTCATGAGTGAAGTAATGTTGTTCT 1481
Db      421  AACNCCGACGACCTTAAGTCTTTGATGATAAGCTCATGAGTGAAGTAATGTTGTTCT 480
QY      1482  CATGGACATTTGTTACAGCAGCATGCATCAATAATATCTTTAGTGGACTGAACATGTTGA 1541
Db      481  CATGGACATTTGTTACAGCAGCATGCATCAATAATATCTTTAGTGGACTGAACATGTTGA 540
QY      1542  CGGCACAGATAGTTGTTACTCTCTGGAGCTCGTGTATCATGATGATGGGATTC 1601
Db      541  CGGCACAGATAGTTGTTACTCTCTGGAGCTCGTGTATCATGATGATGGGATTC 600
QY      1602  CGCCTCTTTAACTAATGAACTGGCAGTACTTAGGTATCTTCTCAAAATCCGAGATG 1661
Db      601  CGCCTCTTTAACTAATGAACTGGCAGTACTTAGGTATCTTCTCAAAATCCGAGATG 660
QY      1662  GTGGTTGGATGAGTGCAAAATTTGRTGATTTAGATTTGATGTTGTTGACATCAATGATGA 1721
Db      661  GTGGTTGGATGAGTTCAAAATTTGATGATTTAGATTTGATGTTGTTGACATCAATGATGA 720
QY      1722  TACTCACCAGCATATCGTGGGATTCCTCTGGAGTACTGGAGTACTGGAGTACTTTGGACTCG 1781
Db      721  TACTCACCAGCATATCGTGGGATTCCTCTGGAGTACTGGAGTACTTTGGACTCG 780
QY      1782  AACTGATGRTGATGCTGCGGTATCTGATGCTGCGCAAGCATCTTATTCATGGGCTTT 1841
Db      781  AACTGATGRTGATGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840
QY      1842  CCCAGATGCAATACCAATGGTGAAGATCTTACCGGAATCCGACATTTTGTATCCCGT 1901
Db      841  CCCAGATGCAATACCAATGGTGAAGATCTTACCGGAATCCGACATTTTGTATCCCGT 900
QY      1902  TCAAGATGGGCTGTTGGCTTTGACTATCGGCTGCATATGGCAATTCGTCATAAATGGAT 1961
Db      901  TCAAGATGGGCTGTTGGCTTTGACTATCGGCTGCATATGGCAATTCGTCATAAATGGAT 960
QY      1962  TGAGTTGCTCAAGAAACGGGATGAGATTTGGAGTGGGTGATTTGTTCAATCACTGAC 2021
Db      961  TGAGTTGCTCAAGAAACGGGATGAGATTTGGAGTGGGTGATTTGTTCAATCACTGAC 1020
QY      2022  AAATGAAGATGGTCGGAAGATGTTTTCATACGCTGAAGTCAAGTCAAGCTAGT 2081
Db      1021  AAATGAAGATGGTCGGAAGATGTTTTCATACGCTGAAGTCAAGTCAAGCTAGT 1080
QY      2082  CGGTGATAAACTATAGCATCTCGCTGATGGACAGGATGATGATGATTTATGCTTT 2141
Db      1081  CGGTGATAAACTATAGCATCTCGCTGATGGACAGGATGATGATGATTTATGCTTT 1140
QY      2142  GGATGACCGCTCAACATCATTAATAGATCGTGGGATAGCATTCGCAAGATGATAGGCT 2201
Db      1141  GGATGACCGCTCAACATCATTAATAGATCGTGGGATAGCATTCGCAAGATGATAGGCT 1200
QY      2202  TGTAACTATGGGATAGGAGGAGAGGTTACCTAAATTCATGGGAAATGAATTCGGCCA 2261
Db      1201  TGTAACTATGGGATAGGAGGAGAGGTTACCTAAATTCATGGGAAATGAATTCGGCCA 1260
QY      2262  CCTGAGTGGATTTGATTTCCCTAGGCTGACACACCTCTCTGATGGCTCAGTAATTC 2321
Db      1261  CCTGAGTGGATTTGATTTCCCTAGGCTGACACACCTCTCTGATGGCTCAGTAATTC 1320
QY      2322  CGGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATCAGAATA 2381
Db      1321  CGGAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGGAGATCAGAATA 1380
QY      2382  TTTAAGATACCGT 2394
Db      1381  TTTAAGATACCGT 1393

RESULT 5
US-09-257-894-1
; Sequence 1, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.
; APPLICANT: Hubbard, Natalie L.
; APPLICANT: Lightner, Jonathan E.
; TITLE OF INVENTION: No. 6376749el Starches via Modification of
; TITLE OF INVENTION: Expression of Starch Biosynthesis
; TITLE OF INVENTION: Enzyme Genes
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESS: E. I. du Pont de Nemours and Company
; CITY: Wilmington
; STATE: Delaware
; COUNTRY: USA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Microsoft Windows 95
; SOFTWARE: Version 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/257,894
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/091,052
; FILING DATE: JUNE 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Majarian, William R.
; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2665 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 79..2476
; US-09-257-894-1

Query Match 38.0%; Score 1200.4; DB 4; Length 2665;
Best Local Similarity 73.3%; Pred. No. 0;
Matches 1534; Conservative 2; Mismatches 558; Indels 0; Gaps 0;

QY      663  TGATGATCTGATAGGATCAGAGAGAGGGGCGATCCCTCCACCTGGACTTGGTCAGAGAT 722
Db      381  TGATGTCAGAGCCTTGAACAGAGTTCGAGTGGTCCCGCCACCAAGCGATGGACAAAAAT 440
QY      723  TTAATAAATAGACCCCTTTTGACAACTATCGTCACAACTATCGTCACAACTATCGTCAC 782
Db      441  ATTCCAGATTTGACCCCTATGTTGCAAGGCTATAAGTACCATCTTGGATGATCGTACAG 500
QY      783  GTACAGAAAATGAGGAGGCAATTCGAAAGTATGAGGGTGGTGGTGGAGCTTTTTCG 842
Db      501  CTATAGAGATCCGTTACAGATTTGATGACATGATGACATGATGACATGATGACATGATG 560
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Db 1893 CATGTATCGTGGGATAGCAATACATAGATGATTAGACTTATCACAAATGGGTTAGGAGG 1952
QY 2223 AGAAGGTTACCTAAATTTTCATGGGAATGAATTCGGCCACCCCTGAGTGGATTGATTTCC 2282
Db 1953 AGAGGCTATCTTAATTTTCATGGGAATGAGTTGGACATCTGGAATGGATAGATTTC 2012
QY 2283 TAGGCTGTACACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTATGA 2342
Db 2013 AAGAGTCCGCAAGAGCTCCAGTGTGAAGTTATTCAGGGAATAACACAGTTATGA 2072
QY 2343 TAAATCCACGAGGATTTGACCTGGGAGATGAGCAATATTTAAGATACCGTGGGTGCA 2402
Db 2073 CAAATGCTCGAAGATTTGACCTGGGTGATGAGACTATCTTAGGTATCATGGTATGCA 2132
QY 2403 AGAATTTGACGGGCTATCAGTATCTTGAAGATAAATATGACTTTATGACTTCAGACA 2462
Db 2133 AGATTTGATCAGGCAATGCAATCTTGAGCAAAATATGAATTCATGACATCTGATCA 2192
QY 2463 CCAGTTTATATCACGAAAGGATGAAGGAGATAGGATGATTTGAAAGGAAACCT 2522
Db 2193 CCAGTATATTTCCGGAACATGAGGAGGATAGGTGATTTGTCGAAAGGAGATT 2252
QY 2523 ACTTTTGTCTTAATTTTCACTGGACAAAGCTATTCAGACTATCGATAGGCTGGCT 2582
Db 2253 GGTATTTGTTCAACTTCCACTGCAACACAGCTATTTGACTACCGTATTTGGTTGTCG 2312
QY 2583 GAAGCTCGGAAATACAAAGTTGCCCTTGGACTCAGATGATCCACTTTTGGTGGCTCGG 2642
Db 2313 AAAGCTGGGTCTATAAGTGTCTTGGACTCCGACGTGGACTATTTGGTGGATTTAG 2372
QY 2643 GAGATGATCATATGCGGAATGTTTCACCTTTGAAGGATGGTATGATGATCGTCTCG 2702
Db 2373 CAGGATCCATCCGACGCGAGCACTTCACCGCGGACTGTTCGATGATAATAGGCCATA 2432
QY 2703 TTCAATTTATGTTGATGACCTAGTAGACAGACAGTGGTCTATGCACTAGTAGA 2756
Db 2433 TTCATCTCGTTTATACACCANGCAGAACATGTGCTGCTATGCTCCAGTGA 2486

RESULT 7

US-09-257-894-9

; Sequence 9, Application US/09257894

; Patent No. 6376749

; GENERAL INFORMATION:

; APPLICANT: Broglie, Karen E.

; APPLICANT: Klein, Theodore M.

; APPLICANT: Hubbard, Natalie L.

; APPLICANT: Lightner, Jonathan E.

; TITLE OF INVENTION: No. 6376749el Starches via Modification of

; TITLE OF INVENTION: Expression of Starch Biosynthesis

; NUMBER OF SEQUENCES: 25

; CORRESPONDENCE ADDRESS:

; ADDRESS: E. I. du Pont de Nemours and Company

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19898

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Microsoft Windows 95

; SOFTWARE: Version 7.0A

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/257,894

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/091,052

; FILING DATE: JUNE 10, 1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Majarian, William R.

; REGISTRATION NUMBER: 41,173
; REFERENCE/DOCKET NUMBER: BB-1066-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-4926
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-257-894-9

Query Match 33.38; Score 1049.8; DB 4; Length 2087;
Best Local Similarity 74.28; Pred. No. 4.3e-308;
Matches 1324; Conservative 2; Mismatches 459; Indels 0; Gaps 0;

QY 663 TGATGATCTGTAGGATCAGAGAGGGGCATCCCTCCACCTGGGACTTGTGTCAGAAGAT 722
Db 303 TGATGCTCAAGCCTTGACAGAGTTCGAGTGGTCCCCCACCACAGCGATGACAAAAAT 362
QY 723 TTATGAATAGACCCCTTTTGACAAACTATCGTCAACACCTTTGATTACAGGATTCACA 782
Db 363 ATTCCAGATTGACCCCAATGTTGCAAGGCTATAAGTACCACTCTTGAGTATCGGTACAGCT 422
QY 783 GTACAAGAAATGAGGGAGGCAATTGACAGTATGAGGGTGGTTTGAAGCTTTTCTCG 842
Db 423 CTATAGAAGAAATCCGTTTCAGACATTTGATGAACATGAAGSAGGCTTGAAGCCTTCTCCCG 482
QY 843 TGGTTATGAAAAAATGGGTTTCACCTCGTAGTGTACAGGATCACTTACCCTGAGTGGGC 902
Db 483 TAGTTATGAGAATTTGGATTTAATGCCAGCGGAGGATACACATATCGAGATGGGC 542
QY 903 TCCTGGTGGCCACTGAGCTGCTCTCATTTGAGAGATTTCACAAATTTGGGACCAAAATGCTGA 962
Db 543 TCCTGGAGCAATTTTCTGCAGCATTTGGTGGGTGACTTCACAACTGGGATCCAAATGCGA 602
QY 963 CATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATTAATGTGGATGG 1022
Db 603 TCGFATGAGCAAAAATGAGTTTGGTGTTCGGGAAATTTTCTGCCTTACATTCAGATGG 662
QY 1023 TTCTCTGTCAATTCCTCATGGGTCAGAGTGAAGATACGCACTGACACTTCATCAGGTGT 1082
Db 663 TACATCACCTATTTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATCTCACTCAGGAT 722
QY 1083 TANGGATTCACCTTCCTGCTTGGATCACTACTCTTACAGCTTCCTGATGAAATTCATA 1142
Db 723 AAAGGATTCAAATTCACGCTGGATCAAGTACTCAGTGCAGGCCCCCAGGAGAAATACATA 782
QY 1143 TAAATGAATATATATGATCCACCGAAGAGGAGAGGTATGTCTTCCACACACCCAGGCC 1202
Db 783 TGATGGATTTATATGATCCTCTGAGAGGTAAAGTATGTTTTCAGGATCGGCAACC 842
QY 1203 AAAGAAACCAAGTCCGTGAGAAATATGAAATCTCATATTGGAATGAGTAGTCCGAGCC 1262
Db 843 TAAACGACCAAAATCATTCGGGATATATGAACACACATGTCGGAATGAGTAGGCGGAAAC 902
QY 1263 TAAATTAATCATACGTGAAATTTAGAGATGAGTTCTTCCCTCGCATAAAAACCTGG 1322
Db 903 GAAGATAAACACATATGTAACCTTTAGGGATGAAGTCCCTCCCAAGAAATAAAAAATTTGG 962
QY 1323 GTACAAATGGGTGCAAAATATGCTATTCAAGAGCATTTCTTATGCTAGTTTGGTGA 1382
Db 963 ATACAATGCAATGCAATATGCAATTCGAAGGCACTCATATTAAGGAGCTTTGGATA 1022
QY 1383 TCATGTCAAAATTTTTTGGCAACAGCCCGTTTGGAAACGCCCGACGACCTTAAGTC 1442
Db 1023 CCATGTAACATAATTTTTTGGCCAAAGTAGTCTGTTTGGTGTACCCCAAGAGATTGAATC 1082
QY 1443 TTTGATTGATAAGGCTCATGAGTAGGAATTTGTTCTCATGAGCAATTTGTTTCACAGCCA 1502
Db 1083 TTTGATTGATAGAGCACATGAGCTTGGTTTGGTAGTTCATGAGTGTGTTGTTCAATAGTCA 1142

QY	1503	TGCATCAAAATAACTATTAGATGSACTGAACATGTTTGACGGCACAGATAGTGTTCATT	1561
Dd	1143	TGCCGTCAAGTAATACTCTGGATGGGTTGAATGGTTTTGATGGTACAGATACACAATTACITT	1202
QY	1563	TCACTCTGGAGCTCGTGTTGATCATTTGGATGTGGGATTCGGCCTCTTTAACHATGAAA	1622
Dd	1203	TCACAGTGTGCCAGTGGCCATCACTGGATGTGGGATTCCTGGCTATTTAACTATGGAA	1262
QY	1623	CTGGGAGGTACTTTAGGTATCTCTCAAATCGAGATGCTGGTTGGATGAGTGCRAAATT	1682
Dd	1263	CTGGGAAGTTTTAAGATTCTCTCHCAAIGCTAGATGGCTCGAGGAATATAAGTT	1322
QY	1683	TGRTGGATTTAGATTTGATGGTGTGATCCAATATGATATATACACCACGGATATATCGGT	1742
Dd	1323	TGATGGTTTCCGTTTTGATGGTGTGACCTCCATGATGTACACTCACACACGGATTACAAGT	1382
QY	1743	GGGATTCACHTGGNACTACGAGAANTACITTTGACATCGCAACTGANGTGRGATGCTGGCGT	1802
Dd	1383	AACATTTACGGGGAACTTCAATGAGTATTTTGGCTTGGCCACCGATGTAGATGCACTGGT	1442
QY	1803	GTACTCTGATCTGGCCAAACGATCTTATCATGGCTTTTCCCAGATGCAATTACCATTGG	1862
Dd	1443	TTACTTTGATGCTCGTAAATGATCTAATTCATGACATTTATCCTGAGGCTGTACCAATTGG	1502
QY	1863	TGAAGATGTTAGCGGAATGCCGACATTTTGATTCCGHTCAAGATGGGGGTGTTGGCTT	1922
Dd	1503	TGAAGATGTTAGTGAATGCCTACATTTGGCCTTCTGTTTACAGATGGTGGGCTTAGGTTT	1562
QY	1923	TGACTATCGGCTGCATATGGCAATTCGTGNATAATGGATAGTTGCTCNAGAAACGGGA	1982
Dd	1563	TGACTATCGGATGCATATGGCTGTGGCTGCACAAATGATTTGACCTTCTCAAGCAAAAGTGA	1622
QY	1983	TGAGGATGTTGAGAGTGGGTGATATTGTCATACACTGCACAAATAGAAAGATGGTCGGAAA	2042
Dd	1623	TGAACCTTGAAGATGGGTGATATTGTGCACACACTGCACAAATAGGAGGTGGTTAGAGAA	1682
QY	2043	GTGTGTTTCATACGCTGAAAGTCATGATCAAGCTCTAGTCGGTGATAAAACTATAGCATTT	2102
Dd	1683	GTGTGTAACTTATGCTGAAAGTCATGATCAAGCATTAGTCGGCGACAAGACTATTGCGTTT	1742
QY	2103	CTGGCTGATCGGCAAGGATATGATGATTTTATGGCTTTGGATAGACCGTCAACATCATTT	2162
Dd	1743	TTGGTTGATGGCAAGGATATGATGATTTTCATGGCCCTCGATAGACCTTCAACTCCTAC	1802
QY	2163	AATAGATCGTGGGATAGCATTTGCACAAGATGATTAGGCTTGTAACATATGGGATTAGGAGG	2222
Dd	1803	CATTGATCGTGGGATAGCATTTACATRAGATGATTAGCTTATCACAAATGGGTTTAGAGG	1862
QY	2223	AGAAGGTACTTAAATTTCAATGGGAATGAATTCGGCCACCCTCGAGTGGATGATTTCCTCC	2282
Dd	1863	AGAGGGCTATCTTAATTTCAATGGGAATGAGTTTGGACATCTTGAATGGATAGATTTTCC	1922
QY	2283	TAGGGCTGGAACAACACCTCTCTCATGGCTCAGTAAATTCGGGAAACCAATTCAGTTATGA	2342
Dd	1923	AGAGGTCCGCAAGACTTCCAGTGGTAAGTTTATTCCAGGGAATAAACACAGSTTATGA	1982
QY	2343	TAAATCGACACGGAGATTTGACCTGGGAGATGCAGAAATATTTAAGATACCGTGGGTTGCA	2402
Dd	1983	CAAAATGCTGCGAAGATTTGACCTGGGTGATGCAGACTATCTTAGGTATCATCGGTATGCA	2042
QY	2403	AGAAATTTGACCGGGCTATGCAGTATCTTGAAGATAAANTATGAGTT 2447	
Dd	2043	AGAGTTTGTATCGGCAATGCAATCTTGTAGCAAAAATATCAATT 2087	

```

1  APPLICANT: Hubbard, Natalie L.
2  APPLICANT: Lightner, Jonathan E.
3  TITLE OF INVENTION: No. 6376749e1 Starches via Mod
4  TITLE OF INVENTION: Expression of Starch Biosynth
5  TITLE OF INVENTION: Enzyme Genes
6  NUMBER OF SEQUENCES: 25
7  CORRESPONDENCE ADDRESS:
8  ADDRESSER: E. I. du Pont de Nemours and Company
9  STREET: 1007 Market Street
10 CITY: Wilmington
11 STATE: Delaware
12 COUNTRY: USA
13 ZIP: 19898
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC Compatible
17 OPERATING SYSTEM: Microsoft Windows 95
18 SOFTWARE: Version 7.0A
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/257,894
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 09/091,052
25 FILING DATE: JUNE 10, 1998
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Majarian, William R.
28 REGISTRATION NUMBER: 41,173
29 REFERENCE/DOCKET NUMBER: BB-1066-A
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 302-992-4926
32 TELEFAX: 302-773-0164
33 INFORMATION FOR SEQ ID NO: 8:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 2165 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 MOLECULE TYPE: DNA (genomic)
40 US-09-257-894-8

```

Query Match	33.28;	Score 1048.2;	DB 4;	Length 2165;
Best Local Similarity	74.1%;	Pred. No. 1.4e-307;		
Matches 1323;	Conservative 2;	Mismatches 460;	Indels 0;	Gaps 0;
Qy	663	TGATGAATCTGTAGAGATCAGAGAGAGGGGCATCCCTCCACCTCGACCTTGGTCAGAGAT	722	
Db	1785	TGATGCTCAGCCTTGAACAGAGTTCAGTGGTCCCTCCACCCACCCAGCGATGGACAAAAAT	1726	
Qy	723	TTATGAATAGACCCCTTTTGTGCAAACTATPGCTAACACACTTGATTTACAGGTATTCACA	782	
Db	1725	ATCCAGATTACCCCATGTGTGAAGGCTATAAGTAGCATCTTGTAGTATCGGTACAGCCT	1666	
Qy	783	GTACAAGAAATGAGGGAGGCAATTGTACAAAGTATGAGGGTGGTTTGGAACTTTTCTCG	842	
Db	1665	CTATAGAAGAAATCCGTTACACATTTGATGACATGCAAGAGGCTTGAAGCCTTCCTCCG	1606	
Qy	843	TGSETATGAAAAAATGGGTTTCACTCGTAGTGTCTACAGTATCACTTTACCCTGAGTGGC	902	
Db	1605	TAGTTATGAGAAGTTTGGATTTAATGCCAGCGGGAAGGTATCACATATCGAAGTGGC	1546	
Qy	903	TCTGTGTCCGAGTCAGCTGCTCTCATTGTGAGATTTCAACAATTGGGACCAAAATGCTGA	962	
Db	1545	TCTGTGAGCAATTTTCTCAGCATTTGGTGGGTGAGCTCAACAACITGGGATCCAAATGCAG	1486	
Qy	963	CATTATCACTCGGAATGAAATTTGGTGTCTCGGAGATTTTTCGCCAAATTAATGTGATGG	1022	
Db	1485	TCGTATGAGCAAAAATGAGTTTGGTGTGTGGRAATTTTCTGCCTAACAAATGCAGATGG	1426	
Qy	1023	TTCTCTGCAATTCCTCATGGGTCAGAGTGAAGATACGCAATGGACACTTTCATCAGGTGT	1082	
Db	1425	TACATCACCTAATTCCTCATGGATCTCGTGTAAAGGTGAGAATGGATCTCCATCAGGAT	1366	

RESULT 8
US-09-257-894-8/c
; Sequence 8, Application US/09257894
; Patent No. 6376749
; GENERAL INFORMATION:
; APPLICANT: Broglie, Karen E.
; APPLICANT: Klein, Theodore M.

1083 TAAGGATTCATCTCCCTGGATCAACTACTCTTTACAGCTTCCTGATGAATTCCTATA 1142
1365 AAAGGATTAATTCAGCTGGATCAAGTACTCAGTGCAGGCCAGGAAATACCATTA 1306
1143 TAATGAAT 1202
1305 TGATGGATTTAT 1246
1203 AAGAAACCAATCTCTGAGATATATATATATATATATATATATATATATATATATAT 1262
1245 TAAACGACCAAAATCATCTGGATATATGAACACATGTCGGAATGAGTACCGGAC 1186
1263 TAAATTAATCTATCTGAT 1322
1185 GAAGATTAACACAT 1126
1323 GTACAAATGGGTGCAAAAT 1382
1125 ATACAATGAGTGCAT 1066
1383 TCATGTCACAAATTTTTTGCACCAAGCAGCCGTTTGGAAACCCGACGACCTTAAGTC 1442
1065 CCATGTAACATATTTTTTGGCCAGTAGTCTGTTTTGTTACCCAGAGATTTGAGTC 1006
1443 TTTGATGATTAAGCTCATGACCTAGGATTTGTTGTCATGAGCATGTTCCACAGCCA 1502
1005 TTTGATGATGAGCAGACATGAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 946
1503 TGCATCAATAAT 1562
945 TCCGTCACATATATCTCTGATGGTGTGATGGTTTGTGATGTTGATGTTGATGTTGAT 886
1563 TCACCTCTGAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1622
885 TCACAGTGTCCAGCTGGCCACTGATGTTGGATTTCTGCGCTATTTAACTATGGAA 826
1623 CTGGAGGACTTAGTATCTCTCAATCGAGATGTTGTTGATGAGTGCATTAAT 1682
825 CTGGAGGATTTAAGATTTCTCTCAATGATGTTGTTGATGAGTGCATTAAT 766
1683 TGTGATTTAGATTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTT 1742
765 TGATGTTTCCGTTTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTGAT 706
1743 GGGATCTAGGACTAGGAGATATCTTTGAGTTCGCACTGATGTTGATGTTGATGTTGAT 1802
705 AACATTTACGGGAACTTCAATGATTTTGGCTTTCGACCGATGATGATGATGATGAT 646
1803 GTATCTGATGCTGGCCAGCATCTTATTCATGCGCTTTTCCAGATGCAATACCATGG 1862
645 TTACTTGATGCTGGTGAATGATCTAATTCATGAGCTTTATCTGAGGCTGTAACCAT 586
1863 TGAAGATGTAGCGGAATGCCACATTTTGTATCCGTTCAAGATGGGGGTTTGGCTT 1922
585 TGAAGATGTAGTGAATGCCATATTTGCTTCTGTTACGATGGTGGGTTAGTTT 526
1923 TGACTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1982
525 TGACTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 466
1983 TGAGGATTTGAGAGTGGGTGATTTGATGATGATGATGATGATGATGATGATGATGAT 2042
465 TGAACATTTGAGAGTGGGTGATTTGATGATGATGATGATGATGATGATGATGATGAT 406
2043 GTGCTTTTATACGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2102
405 GTGTGTAATCTATGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 346
2103 CTGGCTGATGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
345 TTGGTTGATGACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 286
2163 AATAGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222

285 CATTGATCGTGGATAGCAATACATAAGATGATTAGACTTATCAATGGGTTTGGAGG 226
2223 AGAAGGCTACTAAATTTTCAATGGGAATGAATTCGGCCACCCTGAGTGGATTTCC 2282
225 AGAGGGCTATCTTAAATTTTCAATGGGAATGAATTTGGACATCTCTGAATGGATTTCC 166
2283 TAGGGCTGAACAACACCTCTCTGATGGCTCAGTAATTCGGGAAACCAATTCAGTTATGA 2342
165 AAGAGTCCCAAGACTTCCAAGTGTAGTTTATTCAGGGNATPACACAGTTATGA 106
2343 TAAATGACAGCAGGATTTGACCTGGAGATGACAGATATATTAAGATACCGTGGTTGCA 2402
105 CAAATGCTGCGAAGATTTGACCTGGGTGATGACAGACTATCTTAGTATCATGTTATGCA 46
2403 AGAATTTGACCGGCTGATGACAGTATCTTGAAGATATAATGATTT 2447
45 AGAGTTGATCAGGCAATGCAACATCTTGACCAAAATATGAATT 1

RESULT 9

US-08-716-449-1

; Sequence 1, Application US/08716449

; Patent No. 6103893

; GENERAL INFORMATION:

; APPLICANT: National Starch and Chemical Investment

; APPLICANT: Holding Corporation

; TITLE OF INVENTION: Method for Producing Altered Starch

; TITLE OF INVENTION: Method for Producing Altered Starch

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scott & Ayleen

; STREET: Box 194, 24th Floor, Toronto-Dominion Bank Tower

; CITY: Toronto

; STATE: Canada M5K 1H6

; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: IMB 1.44 MB High Density Diskette

; COMPUTER: COMPAQ Deskpro 590 (IBM PC compatible)

; OPERATING SYSTEM: WINDOWS 95

; SOFTWARE: Word 7.0 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/716,449

; FILING DATE: FILED CONCURRENTLY HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/00634

; FILING DATE: 22.03.95

; ATTORNEY/AGENT INFORMATION:

; NAME: Anita E. Nador

; REGISTRATION NUMBER:

; REFERENCE/DOCKET NUMBER: 1552

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 368-2400

; TELEFAX: (416) 363-7246

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3128 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: cDNA encoding starch branching enzyme

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE:

; ORIGINAL SOURCE: clone 1.2.1 and E2

; ORGANISM: Solanum tuberosum

; STRAIN: cv desiree

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE: mature tuber

; HAPLOTYPE:

; TISSUE TYPE:

CELL TYPE:	20.2%;	Score 637.4;	DB 3;	Length 3128;
ORGANELL:	Best Local Similarity 60.3%;	Pred. No. 7.3e-183;		
ORGANELLE:	Matches 1190;	Conservative 1;	Mismatches 727;	Indels 57; Gaps 6;
IMMEDIATE SOURCE:				
LIBRARY: lambda Zap tuber cDNA				
CLONE: 1.2.1 and E2				
POSITION IN GENOME:				
CHROMOSOME/SEGMENT:				
MAP POSITION:				
UNITS:				
FEATURE: open reading frame				
NAME/KEY: starch branching enzyme				
LOCATION: 44-2788				
IDENTIFICATION METHOD: lone ORF with homology to other starch				
IDENTIFICATION METHOD: branching enzymes				
OTHER INFORMATION: complements KV832 E. coli glycogen				
OTHER INFORMATION: branching enzyme mutant				
US-08-716-449-1				
QY	731	TAGACCCCTTTTGACAAACTATCGTCACACACCTTGATTACAGGTATTCACAGTCAAGA	790	
Db	345	TGGATCCAACTTTTGGAACTTATCTAGATCACTTCAGACACAGAATGAAGATATGTGG	404	
QY	791	AAATGAGGGAGGCAATTGCAAGTATGAGGTGGTTTGGAGCTTTTCTCGTGGTTATG	850	
Db	405	ATCAGAAATGCTCATVGAANAATATGAGGAGCCCTTGAGGAATTTGCTCAAGGTATT	464	
QY	851	AAAAATGGGTTTCACTCGTAGTCTACAGGTATCACTTACCGTGAAGTGGCTCCCTGGT	910	
Db	465	TAAATTTGGATTCAACAGGGAAGTGGTTGCATAGTCATCTGTAATGGCTCCCTGCTG	524	
QY	911	CCAGTCAGCTGCTCTATTTGGAGATTCACAAATTTGGAGCGCAATGCTGACATATGA	970	
Db	525	CTCAGGAAGCAGAAGTATTGGCGATTTCAATGATCGAACCGTCTTAACCAATGATGG	584	
QY	971	CTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAATATATGTTGGATGGTTCCTG	1030	
Db	585	AGAAGACCAAGTTGGTGTGGAGTATAGAAATCC---TGATGTTGACAGTAAGCCAG	641	
QY	1031	CAATTCCTCATGGTCCAGAGTCAAGATACGCAATGGACACTTCATCAGGTGTTAAG---G	1087	
Db	642	TCATCCACACAACCTCCAGATTAAAGTTTCGTTTCAACATGTTAATGAGTGGGTAG	701	
QY	1088	ATTCCATTCCTGTTGGATCACTACWTCTTACAGCTTC-----TGATGAATTTCCAT	1141	
Db	702	ATCGTATCCCTGCTGGATAAAGTATGCCACTGCACACGCCACAAAGTTTGCAGCAACAT	761	
QY	1142	ATAATGGAATATATTATGATCCACCGAGAGAGAGAGGTATGCTTCCACACCCACGGC	1201	
Db	762	ATGATGGTCTACTGGGACCCACCACTTCAGAAAGGTACCACTCAAAATACCCCTGCC	821	
QY	1202	CAGAAGAACCAAAAGTCGCTGAGAAATATATGAATCTCATATTGGAATGAGTAGTCCGAGC	1261	
Db	822	CTCCCAAAACCCGAGCCCCAGAACTACGAAGCACATGTCGCGATGAGCAGCTCTGAGC	881	
QY	1262	CTAAATTAATCAATGAGTGAATTTAGAGATGAAGTTCTTCTCGATTAATAAACCTTG	1321	
Db	882	CAGGTGTAAATTCGTATCGTGGTGTTCGATGATGTTTACCTCGGATTAAGGCAAAAT	941	
QY	1322	GGTCAATGCGGTGCAAAATATGCTATTCAACAGCATCTCTTATATGCTAGTATTGGTT	1381	
Db	942	ACTATAATCTGCTCAGTTGATGCCAAATAGGAACATCTTCTATGATCAATTTGGAT	1001	
QY	1382	ATCATGTCAAAAATTTTTTTCACCAAGCAGCGCTTTTGGAGCCCGCAGCAGCTTAAGT	1441	
Db	1002	ATCATGTCAAACTTTTTTGTCTGAGCAATAGATATGAACCCGGAGCAGCTTAAGT	1061	
QY	1442	CTTTGATGATAAAGCTCATGAGTATAGGAATTTGTTCTCATGGACATTTGTCACAGCC	1501	

Db 910 TTGGGTACCATGTGACAAATTTCTTTGGGGTTAGCAGCAGATCAGGCACACACAGAGGAC 969
QY 1435 CTTAAGCTCTTTGATTCATAAAGCTCATGAGCTAGGAAATTTCTTCTCTCATGGACATGTT 1494
Db 970 CTCAAATATCTTGTGTATGATGAGCACAACATTTGGGGTTTGGAGTTCTGTATGGATGTGC 1029
QY 1495 CACAGCCATGCATCAATAATATCTTTAGATGGACTGAACATGTTTGACG-----GC 1545
Db 1030 CATAGCCATGCAAGTAATAATCTCACAGATGGTTTAAATGGCTATCATGTTGACAAAGC 1089
QY 1546 ACAGATAGTGTGTACCTTCACTCTGGAGCTCGGGTTATCATATGGATGGGATTCGCCG 1605
Db 1090 ACCCAAGAGTCTATTTTCATCGGGGAGATAGAGGTTATCATAAACTTTGGGATAGTCGG 1149
QY 1606 CTCCTTAATATATGGAACCTGGAGGTACTTAGTATCTCTCTCAATCGGAGATGGTG 1665
Db 1150 CTGTTCACTATGCTAACTGGAGGTATTAAGTTTCTTCTTCACTGAGATGATGG 1209
QY 1666 TTGGATGACTGCAAAATTTGRTGGATTTAGATTTGATGGTCTGACATCAATGATGATACT 1725
Db 1210 TTGGATGAATTCATGTTTATGCTTCCGATTTGATGGAGTTACATCAATGCTGTATCAT 1269
QY 1726 CACCGAGATTCGTTGGATTCACCTGGAACCTAGCAGGATACCTTTGACCTCGCACT 1785
Db 1270 CACCATGGTATCAATGTGGGGTTTACTGGAACCTACCGAGGATATTTCACTTTGGACACA 1329
QY 1786 GATGRTGATGCTGCCGTGATCTGATGCTGGCCCAACGATCTTATTCATGGCTTTTCCCA 1845
Db 1330 GCTGTGGAGCAGTTGTTTACATGATGCTTGAACCACTTATGACACAACTCTTGCCA 1389
QY 1846 GATGCAATACCATGGTGAAGATTTAGCGGAATGCCGACATTTTGTATTCOOGTTCAA 1905
Db 1390 GAAGCAACTGTTTGTCTGAAGATGTTTTCAGGCATGCCGTCTTTCGCCGCCAGTTGAT 1449
QY 1906 GATGGGGTGTGGCTTTGACTATCGCTGCATATGCGCAATGTCCTGATTAATGATGGATGAG 1965
Db 1450 GAAGTGGGGTGTGGCTTTGACTATCCCTGCAATGGCTATCCCTGATAGATGGATGATGAC 1509
QY 1966 TTGCTCAAGAAACGGGATGA---GGATGGAGAGTGGGTGATATTTTCATACACTGACA 2022
Db 1510 TACCTGAAGATAAAGATGACTCTGAGTGTGCTGATGGTGAATAGCGCATCTTTGACT 1569
QY 2023 ATAGAAGATGTCGGAAGATGTTTTCATGCTGAAAGTCAATGATCAAGCTCAGTC 2082
Db 1570 AACAGGAGATATACTCAAAATGCTATGCTGATGCTGAGAGCATGATCAGTCTATGTT 1629
QY 2083 GGTGATAAACTATAGCATCTGCTGATGGACAAGGATATGATGATTTTATGGCTTTG 2142
Db 1630 GCGCACAAACTATTGCAATTTCTCTGATGGACAAGGAATGATGCTGGCATGTGACAC 1689
QY 2143 GATAGCCGTCAACATCATTAATAGATCGTTGGATAGCATTTGCACAAGATGATTAGGCTT 2202
Db 1690 TTGCAGCCTGCTTCACTTACATTTGATCGAGGATGCTCCTCAAAAGATGATTCACCTC 1749
QY 2203 GTAACATGGGATTTAGGAGGACAGGTTACCTAAATTTTCATGGGAAATGAAATCGGCCAC 2262
Db 1750 ATCAATATGGCCCTTGGAGGTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1809
QY 2263 COTGATGATGATTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAGTAATTCOC 2322
Db 1810 CCAGATGGATGACTTTCCAGAGAA----- 1836
QY 2323 GGAACCAATTCAGTTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAATAT 2382
Db 1837 GGAACCAATTCAGTTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAATAT 1896
QY 2383 TTAAGATACCGTGGGTTGCAAGATTTGACCGGCTATGCTGATCTTGAAGATAATAT 2442
Db 1897 TTGGGTACAGTACATGATGCTGTTTGAACCAAGCGGATGATGCTGCTGATGAGATTT 1956
QY 2443 GAGTTATGACTTCAGACACACAGTTTCATATCACGAAGGATGAAGGAGATAGGATGAT 2502

Db 1957 TCCTCTCTCTTCTGCTCAAAAGCAGATCGCTCAGCAGATGAACGATGAGAAAAGGTTAT 2016
QY 2503 GTATTTCAAAAGGAAACCTAGTTTGTCTTTTAAATTTTCACTGCAAAAAGCTATTTCA 2562
Db 2017 GTCTTTGAACGTGGAGATTTAGTTTGTCTTTTCAATTTCCATGCCAAGAACTTACGAG 2076
QY 2563 GACTATCGCATAGCTGGCTGAAGCCTTGGAAATACAAAGTTGCTTGGACTTCAGATGAT 2622
Db 2077 GGCTACAAAGTGGATGCGATTTTCCCTGGGAATACAGATAGCCCTGGACTCTGATGCT 2136
QY 2623 CCACCTTTTGGTGGCTTCGGGAGAAATGATCATATAAGCCGAATGTTTCACT 2674
Db 2137 CTGGCTCTGCTGATGATGAAGAGTTGGCCACGACGCTGATCAGTCTCACT 2188

RESULT 12

US-08-941-445A-16
; Sequence 16, Application US/08941445A
; Patent No. 6107060
; GENERAL INFORMATION:
; APPLICANT: Keeling, Peter
; APPLICANT: Guan, Hanping
; TITLE OF INVENTION: Starch Encapsulation
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 30-SEP-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/026,855
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Winner, Ellen P.
; REGISTRATION NUMBER: 28,547
; REFERENCE/DOCKET NUMBER: 89-97
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: mRNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: 2..190
; NAME/KEY: mat_peptide
; LOCATION: 191..2467
; NAME/KEY: CDS
; LOCATION: 2..2470
US-08-941-445A-16

Query Match 20.0%; Score 632.4; DB 3; Length 2763;
Best Local Similarity 59.7%; Pred. No. 2.2e-181;

	Matches	1178;	Conservative	2;	Mismatches	738;	Indels	54;	Gaps	5;
QY	721	ATTATGAAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATATACAGGTATTCA	780							
Db	251	ATATACGACCTGGACCCCAAGCTGGAGATATTCAAGGACCATTTTCAGGTACCGGATGAAA	310							
QY	781	CAGTACAGAAATAGGGAGGCAATWTGACAAGTATGAGGGTGGTTTGGAAAGCTTTTTCT	840							
Db	311	AGATTCCTAGACGAGAAAGCATCAATTTGAAGAAAAATGAGGAAAGCTTTGAATCTTTTCT	370							
QY	841	CGTGGTTATGAAAAATGGCTTCACCTCGTAGTCCTACAGGTATCACTTACCGTGAGTGG	900							
Db	371	AAAGGCTATTTGAAATTTGGGAATTAACAAATGAGGATGGAATGTATATCGTGAATGG	430							
QY	901	GCTCCTGGTCCCACTCAGCTGCTCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCT	960							
Db	431	GCACCTCTCGCAGGAGGCAGAGCTTATTGGTGACTTCAATGACTGGAATGGTGCAAC	490							
QY	961	GACATATGACTCGGAATGAATTTGGTGCTGGGAGATTTTTCGCCAAATATGTGGAT	1020							
Db	491	CATAAGATGAGAGGATAAATTTGGTTGGTTGGTTCGATCAAAAT--TGACCATGTCAAA	547							
QY	1021	GGTTCTCTGCAATTCCTCTGCTGGTCCAGAGTGAAGATACGCATGGACCTTCATCAGGT	1080							
Db	548	GGGAACCTGCCATCCCTCAATTCCAAGGTTAAATTCGCTTTCACATGGTGGAGTA	607							
QY	1081	GTTAAGGATPCCATTCCTGCTTGGATCAACTACTCTTTACAGCTTCTCGATGAAAT---	1136							
Db	608	TGGTTTCATGTTATCCAGCATTGATTCGTTATGCGAGCTGTGATGCCICTAAATTTGGA	667							
QY	1137	--TCCATATTAATGGAATATATTATGATCCACCCGAGAGGAGGATGTTCTTCCAAAC	1194							
Db	668	GCTCCCTATGATGGTGTTCATTGGGATCCCTCCCTGCTCTGAAAGGTACACATTTAAGCAT	727							
QY	1195	CCAGGCCAAAGAAACCAAAGTCGCTGAGAAATATATGAATCTCATATTGGAATCAGTAGT	1254							
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Db	848	GCAAAATAACTACAAACAGCATGTCAGTTGATGGCAGTTATGGAGCATTCGTACTATGCTTCT	907							
QY	1375	TTTGGTTATCATGTCACAAATTTTTTTCACCACAGCAGCGTTTGAACGCCCGCAGCAC	1434							
Db	908	TTCCGGTACCATGTGCACAAATTTCTTTGCGGTAGCAGCAGATCAGGCACACACAGAGGAC	967							
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QY	1546	ACAGATAGTTGTATCTTCACTCTGGAGCTCGTGGTTATCATTTGGATGGGATTCGCCG	1605							
Db	1088	ACCCAGAGTCCTATTTTTCATGGGAGATAGAGGTTATCATAACTTTGGGATGTCGG	1147							
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Db	1208	TTGGATGAATTCATGTTTGATGGCTCCGATTTTGTGAGTTCATACATCAATGCTGTA	1267							
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Db	1268	CACCATGGTATCAATGTGGGGTTTACTGGAACCTACGAGGAATTTTCACTTTGGACACA	1327							

RESULT 13

RESULT 13
US-09-257-894-12

US-09-237-894-12
; Sequence 12, Application US/09257894

; Patent No. 6376749

; FILE NO: 6376749
; GENERAL INFORMATION:

APPLICANT: Broglie, Karen E.

APPLICANT: BLOTT, Karen E.
; APPLICANT: Klein, Theodore M.

APPLICANT: KERN, Theodore M.
; APPLICANT: Hubbard, Natalie L.

APPLICANT: Lightner, Jonathan E.

TITLE OF INVENTION: No. 6376749el Starches via Modification of

TITLE OF INVENTION: Expression of Starch Biosynthesis Enzymes via Recombinant Plasmids

;; TITLE OF INVENTION: Enzyme Genes
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: E. I. du Pont de Nemours and Company
;; STREET: 1007 Market Street
;; CITY: Wilmington
;; STATE: Delaware
;; COUNTRY: USA
;; ZIP: 19898
;; COMPUTER READABLE FORM: disk
;; MEDIUM TYPE: Floppy
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: Microsoft Windows 95
;; SOFTWARE: Version 7.0A
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/257,894
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/091,052
;; FILING DATE: JUNE 10, 1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Majarian, William R.
;; REGISTRATION NUMBER: 41,173
;; REFERENCE/DOCKET NUMBER: BB-1066-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 302-992-4926
;; TELEFAX: 302-773-0164
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2772 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 49..2580
;; US-09-257-894-12

Query Match 20.0%; Score 632.4; DB 4; Length 2772;
Best Local Similarity 59.7%; Pred. No. 2.2e-181;
Matches 1178; Conservative 2; Mismatches 738; Indels 54; Gaps 5;
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Db 1921 CCAGATGGATTGACTTTCCAGAGAA----- 1947
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Db 1948 GGAACCACTGGAGCTATGATAATGACAGCGAGATGGAGCTTTGGACACTGATCAC 2007
QY 2383 TTAAGATACCGTGGTGGTGAAGAAATTTGACCGGCTATGAGTATCTTTGAAGATAATAT 2442
Db 2008 TTGCGGTACAGTACATGATGATGCTTGAACCAAGCGATGAATGCGCTCGATGAGATTT 2067
QY 2443 GAGTTTATGACTTCAGAACACCACTATATACAGAAAGATGAAGAGATAGATGATT 2502
Db 2068 TCCTTCTTTCGTCGTCGCAAGCAGATCGTCAGCAGATGAACGATGAGGAAAGGTTATT 2127
QY 2503 GTATTTGAAAAGAAACCTAGTTTGTCTTTTAAATTTTCACTGGACAAAAAGCTATCA 2562
Db 2128 GTCTTGAAGTGGAGATTTAGTTTGTCTTTTCAATTTCCATCCCAAGAAACTTAGGAG 2187
QY 2563 GACTATCGCATAGCTGGCTGGAAGCTGGAAATACAAAGTTGCTTGGACTGAGATGAT 2622
Db 2188 GGCTACAAAGTGGATGCGATTTGCTGCGGAAATACAGAGTAGCCCTGGACTCTGATGCT 2247
QY 2623 CCACCTTTTGGTGGCTTGGGAGAAATGATCATAATGCGAATGTTTCACT 2674
Db 2248 CTGGTCTTGGTGGACATGGAAGATGTTGGCCAGCAGCTGATCATCTCAGT 2299

RESULT 14

US-08-104-158-1
Sequence 1 Application US/08104158
Patent No. 6215042
GENERAL INFORMATION:
APPLICANT: Willmitzer, Iothar
APPLICANT: Sonnewald, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Mueller-Roerber, Bernd
APPLICANT: Visser, Richard Gerardus Franciscus
APPLICANT: Jacobsen, Evert
TITLE OF INVENTION: PLASMIDS CONTAINING DNA-SEQUENCES THAT
CAUSE CHANGES IN THE CARBOHYDRATE CONCENTRATION AND THE
CARBOHYDRATE COMPOSITION IN PLANTS, AS WELL AS PLANT CELLS
CONTAINING THESE PLASMIDS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/104,158
FILING DATE: 13-AUG-1993
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: EP PCT/EP92/00302
FILING DATE: 11-FEB-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE P 41 04 782.6
FILING DATE: 13-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward A.
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: FA-1996 PCT (951-91)

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-382-0700
TELEFAX: 212-382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2909 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Solanum tuberosum cv. Desiree
STRAIN: Desiree
DEVELOPMENTAL STAGE: growing tuber
TISSUE TYPE: tuber
CELL TYPE: total tuber
IMMEDIATE SOURCE:
LIBRARY: cDNA of total tuber mRNA in pUC 19 (Hinc II)
FEATURE:
NAME/KEY: CDS
LOCATION: 2..1699
OTHER INFORMATION: /note= "for Branching enzyme I
(partial) truncated protein; 97,11 & identity to
other information: active potato branching enzyme"
US-08-104-158-1

Query Match 19.78; Score 623.2; DB 4; Length 2909;
Best Local Similarity 60.1%; Pred. No. 1.4e-178;
Matches 1188; Conservative 1; Mismatches 729; Indels 58; Gaps 7;
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QY 791 AAATGAGGAGCAATGACAAAGTATGAGGTTGTTGGAAGCTTTTCTCGTGGTTATG 850
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QY 971 CTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAAATAATGTGGATGGTCTGCTG 1030
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QY 1031 CAATTCCTCATGGTCCAGATGAAGATAGCATGGACATTCATCAGGTGTTAAG---G 1087
Db 462 TCATTCACACAACTCCAGATTAGTTTCTTCAACATGTAATGAGTGGTGGTAG 521
QY 1088 ATTCCATTCCTGCTTGGATCACTACTCTTTACAGCTTC-----TGATGAATTCAT 1141
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Db 253 ATATACGACCTGGACCCCAAGCTGGAGATATTCAGGACCAATTCAGGTACCGGATGAAA 312
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Db 373 AAGGGTATTTGAAATTTGGGATTAATACAAATGAGGATGGAACTGTATATCGTGAATGG 432
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Db 1030 CATAGCCATGAAGTAATATGTCACAGATGTTTAAATGGCTATGATGTTGGACAAAGC 1089
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OM nucleic - nucleic search, using sw model

Run on: July 5, 2003, 13:51:57 ; Search time 486.292 Seconds
(without alignments)
10130.730 Million cell updates/sec

Title: US-10-056-454A-18_COPY_45_3200

Perfect score: 3156

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1085931 seqs, 780495707 residues

Total number of hits satisfying chosen parameters: 2171862

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1372.2	43.5	1393	9	US-10-254-534-3
3	1323	41.9	2418	9	US-09-938-842A-872
4	1296	41.1	2577	9	US-09-938-842A-337
5	1185.6	37.6	3039	10	US-09-792-127-3
6	1185	37.5	2559	10	US-09-792-127-1
7	598.2	19.0	2994	9	US-10-084-817-92
8	596.6	18.9	2955	9	US-09-918-624B-30
9	596.6	18.9	2955	10	US-09-880-107-2148
10	257.8	8.2	602	10	US-09-770-143-955
11	139.6	4.4	604	10	US-09-925-300-453
12	114.6	3.6	441	10	US-09-770-444-893
13	108	3.4	601	9	US-10-025-380-304
14	108	3.4	601	10	US-09-922-217-304
15	108	3.4	601	10	US-09-833-263-304
16	88.2	2.8	1877	10	US-09-974-300-653
17	87.2	2.8	204	10	US-09-878-574-12567
18	85.4	2.7	1830121	9	US-10-329-960-1
19	81.4	2.6	2193	9	US-09-738-626-1354

c	20	81.4	2.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
c	21	79.4	2.5	310	9	US-10-102-524-1616	Sequence 1616, Ap
c	22	69.8	2.2	543	10	US-09-815-343-373	Sequence 373, App
c	23	68.8	2.2	576	10	US-09-815-343-924	Sequence 924, App
c	24	59	1.9	261	10	US-09-864-761-19524	Sequence 19524, A
c	25	59	1.9	261	10	US-09-864-761-25517	Sequence 25517, A
c	26	59	1.9	448	10	US-09-864-761-557	Sequence 557, App
c	27	59	1.9	513	10	US-09-864-761-8851	Sequence 8851, App
c	28	55.4	1.8	255883	9	US-10-175-523-57	Sequence 57, Appl
c	29	54.6	1.7	381	10	US-09-864-761-21610	Sequence 21610, A
c	30	54.6	1.7	90650	9	US-10-175-523-80	Sequence 80, Appl
c	31	54.2	1.7	419	10	US-09-864-761-6432	Sequence 6432, Ap
c	32	53.8	1.7	8895	9	US-10-091-438-250	Sequence 250, App
c	33	53.8	1.7	8895	9	US-10-091-438-256	Sequence 256, App
c	34	53.8	1.7	8895	10	US-09-764-853-887	Sequence 887, App
c	35	53.8	1.7	8895	10	US-09-764-853-937	Sequence 937, App
c	36	53.8	1.7	9656	9	US-10-091-438-246	Sequence 246, App
c	37	53.8	1.7	9656	9	US-10-091-438-255	Sequence 255, App
c	38	53.8	1.7	9656	10	US-09-764-853-886	Sequence 886, App
c	39	53.8	1.7	9656	10	US-09-764-853-933	Sequence 933, App
c	40	53.4	1.7	1282	9	US-10-002-344A-89	Sequence 89, Appl
c	41	53.4	1.7	16299	9	US-10-175-523-64	Sequence 64, Appl
c	42	53.4	1.7	1691139	9	US-10-067-514-1	Sequence 1, Appli
c	43	53	1.7	312	10	US-09-864-761-22972	Sequence 22972, A
c	44	52.6	1.7	483	10	US-09-864-761-1384	Sequence 1384, A
c	45	52.4	1.7	288	9	US-09-728-444-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-254-534-1
; Sequence 1, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, Bo
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3074
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:belI gene
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (189)..(2825)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (189)..(332)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (333)..(2825)
; FEATURE:

1679 GTTCAAAATTTGATGGATTTAGATTTGATGCTGCACATCAATGATGTAHACTCACCACGG 1738
1734 ATTATCGGTGGGATTTCACTGGGAACATCAGAGGAATATCTTGGACTCGCAACTGATGPRGA 1793
1739 ATTATCGGTGGGATTTCACTGGGAACATCAGAGGAATATCTTGGACTCGCAACTGATGPRGA 1798
1794 TGCCTGCCGTCTATCTGATGCTGGCCCAACGATCTTATTCATGGGCTTTTCCACAGTCAAT 1853
1799 TGCCTGCTGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1858
1854 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTATTCCTCCGTTCAAGATGGGG 1913
1859 TACCATTGGTGAAGATGTTAGCGGAATGCCGACATTTTATTCCTCCGTTCAAGATGGGG 1918
1914 TGTGCTTTGACATCTGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1973
1919 TGTGCTTTGACATCTGCGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1978
1974 GAAACGGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2033
1979 GAAACGGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2038
2034 GTCGGAAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2093
2039 GTCGGAAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2098
2094 TATAGCATCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2153
2099 TATAGCATCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2158
2154 AACATCAATTAATAGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2213
2159 AACATCAATTAATAGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2218
2214 ATTAGAGAGAGAGGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2273
2219 ATTAGAGAGAGAGGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTG 2278
2274 TGATTTCCCTGAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2333
2279 TGATTTCCCTGAGGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2338
2334 CAGTTATGATAATGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2393
2339 CAGTTATGATAATGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2398
2394 TGGGTTGCAAGAAATTTGACGGGCTATGACGGGCTATGACGGGCTATGACGGGCTATGACGGGCTAT 2453
2399 TGGGTTGCAAGAAATTTGACGGGCTATGACGGGCTATGACGGGCTATGACGGGCTATGACGGGCTAT 2458
2454 TTCAGAACACCGATTTATATCAGGAAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2513
2459 TTCAGAACACCGATTTATATCAGGAAGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 2518
2514 AGGAAACCTAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2573
2519 AGGAAACCTAGTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 2578
2574 AGGCTGGCTGAGCCCTGGAATAATACAAAGTTGCTTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTTGG 2633
2579 AGGCTGGCTGAGCCCTGGAATAATACAAAGTTGCTTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTTGG 2638
2634 TGGCTTCGGGAGAAATGATCAATATGCGGAATTTTACCTTTTGAAGGATGGTATGATGA 2693
2639 TGGCTTCGGGAGAAATGATCAATATGCGGAATTTTACCTTTTGAAGGATGGTATGATGA 2698
2694 TGGCTTCCTGCTCAATTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2753
2699 TGGCTTCCTGCTCAATTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 2758
2754 AGACA--AG 2810
2759 AGACAAG 2818

2811 AGAATGAACGAATTTGATCGCTTGAAGATTTGAACGCTACATAGAGCTTCTTGACG 2870
2819 AGAATGAACGAATTTGATCGCTTGAAGATTTGAAGGCTACATAGAGCTTCTTGACG 2878
2871 TATCTGCAATATTGCAATCAGTCTTGGCGGAATTTTCAATGTCACAAAAGGTTTGCATTTCT 2930
2879 TATCTGCAATATTGCAATCAGTCTTGGCGGAATTTTCAATGTCACAAAAGGTTTGCATTTCT 2938
2931 TTCCACTATTAGTAGTGCACATATATGCGCAGATGAAGTGCCTGAACAAACATATGTAA 2990
2939 TTCCACTATTAGTAGTGCACATATATGCGCAGATGAAGTGCCTGAACAAACATATGTAA 2998
2991 AATCGATGAATTTATGCTGAATGCTGGGACGGCTTCAGCAGGTTTGTCTTAGTGAGTTTC 3050
2999 AATCGATGAATTTATGCTGAATGCTGGGACGGCTTCAGCAGGTTTGTCTTAGTGAGTTTC 3058
3051 TGTAAATTTGCTATCTC 3066
3059 TGTAAATTTGCTATCTC 3074

RESULT 2
US-10-54-534-3
; Sequence 3, Application US/10254534
; Publication No. US20030046730A1
; GENERAL INFORMATION:
; APPLICANT: EK, BO
; APPLICANT: KHOSNOODI, Jamshid
; APPLICANT: LARSSON, Clas-Tomas
; APPLICANT: LARSSON, Hakan
; APPLICANT: RASK, Lars
; TITLE OF INVENTION: STARCH BRANCHING ENZYME II OF POTATO
; FILE REFERENCE: 003300-486
; CURRENT APPLICATION NUMBER: US/10/254,534
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US/09/087,277
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01558
; PRIOR FILING DATE: 1996-11-28
; PRIOR APPLICATION NUMBER: SE 9504272-7
; PRIOR FILING DATE: 1995-11-29
; PRIOR APPLICATION NUMBER: SE 9601506-0
; PRIOR FILING DATE: 1996-04-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1393
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: bell gene fragment
; OTHER INFORMATION: (branching enzyme II) from Solanum tuberosum
; OTHER INFORMATION: (potato)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2)..(1393)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (424)..(1150)
; OTHER INFORMATION: Nucleotides 424, 891 and 1150 are n wherein n = A,
; OTHER INFORMATION: C, G or T.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (422)..(424)
; OTHER INFORMATION: Amino acid 141 is xaa wherein xaa = thr.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (890)..(892)
; OTHER INFORMATION: Amino acid 297 is xaa wherein xaa = Tyr, Ser, Cys
; OTHER INFORMATION: or Phe.
; FEATURE:
; NAME/KEY: misc_feature

LOCATION: (1148)..
OTHER INFORMATION: Amino acid 383 is xaa wherein xaa = Pro.
US-10-254-534-3

Query Match 43.5%; Score 1372.2; DB 9; Length 1393;
Best Local Similarity 98.9%; Pred. No. 0;
Matches 1377; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 1002 TCTGCCAAATAAGTGGATGGTCTCTGCAATTCCTCATGGGCCAGAGTGAAGATACG 1061
DB 1 TCGCCAAATAAGTGGATGGTCTCTGCAATTCCTCATGGGCCAGAGTGAAGATACG 60
QY 1062 CATGGACATTCATCAGGTGTTAAGGATTCATTCCTGCTGGATCAACTACTCTTACA 1121
DB 61 TATGGACATTCATCAGGTGTTAAGGATTCATTCCTGCTGGATCAACTACTCTTACA 120
QY 1122 GCTTCTGTGATGAATTCATATATATGAATATATATATGATCCAGAGAGAGGTA 1181
DB 121 GCTTCTGTGATGAATTCATATATATGAATATATATATGATCCAGAGAGAGGTA 180
QY 1182 TGTCTTCCAAACCCAGCGGCAAGAAACCAAGTCGCTGAGATATATGAATCTCATAT 1241
DB 181 TATCTTCCAAACCCAGCGGCAAGAAACCAAGTCGCTGAGATATATGAATCTCATAT 240
QY 1242 TGAATGAGTAGTCCCGAGGCTAAATTAATCACTCATAGTGAATTTAGAGATGAAGTTCT 1301
DB 241 TGAATGAGTAGTCCCGAGGCTAAATTAATCACTCATAGTGAATTTAGAGATGAAGTTCT 300
QY 1302 TCTCGCATAAACACCTTGGGTACATGCGGTGCAATATATGCTATTTCAAGAGCATTC 1361
DB 301 TCTCGCATAAACACCTTGGGTACATGCGGTGCAATATATGCTATTTCAAGAGCATTC 360
QY 1362 TTATTATGCTAGTGGTGTATCATGTCACAAATTTTTCGCCAAGCAGCGGCTTTGG 1421
DB 361 TTATTATGCTAGTGGTGTATCATGTCACAAATTTTTCGCCAAGCAGCGGCTTTGG 420
QY 1422 AAGCCCGAGGAGCTTAAGTCTTTGATGATGAATGAAGTCAATGAGTGAATTTGTTCT 1481
DB 421 AAGCCCGAGGAGCTTAAGTCTTTGATGATGAATGAAGTCAATGAGTGAATTTGTTCT 480
QY 1482 CATGGACATTTTCACAGCCATCATCAATATATCTTATAGTGGAGTGAACATGTTGA 1541
DB 481 CATGGACATTTTCACAGCCATCATCAATATATCTTATAGTGGAGTGAACATGTTGA 540
QY 1542 CGGCACAGATAGTGTACTTCTACCTGAGGCTCGTGGTATCATTTGATGGGATTC 1601
DB 541 CGGCACAGATAGTGTACTTCTACCTGAGGCTCGTGGTATCATTTGATGGGATTC 600
QY 1602 CGCCCTTTTAACTATGGAACCTGGGAGGTACTAGTATCTTCTCAATGGGAGATG 1661
DB 601 CGCCCTTTTAACTATGGAACCTGGGAGGTACTAGTATCTTCTCAATGGGAGATG 660
QY 1662 GTGGTGGATGAGTGAATTTGRTGATTTAGATTTGATGGTGGATCAATGATGTA 1721
DB 661 GTGGTGGATGAGTGAATTTGRTGATTTAGATTTGATGGTGGATCAATGATGTA 720
QY 1722 TACTACCCAGGATATPCGTTGGATTCATCTGGAACTACAGGAAATPACTTTGGACATCG 1781
DB 721 TACTACCCAGGATATPCGTTGGATTCATCTGGAACTACAGGAAATPACTTTGGACATCG 780
QY 1782 AACTGATGATGATGCGCGGTGATCTGATGCTGGCCAGCATCTTATCATGGGCTTTT 1841
DB 781 AACTGATGATGATGCGCGGTGATCTGATGCTGGCCAGCATCTTATCATGGGCTTTT 840
QY 1842 CCCAGATGCAATTTACCATTTGGTGAAGATGTTAGCGGAATCCGACATTTTCTATCCCGT 1901
DB 841 CCCAGATGCAATTTACCATTTGGTGAAGATGTTAGCGGAATCCGACATTTTCTATCCCGT 900
QY 1902 TCAAGATGGGGGTGTTGGCTTTGACTATCGCTGATATGGCAATTCCTGATGAATGAT 1961
DB 901 TCAAGATGGGGGTGTTGGCTTTGACTATCGCTGATATGGCAATTCCTGATGAATGAT 960
QY 1962 TGAGTGTCTCAAGAAACGGGATGAGGATTTGGAGTGGGATGATTTGTTCACTACATGAC 2021

DB 961 TGACTGTCTCAAGAAACGGGATGAGGATTTGAGAGTGGTGTATTTGTTACACTGAC 1020
QY 2022 AAATAGAGATGGTCCGAAAAGTGTGTTTCATAGCTGAAAAGTCAATGATCAAGCTCTAGT 2081
DB 1021 AAATAGAGATGGTCCGAAAAGTGTGTTTCATAGCTGAAAAGTCAATGATCAAGCTCTAGT 1080
QY 2082 CGGTGATAAAACTATAGCATTTCTGCTGATGACGAAAGATATGATGATTTATGGCTTT 2141
DB 1081 CGGTGATAAAACTATAGCATTTCTGCTGATGACGAAAGATATGATGATTTATGGCTTT 1140
QY 2142 GGATAGACCGCTCAACATCATTAATAGATCGTGGGATGACATTCGCAAGATGATAGGCT 2201
DB 1141 GGATAGACCGCTCAACATCATTAATAGATCGTGGGATGACATTCGCAAGATGATAGGCT 1200
QY 2202 TGTAACTATGGGATTTAGGAGAGAGGATGCTAAATTTCTATGGGAAATGATTCGGGCA 2261
DB 1201 TGTAACTATGGGATTTAGGAGAGAGGATGCTAAATTTCTATGGGAAATGATTCGGGCA 1260
QY 2262 CCCTGAGTGGATTTGATTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAGTAATTC 2321
DB 1261 CCCTGAGTGGATTTGATTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAGTAATTC 1320
QY 2322 CGGAAACCAATTCAGTTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAAGATA 2381
DB 1321 CGGAAACCAATTCAGTTATGATAAATGACAGCGGAGATTTGACCTGGGAGATGCAAGATA 1380
QY 2382 TTTAAGATACCGT 2394
DB 1381 TTTAAGATACCGT 1393

RESULT 3
US-09-938-842A-872
; Sequence 872, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 872
; LENGTH: 2418
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-872

Query Match 41.9%; Score 1323; DB 9; Length 2418;
Best Local Similarity 76.9%; Pred. No. 0;
Matches 1604; Conservative 2; Mismatches 480; Indels 0; Gaps 0;

QY 677 GGATCAGAGAGAGGCGCATCCCTCCACTGGATTTGGTCAGCAAGATTTATGAAATAGACC 736
DB 329 GGGTGAACCAAGATAGTCCCGCCCGGGTGTGCGCAAGAAATTTATGAGATAGACC 388
QY 737 CCCTTTTACAAAATATCGTCAACACCTTGATTAAGTATTCACAGTACAGCAAGAAATGA 796
DB 389 CCATGTTACGAACCTTACAAACATCATCTTGATTTACCGTTATGGACAGTATAAAGATTGC 448
QY 797 GGGAGGCAATTCAGCAAGTATGAGGTTGGAGGCTTTTCTCGTGGTATGATGAAAAA 856

Db 449 GTGAGGAATAAGACAAGTATGAGGTGCTTGGGCAATTCCTCGTGGCTATGAAAAGT 508
Qy 857 TGGGTTTCACCTCGTAGTCTACAGTATCACTTACCGTGACTGGGCTCCTGGTCCCAAGT 916
Db 509 TAGGATTTCCGCGAGTATGCGCGTATPACTTATAGAGATGGGCGCTGGAGCTAAGG 568
Qy 917 CAGCTGCTCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTGACATTTATGACTCGGA 976
Db 569 CTGCATCACTTATCGGAGATTTCAACAACCTGGAATTTCTAATGCGAGATCAATGACTCGGA 628
Qy 977 ATGAATTTGGTGTCTGGAGATTTTTCGCGCAAAATTAATGTTGGATGTTCTCCTGCAATTC 1036
Db 629 ATGAATTTGGTGTCTGGAGATTTTTCGCGCAAAATTAATGTTGGATGTTCTCCTGCAATTC 688
Qy 1037 CTCATGGGTCCAGAGTGAAGATACGATGGAACCTTCATCAGGTGTTTAAGGATTCATTC 1096
Db 689 CTCATGGGTCCAGAGTGAAGATTCGATGGAACCTTCATCAGGTGTTTAAGGATTCATTC 748
Qy 1097 CTGCTTGGATCAACTCTCTTACAGCTTCTCTGATGAAATTTCCATATAATGGAATATAT 1156
Db 749 CTGCTTGGATCAACTCTCTTACAGCTTCTCTGATGAAATTTCCATATAATGGAATATAT 808
Qy 1157 ATGATCCACCGAGAGAGAGTATGCTTCCAAACCCAGCGCCAAAGAACCAAGT 1216
Db 809 ATGATCCACCGAGAGAGAGTATGCTTCCAAACCCAGCGCCAAAGAACCAAGT 868
Qy 1217 CGCTGAGAATATATGAATCTCATATTTGGAATGAGTGTCCGAGCCCTAAATTAATCAT 1276
Db 869 CGCTGAGAATATATGAATCTCATATTTGGAATGAGTGTCCGAGCCCTAAATTAATCAT 928
Qy 1277 ACCTGGAATTTAGAGATGAAGTCTTCTCCGATGAAATTTCCATATAATGGAATATAT 1336
Db 929 ATGCTAACTTTAGAGATGATGTTCTTCCCGCATCAAAAGCTTGGATATATGCTGTTC 988
Qy 1337 AATATGAGTATTTCAAGAGCATCTTATATGCTAGTGTGTTGGTATCATGTCACAAAT 1396
Db 989 AATATGAGTATTTCAAGAGCATCTTATATGCTAGTGTGTTGGTATCATGTCACAAAT 1048
Qy 1397 TTTTTCACCAAGCAGCGCTTTTGGAGCGCCGAGACCTTAAGTCTTTGATTCATTAAG 1456
Db 1049 TTTTTCACCAAGCAGCGCTTTTGGAGCGCCGAGACCTTAAGTCTTTGATTCATTAAG 1108
Qy 1457 CTCATGAGCTAGGAATTTGTTCTCATGAGCATTTGTTACAGCCATGCAATCAAAATA 1516
Db 1109 CTCACAGTATGAGCGCTGATGTTCTGATGATTCGTTTCATAGCCATGCTTCAAAACA 1168
Qy 1517 CTTTATGATGACATGACATGTTTACCGGCACAGATGTTGTTACTTTCACTCTGGAGCTC 1576
Db 1169 CATTGATGACATGACATGTTTATGATGAACTGATGCTCACTATTTTCACTCTGGAGCTC 1228
Qy 1577 GTGGTTATCATTTGATGTTGGATTTCCGCTCTTTACTATGAAACTGGGAGTACTTA 1636
Db 1229 GGGATACCATTTGGATTTGGATTTCCAGCTTTTCAATTAAGGAGCTGGAGATTAAC 1288
Qy 1637 GGTATCTCTCTCAATGCGAGATGTTGGTGGATGAGTGCACAAATTTGRTGATTTAGAT 1696
Db 1289 GATACTCTCTTCAAAATGCAAGTGTGGTGTAGAGATACAAAGTTTATGATTTAGAT 1348
Qy 1697 TTGATGTTGATCATCAATGATGATCTACCCACAGGATTTATCGTGGGATTCAGTGGGA 1756
Db 1349 TTGATGTTGATCATCAATGATGATCTACCCACAGGATTTATCGTGGGATTTACTGGGA 1408
Qy 1757 ACTACAGGAATACTTTGGGACTCGCAACTGATGRTGATGCTGCGGTGATCTGATGCTGG 1816
Db 1409 ACTACAGGAATACTTTGGGACTCGCAACTGATGRTGATGCTGCGGTGATCTGATGCTGG 1468
Qy 1817 CCAACGATCTTATCATGGGCTTTTCCAGATGCAATTTACATTTGTTGAAGATTTAGCG 1876
Db 1469 TTAATGATATGATTCATGGGCTCTACCTGAACGATACCTGTTGGTGAAGATTTAGTG 1528
Qy 1877 GAATGCGGACATTTTGTATTCCTGTTCAAGATGGGCTGTTGCTTTGATGATTCGCTGTC 1936
Db 1529 GTAATGCAACATTTCTGATTCCTGTTCAAGATGGTGGGCTTGTGATTTGACTACCGTTAC 1588

Qy 1937 ATATGGCAATTCCTCATTAATTTGGATTTAGTTCCTCAAGAAACGGGATGAGGATTTGAGAG 1996
Db 1589 ACATGGCCATAGCTATAGTAAAGTAGAATACTCTCAAGAAAGAGATGAAGACTGGCAAA 1648
Qy 1997 TGGGATGATTTCTCATACACTGACAAATAGAGATGTTGCGAAAGATGTTTTCATACG 2056
Db 1649 TGGGCGACATCATTTTACACACTTACCAAGAGAGTGGTTCAGAGAGTGTATCTCTTAIG 1708
Qy 2057 CTGAAGATCATGATCAAGCTTCTAGTGGTGTATAAAACTATAGCATTTGGCTGATGGACA 2116
Db 1709 CTGAAGATCATGATCAAGCTTCTTGGTGTATAAAACTATAGCATTTGGCTGATGGACA 1768
Qy 2117 AGGATATGATGATTTTATGCTTTGGATGATGACCTCAACATTAATAGATCGTGGGA 2176
Db 1769 AGGATATGATGATTTTATGCTTTGGATGATGACCTCAACATTAATAGATCGTGGGA 1828
Qy 2177 TAGCATTCACAAGATGATTTAGGCTTGTAACTATGGGATTTAGGAGGAGAGGTTACTTAA 2236
Db 1829 TAGCTTTCACAAGATGATTTAGGCTTGTAACTATGGGATTTAGGAGGAGAGGTTACTTAA 1888
Qy 2237 ATTTTATGCGGAAATGAATTCGCGCACTTGGATGATTTTCCCTAGGCTGACCAAC 2296
Db 1889 ATTTTATGCGGAAATGAATTCGCGCACTTGGATGATTTTCCCTAGGCTGACCAAC 1948
Qy 2297 ACCTCTCTGATGCTCAGTAAATTCGCGGAAACCAATTCAGTTATGATTAATAGCAGCGGA 2356
Db 1949 GTCCTTCTGATGCTCAGTAAATTCGCGGAAACCAATTCAGTTATGATTAATAGCAGCGGA 2008
Qy 2357 GATTTGACCTGGGAGATGACAAATTTAAGATACCTGCTGATTTCCCTAGGCTGACCAAC 2416
Db 2009 GATTTGACCTGGGAGATGACAAATTTAAGATACCTGCTGATTTCCCTAGGCTGACCAAC 2068
Qy 2417 CTATGCACTTCTTGAAGATAAATGATGATTTTATGACTTCAGACACCACTTCATATCAC 2476
Db 2069 CAATGCACTTCTTGAAGATAAATGATGATTTTATGACTTCAGACACCACTTCATATCAC 2128
Qy 2477 GAAAGATGAGGAGATGAGGATGATTTGATTTGAAAGAAAGAACTAGTTTGTCTTTA 2536
Db 2129 GAAAGATGAGGAGATGAGGATGATTTGATTTGAAAGAAAGAACTAGTTTGTCTTTA 2188
Qy 2537 ATTTTCTACTGGACAAAAGATTTTCAAGATATCGTATTCGAAAGAGTGTATCTCTTTGCTTTA 2596
Db 2189 ACTTTCTACTGGACAAAAGATTTTCAAGATATCGTATTCGAAAGAGTGTATCTCTTTGCTTTA 2248
Qy 2597 ACAAGTGTGCTTGGACTCAGATGATCAGCTTTTGGTGGCTTCGGGAGAAATTCATATA 2656
Db 2249 ATAAGATGCTATTTGGACTCGGACGATCTCTCTTTGGTGGATTCATTAAGCTTCATCGCA 2308
Qy 2657 ATGCGGAATGTTTCACTTTTCAAGGATGATGATGCTTCCTGCTTCGTTCAATTTAGGTGT 2716
Db 2309 AGGAGAGATGTTTCACTTTTCAAGGATGATGATGCTTCCTGCTTCGTTCAATTTAGGTGT 2368
Qy 2717 ATGCACCTAGTAGAAGACAGCTGCTGATGATGCTTACCTAGTAGAAGAA 2762
Db 2369 ATGCACCTAGTAGAAGACAGCTGCTGATGATGCTTACCTAGTAGAAGAA 2414

RESULT 4

US-09-938-842A-337

Sequence 337, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Krepis, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPI300-3

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

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; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 337
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-337

Query Match          41.1%; Score 1296; DB 9; Length 2577;
Best Local Similarity 76.2%; Pred. No. 0; Mismatches 496; Indels 0; Gaps 0;
Matches 1593; Conservative 1;

Qy      Db      686 AGAGGGGCATCCCTCCACCTCGGACTTGGTCAGAGAAGATTATGAATAAGACCCCCTTTTGA 745
Db      Qy      443 AGAGGAAGATTCCACCTCCTGGAGATGGGAAGAGAAATATATGACATTGATCTCATGTGTA 502
Qy      Db      746 CAACATATCGTCAACACCTTGATACAGTATTCACAGTACAGAAAATACAGGAGGCCAA 805
Db      Qy      503 ACAGTCATCGTATATCATCTTGATTACCAGTATGGCAGGTACAGAAAACCTCGGTGAAGAA 562
Qy      Db      806 TTGACAAGTATAGGGGTGGTTTGGAAAGCTTTTTCTCGTGGTTATGAAAAATGGGTTC 865
Db      Qy      563 TTGACAAGAATGAAGTGGTTTGGAGSCATTTTCTCGTGGTTATGAATATTTGGCTTCA 622
Qy      Db      866 CTCGTAGTGTCTACAGWATCACTTACGTCAGTGGGCTCTCGTGGCCAGTCAGCTGCTC 925
Db      Qy      623 CTGGAAGCGCCACTGGTATCACTTACCGGAATGGGCACCGGGAGCTAAGGCAGCATCAC 682
Qy      Db      926 TCATTGGAGATTTCAACAATTTGGAGCAAACTGCTGACATTTATGACTCGGAATGAATTTG 985
Db      Qy      683 TGAATCGAGATTTTAATACTTGAATTCGAAATCTGATTTATGGCTCGGAACGACTTTC 742
Qy      Db      986 GTGTCTCGGGAGATTTTTCGCCAAATAAATGTGGATGGTTCTCTCGAAATTCCTCATGGGT 1045
Db      Qy      743 GTGTGTGGGAAATTTTCTGCCAAATAAATGCTGATGGCTCACGAGCAAAATCCCATGGCT 802
Qy      Db      1046 CCAGAGTGAAGATACGCATCGACACTTCATCAGSTGTTAAGGATTCATTCTCTGCTTGA 1105
Db      Qy      803 CCGGTGGAAGATCCGGATGGATACCCCATCTGGTATTAAGACTCCATTCACAGCTTGA 862
Qy      Db      1106 TCAACTACTCTTTACAGCTTCTCTGATGAAATTCATATATGGAATATATATGATCCAC 1165
Db      Qy      863 TCAAGTATTTCTGCCAGCCACTGGGAGATCCCATATATGAGTATATATGACCCCTC 922
Qy      Db      1166 CCGNAGGAGAGGTATGCTTCCACACCCAGGCCCAAGAAACCAAGTCCTCGTAGAA 1225
Db      Qy      923 CTGAGGAGGATAAATATGCGTTCAACATCTCTGTCCAAAGAACCCACATCTCTCGGTA 982
Qy      Db      1226 TATATGAATCTCATATTTGGAATGAGTAGTCGGAGCCTAAAAATTAATCTCATAGTGAAT 1285
Db      Qy      983 TATATGAATCACATGTTGGAATGAGTAGTACGGAACCAAGATAAATACATATGCCAACT 1042
Qy      Db      1286 TTAGAGATGAAGTTCTCTCGCATAAAAACCTTGGGTACANVGCGGTCCAATATATGG 1345
Db      Qy      1043 TTAGAGATGATGACTTTCCCGGTATAAAAAGCTTAGGCTATATGCTGTGCAGATAATGG 1102
Qy      Db      1346 CTATTCAGAGCATCTCTTATTATGCTAGTTTGGTTATCATGTACAAAAATTTTTTGCAC 1405
Db      Qy      1103 CCATTCAGAGCATGCGCTACTATAGCCAGCTTTGGGTATCATGTACAAAAATTTTTTCGAC 1162
Qy      Db      1406 CAAGACGCGGTTTTGGAACGCCGACACCTTAAAGTCTTTGATTGATAAAGCTCATGAGC 1465
Db      Qy      1163 CTAGACGCGGTTTTGGAACACCTCATGACCTTAAATCTTTGATAGACAAAGCTCATGAGC 1222
Qy      Db      1466 TAGGAATTTGTTCTCATGGACATCTTTCACAGCCATGCATCAATTAATACATTAGATG 1525
Db      Qy      1223 TAGGTCGTGGTTTCTCATGTGATTTGTGCACAGCCATGCATCAAAAACACACTGGAG 1382
Qy      Db      1526 GACTTGAACATGTTTTGAGGCGCACAGATAGTTTACTTCTACTCTGGAGCTCGGGTTATC 1585
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Db 2363 TTTTGGACCTCTGATTAACCTCTTTATTTGGAGGCTTCAACGGCTAGATGACTCGCGGAGCT 2422
QY 2666 GTTTCACCTTTGAAGGATGGTATGATGATGCTCTCGTTCATTTATGTTGATGACCTA 2725
Db 2423 TTTTTCACCTCTGATGGAAGGACGACGATAGGCTTGTCTCTTCATGTTGTTGATGACCGT 2482
QY 2726 GTAGAACAGAGTGTCTATCCATCAGATAGTACAAAGAAAGAAAGAA 2775
Db 2483 GCAGAACCGCTGTAGTTTACGCTGCAGTAGATGATGATGATGATGAA 2532

RESULT 5
US-09-792-127-3
; Sequence 3, Application US/09792127
; Patent No. US20020002713A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Beckles, Diane M.
; APPLICANT: Butler, Karla
; APPLICANT: Pearlstein, Rich
; TITLE OF INVENTION: Starch Branching Enzyme IIb
; FILE REFERENCE: BB1439 US NA
; CURRENT APPLICATION NUMBER: US/09/792,127
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/186098
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 3039
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-792-127-3

Query Match 37.6%; Score 1185.6; DB 10; Length 3039;
Best Local Similarity 71.9%; Pred. No. 0;
Matches 1545; Conservative 2; Mismatches 601; Indels 0; Gaps 0;

QY 664 GATGAATCTGATAGGATCAGAGAGGGGCGATCCCTCCACCTGGACTTGGTCAGCAAGATT 723
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QY 724 TATGAATAGACCCCTTTTGAACAACACTATCGTCAACACCTTGATTAAGCTATTCACAG 783
Db 534 TAGAGATTGACCAACACGCTCCGAGACTTTAAGTACCATCTTGATTCATATAGCCTA 593
QY 784 TACAAGAAATAGGAGGCAATGACAACTATCGTCAACACCTTGATTAAGCTATTCACAG 843
Db 594 TACAGAGAAATAGCTTCAGACATTTGATGAACACGAGGAGGCGATGATGATTTTCCCGC 653
QY 844 GGTATGAAAAATGGGTTTCACTCTGCTAGTGTACAGGTATCACTTACCGTGGAGTGGCT 903
Db 654 GGTACGAGAAAGTTGGATTTATGCGCAGGCTGAGAGTATCACTTACCGAGAAATGGGCT 713
QY 904 CTGTGGCCAGTACGCTCTCATTTGAGATTTCAACAATTTGGACGCAAAATGCTGAC 963
Db 714 CTGGAGCAGATTTGACGACATTTAGTTGGCGACTTCAACAATTTGGGATCCAAATGCGAC 773
QY 964 ATTATGACTCGGAATGAATTTGGTGTCTGGAGATTTTCTGCCAATTAATGTTGATGTT 1023
Db 774 CATATGAGCAAAATGACCTTGGTGTGGGAGATTTTCTGCCAACAATGACATGTT 833
QY 1024 TCTCTGCAATTCCTATGGGTCACAGATGAAGATACGATGACACTTCACTACGTTGTT 1083
Db 834 TCGCCACCAATTCCTCACGGTACAGGTTGAGGATGAGATGATGATCTCCATCTGGGATA 893
QY 1084 AAGGATTCATCTCTGTTGGATCACTACTCTTTACAGCTTCTCTGATGAAATTCATAT 1143
Db 894 AAGGATTCATCTCTGTTGGATCACTACTCTCTGAGTACAGTACCTGAGGATATACCATAC 953
QY 1144 AATGGAATATATTATGATCCACCCGAGAGGAGGATGATGCTTCCACACCCACCGGCA 1203
Db 954 AATGGAATATATTATGATCTCTCCGAGAGGAGAGTATGATTTCAAGCATCTCTCAACT 1013

QY 1204 AAGAAACCAAGTCGCTGAGAAATATATGAATATATATGGAATAGTAGTCCGAGCCT 1263
Db 1014 AAGAGCAAAATCATTTGGGATATATGAACACATGTTGGCATAGTAGTCCCGGAACCA 1073
QY 1264 AAAATTAATCATACGTGAATTTTAGAGATGAGTTCTTCCCTGCGCAATAAAACCTTGGG 1323
Db 1074 AAGATCAACACATATGCAAACTTCAGGGATGAGGTGCTTCCRAAGATTAAGACATTGA 1133
QY 1324 TACAATGGGTGCABAATTAATGCTATTCAAGAGCAATCTTATTATGCTAGTTTGGTTAT 1383
Db 1134 TACAATGGGTGCABAATTAATGCTATTCAAGAGCAATCTTATTATGCTAGTTTGGTTAT 1193
QY 1384 CATGTCAAAATTTTTCACCAAGCAGCCGCTTTTGGAAACGCCGACACCTTAAGTCT 1443
Db 1194 CATGTCAAAATTTTTCACCAAGTACCCGCTTTTGGTCCCAAGAGATTTAAATCT 1253
QY 1444 TTGATTGATAAGCTCATGAGCTAGGAATTTGTTCTCATGAGCAATTTGTTTCCAGCCAT 1503
Db 1254 TTGATTGATAAGCTCATGAGCTAGGAATTTGTTCTCATGAGCAATTTGTTTCCAGCCAT 1313
QY 1504 GCATCAAAATATACCTTTAGATGAGTGAACATGTTTGGACGCGACAGATAGTTTACCTT 1563
Db 1314 GCGTCAAAATATACCTTTAGATGAGTGAACATGTTTGGACGCGACAGATAGTTTACCTT 1373
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Db 1374 CATGGCGTTTACCGGGGCCATCCTGGATGTTGGATTCGCGCTCTTTAACTATGAGAAAC 1433
QY 1624 TGGGAGGTACTTAGTATCTCTCAAAATCGAGATGTTGTTGGATGAGTGAATTT 1683
Db 1434 AAGGAAGTTATTAAGTTTCTTCTCAAAATCGAGATGTTGTTGGATGAGTGAATTT 1493
QY 1684 GRTGGATTGATTTGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1743
Db 1494 GATGTTTCCGATTCGATGCGCGACCTTCCGATGATGATGATGATGATGATGATGATGAT 1553
QY 1744 GGATTCATGGAACACTACGAGGAATATCTTTGGACTCGCAACTGATGTTGATGCTCGCG 1803
Db 1554 ACCTTTACGAGAACTACCATGATATTTTGGCTTGGCACTGATGATGATGATGATGATGAT 1613
QY 1804 TATCTGATGCTGGCCACAGATCTTATTAATGAGGCTTTTCCAGATGCAATTTACCATTTG 1863
Db 1514 TACTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1673
QY 1864 GAAGATCTTAGCGGAATCCGACATTTTGTATTTCCCTTCAAGATGAGGTTTGGGCTTT 1923
Db 1674 GAAGATCTTAGCGGAATCCGACATTTTGTATTTCCCTTCAAGATGAGGTTTGGGCTTT 1733
QY 1924 GACTATGGGTGCATATGCAATTTGCTGATAAATGGAATGATTTGCTCAAGAAACGGAT 1983
Db 1734 GACTATGGGTGCATATGCAATTTGCTGATAAATGGAATGATTTGCTCAAGAAACGGAT 1793
QY 1984 GAGGATGAGAGTGGGTGATATGTTTCACTACTGACAAATAGAGATGCTCGGAAAG 2043
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QY 2044 TGTGTTTCACTACCTGAAAGTCAATGATCAAGCTTAGTCTGATGATGATGATGATGATGAT 2103
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QY 2104 TGCTGATGAGCAAGGATATGATGATTTTATGCTTTTGAATAGACCGTCAACATCATTA 2163
Db 1914 TGCTGATGAGCAAGGATATGATGATTTTATGCTTTTGAATAGACCGTCAACATCATTA 1973
QY 2164 ATAGATCGTGGATAGCATTTGCACAGATGATTTAGGCTTTTAACTATGAGATGAGGA 2223
Db 1974 ATGATCGTGGATAGCATTTGCACAGATGATTTAGGCTTTTAACTATGAGATGAGGA 2033
QY 2224 GAAGGTACTTAAATTTTCAATGGAATGAAATTCGCGCCACCTTGAAGTATGATTTCCCT 2283
Db 2034 GAAGGTACTTAAATTTTCAATGGAATGAAATTCGCGCCACCTTGAAGTATGATTTCCCT 2093


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Db 1225 TTCTGTTCAAGTTGGTGGGTTGGTTTGGACTATCGCTTACATATGCGCTGTGCCGACA 1284
QY 1955 AATGATTACAGTTCCTCAAGAAACGGGATGAGGATTTGGAGGTGGGTGATATGTTTCATA 2014
Db 1285 AATGATTGAACTTCTCAAGGAACGATGAGCTTTGGGAGATGGGTAAATATTTGGCACA 1344
QY 2015 CACTGACAAATAGAGATGTCGCGGAAAAGTGTGTTTCATAGCTGAAAGTCATGATCAAG 2074
Db 1345 CACTAACAAACAGAGGTGGCTGGAAAAGTGTGTACTTATGCTGAAGATCAGATCAAG 1404
QY 2075 CTCTAGTCGGGTGAATAAATACTAGCATTTCTGGCTGATGGACAAGGATATGATATTTA 2134
Db 1405 CACTGTTGGAGACAGACTATTTGCTGCTGGTTGATGGACAAGGATATGATATTTC 1464
QY 2135 TGGCTTTGGATAGACCTCAACATCAATTAATAGATCGTGGGATAGCATTTGACACAGATGA 2194
Db 1465 TGGCGCTGAACGGACCTTCGAGCGCTAATAATGATCGGAAATAGCATGCTGATAAAATGA 1524
QY 2195 ITAGGCTGTAACCTATGGGATAGGAGGAGGAGGATACCTAAATTTTCATGGGAATGAAT 2254
Db 1525 TTAGCATTTACAAATGGGCTTAGGAGGAGAGGGTTATCTTAACTTTATGGGAATGAGT 1584
QY 2255 TCGGCCACCTGAGTGATTTGCTTCCCTAGGCTGAACACACCTCTCTGATGGCTCAG 2314
Db 1585 TCGGGCATCTGATGATAGACTTTCCAGAGGCCCAAGTACTTCCAAAGTGGTAAGT 1644
QY 2315 TAATTCGCGAAACCAATTCAGTTATGATAAATGCAGACGGAGATTTGACCTGGAGATG 2374
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QY 2375 CAGAAATTTAAGATACCGTGGGTGCAAGATTTGACCGGGCTATCAGTATCTTTGAAG 2434
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QY 2435 ATAAATATGAGTTTATGACTTCAGAACACACAGTTTCATATCAGCAAGGATGAGGAGATA 2494
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QY 2495 GGATGATGTTATTTGAAAAGGAAACCTAGTTTGTCTTTATTTTCTTCTTCTTCTTCTTCT 2554
Db 1825 AGTGATGCTGTTTGAAGAGGGGACTTGTATTTGTTTCACTTCCACTGGAGTAGTA 1884
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Db 1885 GCTATTTCACATACCGGGTGGCTGTTTAAAGCTGGGAAGTACAAGTGGTCTTAGACT 1944
QY 2615 CAGATGATCCACTTTTGGTGGCTTCGGGAGATTTGATCATATGCTCGGAATGTTTCACT 2674
Db 1945 CGGACGCTGGACTCTTTGGTGGATTTGGTAGATTCATCAGTACCTCCTAGCAGACCT 2004
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Db 2005 CTGATGCTCAACATGACACAGGCCCAATCTCTCAGTGTACCTCCTAGCAGACCT 2064
QY 2735 CAGTGGCTATGCTAGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2794
Db 2065 GTGTGCTATGCTCCATGAACTAACAGCAAGTGCAGATACGCTACGCTGCGGCTGTGT 2124
QY 2795 AAGTAGTAGTGAAGAA 2811
Db 2125 TGCTAGTAGCAAGAAA 2141
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RESULT 7

US-10-084-817-92

; Sequence 92, Application US/10084817

; Publication No. US20030119009A1

; GENERAL INFORMATION:

; APPLICANT: Susan Stuart

; APPLICANT: Jed G. Nuchtern

; APPLICANT: Sharon E. Plon

; APPLICANT: Jason M. Shohet

; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION

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; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 92
; LENGTH: 2994
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 1253978CB1
US-10-084-817-92
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Query Match

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Best Local Similarity 19.0%; Score 598.2; DB 9; Length 2994;
Matches 1175; Conservative 2; Mismatches 800; Indels 48; Gaps 5;
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Db 215 GAGATCGACCCGTACTTGAAGCCCTACCCGTGGACTTCCAGCGAGGTATAAGCAGTTT 274
QY 787 AAGAAATGAGGGAGGCAATTCACAAGTATGAGGGTGGTTTGGAGCTTTTCTCGTGGT 846
Db 275 AGCCAAATTTTGAAGAACATTTGAGAAATCAAGGTGCTATGATAAGTTTCCAGAGCC 334
QY 847 TATCAAAAATGCGTTTTCACCTCTAGTCTGACAGTATCATTACCGT---GAGTGGGCT 903
Db 335 TATGAATCATTTGGCGTCCACAGATGTCTGATGGTGGTTTATCTACTCAAAAGATGGGCC 394
QY 904 CTTGGTCCCGAGTCAGTCTCTCATTTGGAGATTTCAACAATTTGGAGCGCAATGCTGAC 963
Db 395 CCGGACGACAGAGAGTTTCTTACTGGAGATTTTATGTTGGATTCCTTTCGTAC 454
QY 964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCCAAATATGTTGATGGT 1023
Db 455 CCATACAAAATACCTGGATTTATGGAATATGGAGCTGTATATCCCAACCAAGCAATAAA 514
QY 1024 TCTCTCAATTTCTCTAGTTCAGAGTCCAGATGAGTATGAGTATGAGTATGAGTATGAGT 1081
Db 515 TCTGTACTCTGCTCATGATCCAAATTAAGGTAGTTTATTTACTAGTAAAGCGGAGAG 574
QY 1082 -TTAAGGATTCCTTCTGCTGGATCAACTACTCTTTACAGCTTCTCTGATGAAATFCCA 1140
Db 575 ATCTTGTATCGTATTTACCGTGGCAAGTATGTGGTTCGTGAGGTGATATGTAAT 634
QY 1141 TATAATGGAATATATATGATCCACCGGAAAGAGAGAGGTATGTCTTCCAAACCCACGG 1200
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Db 689 CCAGAAAGCCACCGAGTCTAGAAATTTATGATCTCATGTTGGGAAATTTCTTCCCATGAA 748
QY 1261 CTTAAATTAACCTCATACGTGAATTTTAGAGATGAAGTTCTTCTCGCATAAACCTT 1320
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QY 1381 TATCATGTACAAATTTTTCACCAAGAGCCGCTTTTGGAAACCCGAGACCTTAAG 1440
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Db 661 CCAAGAGCCAGCGAGTCTAAGAAATTTATGAATCTCATGTGGGAATTTCTTCCCATGAA 720
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Db 721 GGAAGAGTAGCTTCTTTATAACAACTTTTACATGCAATGTACTACCAAGAAATCAAGGCGCT 780
QY 1321 GGGTACAAATGGCGTCAAAATTTAGGCTATTTCAAGAGCAATCTTTATATGTAGTTTGGT 1380
Db 781 GGAATCAAGTGCATTCAGTTGATGGCAATCATGGAGCATGCTTACTATGCGACGTTGGT 840
QY 1381 TATCATGTCCAAATTTTTCACCAAGCAGCGCTTTTGGAAAGCGCCGACGACCTTAAG 1440
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QY 1441 TCTTTGATGATAAGCTCATGAGCTAGGAATTTGTGTCTCTCATGACATTTGTTCACAGC 1500
Db 901 GAACTGGTATGACACAGCTCATTCATGGGTATCATAGTCTCTTAGATGGTACACAGC 960
QY 1501 CATGCATCAAAATTAATCTTTAGATGAGCTGAACATGTTTGAAGGACAGATAGTTGTAC 1560
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QY 1561 TTTCATCTGGAGCTCGTGGTATCATTTGGATGAGGATTCGGCTCTTTTACTATGA 1620
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QY 1621 AACTGGGAGTACTTAGGTATCTCTCAAAAGCAGATGTTGGATGAGTGAAGCAAA 1680
Db 1081 AGCTGGGAGTTTAAAGATCTCTCTGCAAAACATAGATGTTGGTGAAGAAATATGCG 1140
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Db 1141 TTTGATGATTTGTTTGTGATGGTGTACGTCATGCTTTATCATCAACATGAGTGGT 1200
QY 1741 GTGGATCTAGTGGGACAGTACTTATTCATGGCTTTTCCAGATGCAATACCAAT 1860
Db 1261 ACTTACCTCATGTTGGCAATCAATTTGTTTACAGCTGTGCTCCGATCTTATACAAATA 1320
QY 1861 GGTCAAGATGTTACGGAATCCGACATTTTGTATTCGGTTCAAGATGGGGGTGTGGC 1920
Db 1321 GCTGAGATGATCAGGAATGCCAGCTGTGCTCTCCAATTTCCAGGAGGGGTGGT 1380
QY 1921 TTTGACTATCGCTGATGCAATGCAATTTGCTGATAAATGATGATGATTCCTCA ---AGAA 1977
Db 1381 TTTGACTATCGCTGATGCAATGCAATTTGCTGATAAATGATGATGATTCCTCA ---AGAA 1977
QY 1978 CGGATCAGATGGAGAGTGGTGAATTTTATACACTGACAAATAGAAGATGCTG 2037
Db 1441 AAGATGAAGACTGGACATGGCGATATAGTATACAGCTCACAAACAGCGCTACTCT 1500
QY 2038 GAAAGTGTCTTTCATACGCTGAAGTCATGATCAAGCTGATGCGGTGAATAAATATA 2097
Db 1501 GAAAGTGTCTTTCATACGCTGAAGTCATGATCAAGCTGATGCGGTGAATAAATATA 2097
QY 2098 GCATTTGGCTGATGGACAGGATATCTATGATTTTATGCTTTGGATACACGCTCA 2157
Db 1561 GCATTTGGCTGATGGACAGGATATCTATGATTTTATGCTTTGGATACACGCTCA 2157
QY 2158 TCATTAATAGATCGTGGATAGATTCACAAAGATGATAGGCTTGTGAATATGGGATTA 2217
Db 1621 CCAGTTATTGATCGTGGATAGATTCACAAAGATGATAGGCTTGTGAATATGGGATTA 2217
QY 2218 GGAGGAGAGGTTACTTAATTTTCAATGGGAATGAATTCGGCACCTGATGATGAT 2277
Db 1681 GGTGAGAGAGGCTATCTCAATTTTCAATGGGATGAATTTGGGATCTTGAATGATGAT 1740
QY 2278 TTCCCTAGGCTGAACAAACACCTCTCTGATGGCTCAGTAATTTCCCGGAAACCAATTCAGT 2337
Db 1741 TTCCCAAGAAA -----GGAAATATGAGAGT 1767

QY 2338 TATGATAAATGACACGAGATTTGACCTGGAGATGCAGAAATTTTAAGATACCGTGGG 2397
Db 1768 TACATTTATGCCAGCGCAGTTTCATTTAACTGACGACGACCTTCTTCGCTACAAGTTC 1827
QY 2398 TTGCAAGAATTTGACCGGCTATGACAGTATCTTGAAGATAAATATGATTTATGACTTCA 2457
Db 1828 CTAATAATTTTGACAGGATATGATAGATTTGAAGAAAGATGATGTTGGCTTGCAGCT 1887
QY 2458 GAACACAGTTTATATCACAAAGGATGAAGGATAGAGATGATGATTTGATTTGAAAAAGGA 2517
Db 1888 CCACAGCCCTACGTGAGTGAAGCAATCAAGGCAATTAAGATCAATGCTTTTGAAGAGCA 1947
QY 2518 AACCTAGTTTCTCTTTTAAATTTTCACTGGACAAAAAGCTATTCAGAGCTATCCATAGGC 2577
Db 1948 GGTCTTCTTTTCAATTTTCACTTCCATCCCAAGCAAGAGCTACACTGACTACCGAGTTGA 2007
QY 2578 TGCGTGAAGCTGGAAATACAAAGTTGCTTGGACTGACATGATCCACTTTTGTGGC 2637
Db 2008 ACAGCATTTGCCAGGGAATTCAAAATTTGCTAGATTCAGATCGACGGAATATGGAGG 2067
QY 2638 TTGCGGAGAAATTCATCAATATGCGGAATGTTTCACTTTTCAAGGATGTTATGATGATCGT 2697
Db 2068 CATCAGAGACTGGACACAGCACTGACTTTTCTGAGGCTTTTGAACATAATGGCGCT 2127
QY 2698 CTTGCTCAATTAATGCTGATGACCTAGTAGAACACAGAGTGGTC 2742
Db 2128 CCTATTCTTTTGTGTACATTTCCAAAGCAGAGTGGCCCTCATC 2172

RESULT 9

US-09-880-107-2148
; Sequence 2148, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 4921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2148
; LENGTH: 2955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L07956
US-09-880-107-2148

Query Match 18.9%; Score 596.6; DB 10; Length 2955;
Best Local Similarity 58.0%; Pred. No. 7e-158;
Matches 1174; Conservative 2; Mismatches 801; Indels 48; Gaps 5;

QY 727 GAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGCATACAGGTATTCACAGTAC 786
Db 187 GAGATCGACCCGTACTTGAAGCCCTAGCCGCTGAGCTTCAGCGCAGGTATTAAGCAGTTT 245
QY 787 ACAAATAGGAGGCAATGACAGTATGAGGGTGGTTTGAAGCTTTTCTCGTGGT 846
Db 247 AGCCAAATTTGAAGAACATTTGGAAGAAATGAAGTGGTATTGTAAGTTTCCAGAGGC 306
QY 847 TATGAAAAATGGTTTCACTCTCTAGTGTACAGGTATCATCTACCTG ---GAGTGGGCT 903
Db 307 TATGAATCATTTGGCGTCCACAGATGCTGTGATGGTGGTTTATATCTCAAGAAATGGGCC 366


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: APPLICANT: Allen, Keith
: APPLICANT: Hoffman, Neil
: APPLICANT: Hurlburt, Patrick
: TITLE OF INVENTION: Expressed Sequences of Arabidopsis
: TITLE OF INVENTION: thaliana
: FILE REFERENCE: 2024 (PARA-013PRV)
: CURRENT APPLICATION NUMBER: US/09/770,149
: CURRENT FILING DATE: 2001-01-26
: PRIOR APPLICATION NUMBER: 60/178,506
: PRIOR FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 999
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 955
: LENGTH: 602
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-770-149-955

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Query Match	8.2%;	Score 257.8;	DB 10;	Length 602;
Best Local Similarity	75.1%;	pred. No. 2.5e-62;		
Matches 322;	Conservative 0;	Mismatches 107;	Indels 0;	Gaps 0;
QY	2334	CAGTATCATAAATGCACAGCGAGATTGGACCTGGGAGATGCAGATATTTAAGATACCG	2393	
Db				
	602	CAGTATGACAAATGCCGCGCAGATTGATCTTGGGATGCAGATTCTCAGATACCG	543	
QY	2394	TGGTTTCACAGAATTTGACCGGGGTATGTCAGTATCTTGAAGATAAATATCAGTTTATGAC	2453	
Db				
	542	CGGACTACAAGAATTTGATCAGGCAATGCAACATCTTGAAGAGAAATTTACGGTTTTATGAC	483	
QY	2454	TTCAGACACCAAGTTCATATCAGAAAGGATGAAGGATAGGATGATTTGATTTGAAAA	2513	
Db				
	482	TTCGGAGACCAATTCATATCAGAAAGACGAGCAGATAGAGTAATCGTATTCGAAG	423	
QY	2514	AGGAACCTAGTTTTGTCTTTAAATTTTCTACGCAAAAAGCTATTCAGACTATCGCAT	2573	
Db				
	422	AGGTGATCTCGTCTTTGTCTTTAACTTCTACGACGACGACTCTTTGATTTACGCGCAT	363	
QY	2574	AGCTGGCTGAAGCCTGGAAAATACAAAGTTGGCTTTGGACTCAGATGATCCACTTTTTGG	2633	
Db				
	362	TGTTTGCTCAAGCCTGGAAAATATAGATCGTATTGGACTCGACCGATCCTCTCTTTGS	303	
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Db				
	302	TGGATTCAATAGCTCGATCGCAAGCAGCAGTACTTCACTTAATGATGGCTTTATACACGA	243	
QY	2694	TGCTCTCTGTTCAATTTATGGTGTATGCACCTAGTAGAACAGCAGTGGTCTATGCACTAGT	2753	
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Db				
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RESULT 11
US-09-925-300-453
; Sequence 453, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL01
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 453

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[illegible]

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RESULT 12
US-09-770-444-893
; Sequence 893, Application US/09770444
; Patent No. US20020023280A1
; GENERAL INFORMATION:
; APPLICANT: Gortlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil

```

```

; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 2027 (PARA-016PRV)
; CURRENT APPLICATION NUMBER: US/09/770,444
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,502
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 893
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-770-444-893

Query Match      3.6%; Score 114.6; DB 10; Length 441;
Best Local Similarity 67.2%; Pred. No. 7.8e-22;
Matches 162; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 2535 TAATTTTCACTGGACAAAAGCTATTTCAGACTATCGACTATCGAGCTGGCTGAAGCTGGAAA 2594
Db 1 TAATTTTCCACTGGACCAACAGTTTACTCTGACTACCGTATCGGTTGCTCTCTTCCCGAAA 60

QY 2595 ATACAAAGGTTGCTTGGACTCAGATGATCCATTTTGGTGGCTTCGGGAGAAATTGATCA 2654
Db 61 GTACAAATCGTTTTGGACTCTGATAACTCTTTATTGGAGGCTTCAACCGGCTAGATGA 120

QY 2655 TAATGCCGATGTTTACCTTTGAAGATGGTATGATGATCGCTCGTTCAATTATGGT 2714
Db 121 CTCGGGGAGTTTTTACCTCTGATGGAAGCGACGAGTAGGCGTTGCTTCTTCTTATGGT 180

QY 2715 GTATGCACTAGTAGACACAGTGGTCTATGCACTAGTAGACAAAAGAAAGAA 2774
Db 181 GTATGCACTAGTAGACACAGTGGTCTATGCACTAGTAGACAAAAGAAAGAA 240

QY 2775 A 2775
Db 241 A 241

RESULT 13
US-10-025-380-304/c
; Sequence 304, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaugchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skelky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-025-380-304
Query Match      3.4%; Score 108; DB 9; Length 601;
Best Local Similarity 52.5%; Pred. No. 7.2e-20;
Matches 312; Conservative 0; Mismatches 270; Indels 12; Gaps 3;

QY 727 GAAATAGACCCCTTTTGACAAACTATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
Db 590 GAGATCGACCGGTACTTTGAAGCCCTACGCGCTGAGACTTCGCGCGAGGTATTAAGCAGTTT 531

QY 787 AAGAAAATGAGGAGGCAATTGACAAAGTATGAGGGTGGTTTGGAAAGCTTTTCTCCGTGGT 846
Db 530 AGCCAAATTTTGAAGACATTTGAGAAAATGAGGGTGGTTTGAATAGTTTTCAGAGGC 471

QY 847 TATGAAAAAATGGGTTTCTACTCGTAGTGTCTACAGGTATCACTTACCGT---GAGTGGCT 903
Db 470 TATGAATCATTTGGCGTCCACAGATGCTGCTGATGGTGGTTTATCTCAAGAATGGGCC 411

QY 904 CTTGGTCCCGAGTCACTGCTCTCATTTGGAGATTTCAACAATTTGGGACGCAAAATGCTCAC 963
Db 410 CCGGGAGCAGAAAGAGTTTCTTCTACTGGAGATTTTAAATGGTTGGAATCCATTTTCGTAC 351

QY 964 ATTATGACTCGGAATGAATTTGGTGTCTGGGAGATTTTCTGCGCAATAATATGTTGATGGT 1023
Db 350 CCATACAAAAAATGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTT 291

QY 1024 TCTCCTGCAATTCCTCATGGTCCAGAGTGAAGATACGATGGACACTTTCATCAGGTG-- 1081
Db 290 TCTTACTCGTGGCTCATGATCCAAATTTAAAGGTAGTTTACTAGTAAAGCGGAGAG 231

QY 1082 -TTAAGGATTCATTCCTGCTTGGATCAACTACTCTTTTACAGCTTCTCTGATCAATTCGA 1140
Db 230 AICTTGATTCGATTTTACCCTGGCAGAAAGTATGTTGGTTCGTGAAGGTGATATGTAAT 171

QY 1141 TATAATGGAATATATATATGATCCACCGGAGAGAGAGTATGTTCTTCCACACCCAGG 1200
Db 170 TATGATTGATACACTGGGATCC-----ACAACACTCATATGAGTTTAAAGCAATTCGCGA 117

QY 1201 CCAAGAAACCAAGTCGCTGAGATATATGATCTCATATTTGAATGATGATGATGTCGGAG 1260
Db 116 CCAAGAAACCAAGTCGCTGAGATATATGATCTCATATTTGAATGATGATGATGATGATGAT 57

QY 1261 CCTAAATTAATCACTACGTTGAATTTTAGAGATGAAGTTCTTTCCTCGCATAAA 1314
Db 56 GGAAGAGTACTTCTTATTAACATTTTATCATCAATGATGATGATGATGATGATGATGAT 3

RESULT 14
US-09-922-217-304/c
; Sequence 304, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaugchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 601
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Query Match 3.4%; Score 108; DB 10; Length 601;
Best Local Similarity 52.5%; Pred. No. 7.2e-20;
Matches 312; Conservative 0; Mismatches 270; Indels 12; Gaps 3;

QY 727 GAAATAGACCCCTTTTGACAAATGATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
DB 590 GAGATCGACCGGTACTTGAGCCCTTACGCCGTGGACTCCAGCGCAGTATTAAGCAGTTT 531
QY 787 AAGAAATGAGGAGGCAATTTGACAAATGAGGTGGTGTGGAAGCTTTTCTCGTGGT 846
DB 530 AGCCAAATTTTGAAGAACTTGAGAAATGAGGTGGTGTGGAAGCTTTTCTCGTGGT 846
QY 847 TATGAAAAATGSGGTTTTCACCTGCTAGTGTACAGGTATTCACCTGCTGCTGCTGCT 903
DB 470 TATGAAATCATTTGGCGTCCACAGATGCTGATGGTGGTGTGGAAGCTTTTCTCGTGGT 903
QY 904 CCTGGTCCCGAGTCCAGTCTCTCATTTGGAGATTTTCAACAATGGGAGCGCAATCTGAC 963
DB 410 CCGGAGCAGAGGAGTTTCTTACTGAGATTTTAAAGGTGGTGTGGAAGCTTTTCTCGTGGT 351
QY 964 ATTATGACTCGGAATGATTTGGTGTCTGGAGATTTTCTGCGCAATGATGATGATGATG 1023
DB 350 CCATACAAAAAATGATTTGAGAAATGGGAGCTGATATCCCAAGCAAGATATAA 291
QY 1024 TCTCTGCAATTCCTGATGGTCCAGAGTGAAGATACGATGCGACATTCATCAGGTG-- 1081
DB 290 TCTGACTCGTCCCTCATGGATCCCAATTAAGGTAGTTTACTAGTAAAGCGGAGAG 231
QY 1082 -TTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGCTTCTCTGATGAAATTC 1140
DB 230 ATCTGTATGCTATTTACCGTGGCAAGTATGTTGTTGTAAGGTGATAATGTGAAT 171
QY 1141 TATAATGGAATATATTAATGATCCACCGGAGAGGAGTATGTTCTTCCACACCCAGG 1200
DB 170 TATGATGGATACACTGGATCC-----AGACACTCATATGAGTTTAAAGCAATCCGGA 117
QY 1201 CCAAGAAACCAAGTCCCTGAGATATATGAATTCATATTTGGAATGAGTAGTCCGAG 1260
DB 116 CCAAGAAACCAAGTCCCTGAGATATATGAATTCATATTTGGAATGAGTAGTCCGAG 1260
QY 1261 CCTAAAATTAACCTCATAGTGAATTTAGAGATGAGTTCTTCTCGCATATAA 1314
DB 56 GGAAGATGAGTCTTCTTATAAATTTTACATGCAATTTTACATGCAATTTTACCAAGATCAAA 3

RESULT 15

US-09-833-263-304/c
; Sequence 304, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 304
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-833-263-304

Query Match 3.4%; Score 108; DB 10; Length 601;
Best Local Similarity 52.5%; Pred. No. 7.2e-20;

Matches 312; Conservative 0; Mismatches 270; Indels 12; Gaps 3;

QY 727 GAAATAGACCCCTTTTGACAAATGATCGTCAACACCTTGATTACAGGTATTCACAGTAC 786
DB 590 GAGATCGACCGGTACTTGAGCCCTTACGCCGTGGACTCCAGCGCAGTATTAAGCAGTTT 531
QY 787 AAGAAATGAGGAGGCAATTTGACAAATGAGGTGGTGTGGAAGCTTTTCTCGTGGT 846
DB 530 AGCCAAATTTTGAAGAACTTGAGAAATGAGGTGGTGTGGAAGCTTTTCTCGTGGT 846
QY 847 TATGAAAAATGSGGTTTTCACCTGCTAGTGTACAGGTATTCACCTGCTGCTGCTGCT 903
DB 470 TATGAAATCATTTGGCGTCCACAGATGCTGATGGTGGTGTGGAAGCTTTTCTCGTGGT 903
QY 904 CCTGGTCCCGAGTCCAGTCTCTCATTTGGAGATTTTCAACAATGGGAGCGCAATCTGAC 963
DB 410 CCGGAGCAGAGGAGTTTCTTACTGAGATTTTAAAGGTGGTGTGGAAGCTTTTCTCGTGGT 351
QY 964 ATTATGACTCGGAATGATTTGGTGTCTGGAGATTTTCTGCGCAATGATGATGATGATG 1023
DB 350 CCATACAAAAAATGATTTGAGAAATGGGAGCTGATATCCCAAGCAAGATATAA 291
QY 1024 TCTCTGCAATTCCTGATGGTCCAGAGTGAAGATACGATGCGACATTCATCAGGTG-- 1081
DB 290 TCTGACTCGTCCCTCATGGATCCCAATTAAGGTAGTTTACTAGTAAAGCGGAGAG 231
QY 1082 -TTAAGGATTCATTCCTGCTGGATCAACTACTCTTTACAGCTTCTCTGATGAAATTC 1140
DB 230 ATCTGTATGCTATTTACCGTGGCAAGTATGTTGTTGTAAGGTGATAATGTGAAT 171
QY 1141 TATAATGGAATATATTAATGATCCACCGGAGAGGAGTATGTTCTTCCACACCCAGG 1200
DB 170 TATGATGGATACACTGGATCC-----AGACACTCATATGAGTTTAAAGCAATCCGGA 117
QY 1201 CCAAGAAACCAAGTCCCTGAGATATATGAATTCATATTTGGAATGAGTAGTCCGAG 1260
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GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 16154066 seqs, 8097743376 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin:**

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8: em_htc:**

9: gb_est1:**

10: gb_est2:**

11: gb_htc:**

12: gb_est3:**

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27: em_gss_rod:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	488.6	15.5	728	14	BU008463

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13	411.8	13.0	717	14	BU005876
14	402.4	12.8	603	10	AW930851
15	398	12.6	825	12	BF065047
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27	371.4	11.8	560	14	BM885252
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33	346.4	11.0	602	12	BG524041
34	345.6	11.0	704	14	BU008407
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36	341.2	10.8	761	13	BM411030
37	340.4	10.8	592	10	BE402623
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VERSION	AY109521.1	GI:21213273		
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ORGANISM	Zea mays			
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AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whittitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.			
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes			
JOURNAL	Unpublished (2002)			
REFERENCE	2 (bases 1 to 2766)			
AUTHORS	Coe,E.C.			
TITLE	Direct Submission			
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA			
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BF065047 HV_CEB002
BQ240494 TaE05016F
BG521671 13-3 Stev
BE427534 PSR7153 I
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AW065909 687002G09
BG526727 63-11 Ste
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AV442128 AV442128
AW244197 687050F06
BI469105 sal07e09.
BI425610 sah9a11.
BM885252 sal97a08.
AW596011 sal96g03.Y
BM309136 sal55b02.
AJ432814 AJ432814
AV913706 AV913706
BU268430 BU268430
BG524041 38-25 Ste
BU008407 QGH7104.Y
BQ253050 sac05e05.
BM411030 EST585357
BE402623 CSB009H05
BO608128 BRY_4030
BQ240653 TaE05014F
BJ233506 BJ233506
BG651974 sac72d10.
AJ432886 AJ432886
BQ716536 AGENCOURT
BQ606935 BRY_2812
BI920158 EST540093

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/db_xref="MaizeDB:633976"
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/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
BASE COUNT 837 a 628 c 790 g 756 t 1 others
ORIGIN
Query Match 19.6% Score 619.8; DB 11; Length 3012;
Best Local Similarity 59.7%; Pred. No. 1.9e-148;
Matches 1177; Conservative 2; Mismatches 739; Indels 55; Gaps 6;
QY 721 ATTATGAAATAGACCCCTTTTGCAAACTATCGTCAACACCTTGATTACAGTATTC 780
DB 407 ATATACACCTGGACCCCAAGCTGGAGATATTCAAGGACCAATTCAGGTACCGGATGAA 466
QY 781 CAGTACAGAAATAGAGGAGGCAATTCACAAGTATGAGGCTGTTGGAGGCTTTTCT 840
DB 467 AGATTCTAGACGAAAGGATCAATTGAGAAAATGAGGAAGTCTTGAATCTTTCT 526
QY 841 CGTGTATGAAAAATGGGTTTCACCTGATGCTACAGGTATCATCTACCTGAGTGG 900
DB 527 AAGGCTATTTGAAATTTGGATTAATCAATGAGGATGGAACGTATATCGTGAATGG 586
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QY 1021 GGTTCCTCGCAATTCCTCATGGGTCCAGAGTGAAGATACGATGGACATTCATCAGT 1080
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QY 1137 ---TCCATATATGGAATATATTATGATCCACCGAGAGAGAGGATGCTCTTCCACAC 1194
DB 824 GTCCTATATGATGGTGTTCATTTGGATCTCTGCTTCTGTTGAAAGGTACACATTTAAGCAT 883
QY 1195 CCACGCGCAAGAAACCAAGTCCGTGAGATATATGATCAATCAVATTCATGAGTGTAGT 1254
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QY 1255 CCGGAGCCPAAATTAACATACATGATTTAGATTTAGATCAAGTCTTCTCTCCATATA 1314
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DB 1004 GCAATTAATATCAACACAGTTCAGTTGATGGGAGTATGAGGATTCGTACTATGCTTCT 1063
QY 1375 TTTGGTTATCATGTCAAAATTTTTCACCAAGCAGCGGTTTTCAGAGCCCGAGAC 1434
DB 1064 TTCGGGTACCATGTGACAAATTTCTTTGGGTTTTCAGCAGAGATCAGCAGCAGAGAC 1123
QY 1435 CTTAAGTCTTTGATTAATGAGCTCATGAGCTAGGATTTCTTCTCATGGACATTTGT 1494
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QY 1495 CACAGCCATGCATCAAAATATACTTTAGATGGAGTGAACATGTTTGACG-----GC 1545

2043 GGTGTTTCATACGCTGAAGATCATGATCAAGCTAGTCTGATGATGATGATGATGATGAT 2102
DB 1783 GTGTGTAACTTATGCTGAAGATCATGATCAAGCTAGTCTGATGATGATGATGATGATGAT 1842
QY 2103 CTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2162
DB 1843 TTTGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1902
QY 2163 AATAGATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2222
DB 1903 CATGATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1962
QY 2223 AGAAGGTTACCTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2282
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QY 2403 AGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2462
DB 2143 AGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2202
QY 2463 CCAATTCATATCAGAAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2522
DB 2203 CCAGTATATTTCCGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2262
QY 2523 AGTTTGTCTTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2582
DB 2263 GGTATTTGTTCAACTTCCACTGCAACACAGCTATTTGATGATGATGATGATGATGATGATGAT 2322
QY 2583 GAACCTCGAAATACAGGTTGCTTGGACTCAGATGATGATGATGATGATGATGATGATGATGAT 2642
DB 2323 AAGCCTGGGGTGTATAGGTTGCTTGGACTCAGCTGATGATGATGATGATGATGATGATGATGAT 2382
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DB 2383 CAGGATCATCAACGAGCGGAGCTTCCAGCGGAGCTTTCAGGATGATGATGATGATGATGATGAT 2442
QY 2703 TTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2756
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RESULT 3
AY105679
LOCUS 3012 bp mRNA linear HTC 25-MAY-2002
DEFINITION Zea mays PC0072723 mRNA sequence.
ACCESSION AY105679
VERSION AY105679.1 GI:21208757
KEYWORDS HTC.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 3012)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanarey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
unpublished (2002)
2 (bases 1 to 3012)
Coe,E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
Location/Qualifiers

Db 1184 CATAGCCATGCAATTAATATGTCACAGATGGTTAAATGCGCTATGATGTTGGCAAAAGC 1243
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QY 1905 AGATGGGGTGTGGCTTTGACTATCGGCTGCATATGCAATGCTGATAAATGATGTA 1964
Db 1604 TGAAGTGGGGTGTGGTTTGACTATCGCTGCAATGGCTATCCCTGATAGATGATGTA 1663
QY 1965 GTTGCTCAAGAAACGGGATGA---GGATGGAGATGGGTGATATGTTTCAATACACTGAC 2021
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QY 2022 AATAGAGATGCTGGGAAAGTGTGTTTCATACCTCAAGCTCAAGTCAAGTCAAGTCTAGT 2081
Db 1724 TAACAGGAGATATCTGAAATGATCCCATATGCTGAGAGCCATGATCATCTATGCT 1783
QY 2082 CGGTGATTAACACTATGACTCTGCTGATGCACAAAGATATGATGATTTATGGCTTT 2141
Db 1784 TGGCGCAAAACTATGCTATTCCTGATGCGACAGGAATGATACCTGGCATGTCAGA 1843
QY 2142 GGATAGACGCTCAACATCAATATAGATCGTGGGATGCAATGCAAGATGATAGGCT 2201
Db 1844 CTTGACCGCTTCTTCACTCAATGATGCGAGGATGCACTCCAAAGATGATTCACCT 1903
QY 2202 TGTAACTATGGGATTAGGAGGAGGAGTACCTAAATTTCTATGGAATGAATTCGGCCA 2261
Db 1904 CATCAAAATGGCCCTTGGAGTATGCTACTTGAATTTATGGGAAATGATGTTGTC 1963
QY 2262 CCTGAGTGTGATTTCCCTAGGGCTGAACACACCTCTCTGATGGCTCAGTAATTC 2321
Db 1964 CCAGATGATGATGCTTCCAGAGAA----- 1991
QY 2322 CGGAACCAATTCAGTTATGATAAATGACAGCGGATTTGACCTGGAGATCGAGAATA 2381
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Db 2051 CTTGCGGTACAAGTACATCAATCGGTTTGACCAAGCGTGAATGCGCTCGATGAGAGAT 2110
QY 2442 TGAGTTTATGACTTACAGACACAGTTCATATCAGAAAGGATGAAGGAGATAGGATGAT 2501
Db 2111 TTCCTTCCCTTCGCTCAAGACAGATGCTGACGACATGACGATGAGGAAGAGTTAT 2170
QY 2502 TGATTTTAAAAAGAAACCTAGTTTGTCTTTTATTTTCTACTGACGAAAAAGCTATTC 2561
Db 2171 TGTCTTTGACGTGAGATTTAGTTTGTCTTCAATTTCCATCCCAAGAAACTTACGA 2230
QY 2562 AGACTATCGATAGGCTGGCTGAAGCTGGAAATACAGGTTGCTTGGATCGATGTA 2621
Db 1184 CATAGCCATGCAATTAATATGTCACAGATGGTTAAATGCGCTATGATGTTGGCAAAAGC 1243

Db 2231 GGGCTAACAAAGTGGGATCGGATTGCTGCTGGGAAATACAGAGTAGCCCTGGACTCGATGC 2290
QY 2622 TCCACTTTTGTGCTCGGGAGAAATGATCATATGATGCGCAATGTTTCACCT 2674
Db 2291 TCTGGTCTCGGTGGACATGGAAGAGTTGGCCACGACGTGGATCATTTCAGT 2343
RESULT 4
AK009815 2738 bp mRNA linear HTC 19-JAN-2002
LOCUS Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310045H19:homolog to 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING ENZYME) (BRANCHER ENZYME), full insert sequence.
ACCESSION AK009815.1 GI:12844841
VERSION HFC: CAP trapper.
KEYWORDS Mus musculus
SOURCE Mus musculus (strain:C57BL/6J) adult male tongue cDNA to mRNA, clone:2310045H19.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20493374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Konno, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kado, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schiraldi, L., Staudli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schombach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S. and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660

Db	1011	ACCTGGGAAGTTTTAAGATTCCCTCTGTCGAACATAGATGGTGGTGGAGGAGTACTGC	1070
Qy	1681	TTTGTGTGATTTAGATTTTCATCGTGTGACATCAATAGATGTATCTACCACGGATTATCG	1740
Db	1071	TTTGATGGCTCCGTTTGTGAGGTGTACCTCTATCTATCATCATCACCACGGAATGGGT	1130
Qy	1741	GTGGGATTCACHTGGGAATCTACGAGAAATACTTTGGACTCGCAACTCATGTGRATGCTGCC	1800
Db	1131	CAAGGTTTTTCGGGTGACTATTAATCAATATTTTGGACTACAAGTAGATGAAGAAGCTTTG	1190
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Db	1191	ATTTATCTCATGTTGGCAAAATCATTTGGCTCACAGTTGTACCCAGACTCGATACAAATA	1250
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Db	1251	GCAGAGGATGATCAGGGATCGCGCTCTCTGTTCTCCAACATTCACGAGGAGCGGTGT	1310
Qy	1921	TTTTCACATCCGCTGCATATGCGCAATTCGTGATAAATGGATGTGCTCAAGAAA---	1977
Db	1311	TTTGACTACAGATTAGCAATGGCTATTCAGATAAATGSATCCCAATTACTTAAAGNATTT	1370
Qy	1978	CGGATCAGGATTCGGAGTGGGTGATATCTTATACACACTGCACAAATAGAGATGGTGG	2037
Db	1371	AAAGATGAAGACTGGAATATGGGCAATAAGTGTATACTCTCACAAATCGACGCTACCTT	1430
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Db	1431	GAAAAATGTGTGGCTTATGCAGAGAGTCATGATCAGGCATTTGGTGTGTGCACAGACATG	1490
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Qy	2218	GGAGGAGAAGGTTACCTAAATTTTCATGGGAAATGAATTCGCCACCTCGATGATTTGAT	2277
Db	1611	GGTGGAGAAGGCTATCTCAATTTTCATGGGTAAATGAGTTTGGGCATCTGAAATGTTGAC	1670
Qy	2278	TTCCCTAGGGCTGAACAACACCTCTCTGTAGGCTCACTAATCCCGGAAACCAATTCAGT	2337
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Qy	2638	TTCCGGGCAATTGATCATATATGCCGAATGTTTCACCTTTTGAAGGATGGTATCATGATCGT	2697
Db	1998	CATCAGAGACTTGGACCACAAACCAACTACTTTTGTGAGGCTTTTGACATAATGGCGC	2057
Qy	2698	CCTCGTTCAATTTATGGTGTATGCACTAGTAGACAGCAGTGGTCTATGCCTAGTAGAC	2757

Db	2058	CCCTATTCTCTTCGTGACATTCCAAGCCGAGTGGCTCTCATCTTCAGAAATGTGGAT	2117
Qy	2758	AAAGAAGAAGAAGA	2774
Db	2118	CTGCAAAACTGAAGAGA	2134
RESULT 5			
AI487345			
LOCUS			
DEFINITION	AI487345	656 bp	linear
ACCESSION	EST245667	tomato ovary,	TAMU Lycopersicon esculentum cDNA clone
VERSION	CLD13M4,	mrna	sequence.
KEYWORDS	AI487345		
SOURCE	EST		
ORGANISM	tomato.		
AUTHORS	Lycopersicon esculentum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.		
	1 (bases 1 to 656)		
	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,I., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.		
TITLE	Generation of ESTs from tomato carpel tissue		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: CUCI		
	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Email: http://www.genome.clemson.edu/orders/index.html .		
FEATURES	Location/Qualifiers		
source	1..656		
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	/tissue_type="carpel"		
	/dev_stage="5 days pre-anthesis to 5 days post-anthesis"		
	/lab_host="Xil-Blue MRF"		
	/note="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST library. Oligodm-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."		
BASE COUNT	207 a	106 c	149 g
ORIGIN			194 t

Query Match	15.8%;	Score 499.6;	DB 9;	Length 656;
Best Local Similarity	90.7%;	Pred. No. 1.2e-117;		
Matches 584;	Conservative 0;	Mismatches 39;	Indels 21;	Gaps 4;
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QY	2488	GGAGATAGGATGATGTATTTGAAAAGGAAACCTAGTTTTTGCTTTAAATTTTCACTGG	2547	
Db	61	GGAGATAGGATGATGTATTTGAAAAGGAAACCTAGTTTTTGCTTTAAATTTTCACTGG	120	
QY	2548	ACAAAAGCCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAATACAAAGTTGCC	2607	
Db	121	ACAAATAGCTATTCAGACTATCGCATAGGCTGGCTGAAGCCTGGAAATACAAAGTTGCC	180	
QY	2608	TTGGACTCAGATGATCCACATTTTGGTGGCTTCGGGAGAAATGATCATAATGCCGAATGT	2667	
Db	181	TTGGACTCAGATGATCCACATTTTGGTGGCTTCGGGAGAAATGATCATAATGCCGAATGT	240	
QY	2668	TTCACTTTTCAAGAGTGGTATGATGATCGTCTCGTTCAATATATGGTGTATGCACCTAGT	2727	

KEYWORDS
SOURCE EST
ORGANISM Lactuca sativa.
 Lactuca sativa.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
 Lactuca.
 1 (bases 1 to 713)
REFERENCE
AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
 Church, S., Jackson, L., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://compenomics.ucdavis.edu/
 Unpublished (2002)
TITLE Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.org [michelmore@vegmil.ucdavis.edu]
 belongs to contig QG_CA_Contig6851, see http://cgpdb.ucdavis.edu/
 for details.
FEATURES Plate: QGF10 row: L column: 08.
 Location/Qualifiers
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 /cultivar="L. serriola"
 /db_xref="taxon:4236"
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 /clone_lib="QG_EFGHJ lettuce serriola"
 /lab_host="E.coli"
 /note="Vector: pBRCDNASFIAB; The library was constructed
 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize
 size bias. Details of each source of RNA and library
 construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_LIB-QG_EFGHJ lettuce serriola
 TAG_TISSUE=flowers post-fertilized
 TAG_SEQ-TGCCATCGGG"
BASE COUNT 221 a 132 c 146 g 214 t
ORIGIN
 Query Match 15.2%; Score 479.4; DB 14; Length 713;
 Best Local Similarity 79.5%; Pred. No. 2e-112;
 Matches 567; Conservative 0; Mismatches 146; Indels 0; Gaps 0;
 QY 859 GGTTCCTACTGCTAGCTACAGGTATCACTACCTGAGTGGCTCTCTGGTGGCCAGTCA 918
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 QY 919 GCTGCTCTCATGTGAGATTTCAACAATTTGGGACGCAATGTCACATTATGACTCGGAAT 978
 Db 61 GCTTCACCTTATGGAGATTTCAACAACCTGGAATCCAAATGCTGATGTAAGACCCGGAAT 120
 QY 979 GAATTTGGTGTCTGGAGATTTTCTGCCAAATTAATGTGGATGTTCTCTCGCAATTCCT 1038
 Db 121 GAATTTGGTGTCTGGAGATTTTCTGCCAAACATGTTGATGTTCTTCACCTATTCCT 180
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 Db 181 CATGGTTCGAGTAAGATTCGTATGATGATGACGCAATGATTAAGACTCGATTCCT 240
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 Db 241 GCTTGGATCAAGTTTTCAGTACAAGCACCTGGTGAAGTTCCTTATATGAATGAATATAT 300
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Db 301 GATCCCCCACAAGAGAGAAAATACGTTTTCACATCCAGACCAAGAGCGGAATCT 360
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RESULT 8
BI308555
LOCUS
DEFINITION EST529965 GP0D Medicago truncatula cDNA clone pgPOD-7017 5' end,
 mRNA sequence.
ACCESSION BI308555
VERSION BI308555.1 GI:14982882
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 689)
REFERENCE Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho
 J., and Fraser, C.M.
AUTHORS ESTs from developing reproductive tissues of Medicago truncatula
 Unpublished (2001)
TITLE Contact: Michael A. Grusak
JOURNAL USDA/ARS Children's Nutrition Research Center
COMMENT Baylor College of Medicine
 1100 Bates Street, Houston, TX 77030-2600, USA
 Tel: 713-798-7044
 Fax: 713-798-7078
 Email: mgrusak@bcm.tmc.edu
 B395410e

FEATURES TIGR sequence name: MTOAQ93TK
 More information is available at: www.medicago.org
 Seq primer: SKmod (CTA GAA CTA gta gAT CC).
 Location/Qualifiers
 1..689
 /organism="Medicago truncatula"
 /cultivar="Al7"
 /db_xref="taxon:3880"
 /clone="pgPOD-7017"
 /clone_lib="GP0D"
 /tissue_type="immature pod walls"
 /dev_stage="Immature pods, ranging in age from 15 to 30
 days after pollination"
 /note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; Immature pods, ranging in age from 15 to 30 days
 after pollination, were collected from greenhouse-grown
 plants. At harvest, seeds were removed from pods and
 isolated pod walls were collected and immediately frozen


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Db      122 GCGATTAATGGAATGAACTCTCAAGCAAGAGTGAGCAATCTTGGAAATGGCGCATATT 181
QY      2008 GTTCAATACACTGACAAATAGAAGATGGTCGGAAGAGTGTTTCATACGCTGAAAGTCAT 2067
Db      182 GTGCACACCCCTAACAAATAGAAGTGCGGTGAGAAGTGTTGCTCATTATGCAAAAGTCAT 241
QY      2068 GATCAAGCTCTAGTGGTGGTGAATAAATACTATAGCATTTCTGGCTGATGGCAAGGATATGAT 2127
Db      242 GATCAAGCACTAGTTGGTGACAAGACTATGTGATCTGTTGATGGATAGGATATGAT 301
QY      2128 GATTTTATGGCTTGGATAGACCGTCAACATCAATTAATAGATCGTGGGATAGCATTCAC 2187
Db      302 GATTTTATGGCTTGGATAGACCGTCAACCCCTCGCATTTGATCGTGGCATAGCATTACAT 361
QY      2188 AAGATGATAGGCTTGAATGATGGATAGGATAGGAGGAGGATGATCTTAATTTTCAATGGA 2247
Db      362 AAAATGATCAGGCTTGTCACCATGGTTTGGTGGCAGAGGCTATCTTAATTTTCAATGGA 421
QY      2248 AATGAATTCGCCACCCCTGAGTGGATGATTTCCCTAGGCTGGAACAACACCTCTCTGAT 2307
Db      422 AATGAGTTTGGCATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 481
QY      2308 GGCTCAGTAATTCGCCGGAACCAATTCAGTTATGATTAATGATGATGATGATGATGATGAT 2367
Db      482 GGCAAGTCTCCCTGGCAATAACAATAGTTATGATTAATGATGATGATGATGATGATGAT 541
QY      2368 GGAGATCAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2427
Db      542 GGAGATCAGAAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 601
QY      2428 CTTGAAGATAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2487
Db      602 CTTGAGGAAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 661
QY      2488 GGAGATAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2546
Db      662 GAAGATAAGTGAACATCTTTGAAAGAGGAAATTTGGTATTTGTTTCACTTCCCTG 721
QY      2547 G 2547
Db      722 G 722

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AV939010      678 bp mRNA linear EST 18-JAN-2002
AV939010 K. Sato unpublished cDNA library, strain H602 adult,
heading stage top three leaves Hordeum vulgare subsp. spontaneum
cDNA clone bah20e24 5', mRNA sequence.
AV939010      1 GI:18234807
EST.
Hordeum vulgare subsp. spontaneum.
Hordeum vulgare subsp. spontaneum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Hordeum.
1 (bases 1 to 678)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
1..678
/organism="Hordeum vulgare subsp. spontaneum"
/strain="H602"

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/db_xref="taxon:77009"
/clone_lib="bah20e24"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT      193 a      135 c      154 g      194 t      2 others
ORIGIN

Query Match      13.6%; Score 430.6; DB 10; Length 678;
Best Local Similarity 78.3%; Pred. No. 7.6e-100;
Matches 528; Conservative 0; Mismatches 145; Indels 1; Gaps 1;

QY      880 GGTATCAGTACCGTG-AGTGGCTCCTGTCGCCAGTCAGCTGCTCTCATGGAGATT 938
Db      5 GGTATCAGTACCGAGNAATGGCTCTCTGGNGCCATCTCTGAGCATATTAGTAGTACCT 64
QY      939 CAACAATTGGGACGCAAAATGCTGACATATTGACTCGGAATGAATTGGTGTCTGGGAGAT 998
Db      65 CAACAATTGGAAACCCAAATGCGATATGATGACGAGAGATGATTATGGTGTGGAGAT 124
QY      999 TTTTCTGCCAAATATGTTGGTGTCTCTCGAATTCCTCAATTCCTCAATTCCTCAATTCCT 1058
Db      125 TTTCTCTCCCTAACAAATGCTGATGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 184
QY      1059 ACAGATGACACTTTCATCAGGTGTTAAAGGATTCCTGCTTGGATCACTACTCTTT 1118
Db      185 ACGGATGATGATCTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY      1119 ACAGTCTCTGATGAATTCATATGGAATATATGATGATGATGATGATGATGATGATGAT 1178
Db      245 GCAGGCTCCAGGTGAAATACCATTCATGCGCATATATGATGATGATGATGATGATGATGAT 304
QY      1179 GTATGCTCTCAACACCCACCGCCCAAGAACCAAGTCCGTGAGATATATGATGATGATGAT 1238
Db      305 GTATGCTCTCAACATCTCTCAACCTAAACGACGAGTCACTAAAGGATATGATGATGATGAT 364
QY      1239 TATTGGAATGAGTACGCGAGCGCTTAAATTAACCTCATACCTGATGATGATGATGATGATGAT 1298
Db      365 CATTGGAATGAGCAGCGCGGACCGAAGATTAATTCATATGCTAATTTAGGATGAGGT 424
QY      1299 TCTTCTCGCATAAAAACCTTGGGTACAATTCGCGTCAAAATATGCTATTCAGAGCA 1358
Db      425 GCTGCCAAGAATTAAGAGGCTTGGATACAATGCAATGCAATGCAATGCAATGCAATGCAAT 484
QY      1359 TTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1418
Db      485 TTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 544
QY      1419 TGAACGCGCGACGAGCTTAAAGTCTTTGATGATGATGATGATGATGATGATGATGATGAT 1478
Db      545 TGGAACTCCAGAGGACTTAAATCCCTTGATGATGATGATGATGATGATGATGATGATGAT 604
QY      1479 TCTCATGAGCATGTTTTCACAGCGCATGATCAATCAATCAATCAATCAATCAATCAATCAAT 1538
Db      605 TCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
QY      1539 TGAAGGCGCAGATA 1552
Db      665 CGATGGCACTGATA 678

RESULT 11
BE602527
LOCUS
DEFINITION
HVSMEh0099J22f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0099J22f,
mRNA sequence.
ACCESSION
BE602527
VERSION
BE602527.2 GI:13190371
KEYWORDS
EST,
SOURCE
Hordeum vulgare.
ORGANISM
Hordeum vulgare

```


Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact: cou@resgen.com web site:
www.resgen.com

Seq primer: -40RP from Gibco
High quality sequence stop: 421.

FEATURES

Location/Qualifiers
1..573

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1059-4491"
/clone_lib="Gm-c1059"
/tissue_type="Whole seedling, 2 week old, etiolated"
/lab_host="DH10B"

/note="Vector: pBluescript II SK+; Site:1: EcoRI; Site:2:
XhoI; The cDNA library was constructed from mRNA isolated
from 2 week old etiolated whole seedlings of PI468916.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The cDNA fragments
were directionally cloned into the EcoRI- XhoI restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker at Iowa state university."

169 a 110 c 126 g 167 t 1 others

Query Match 13.1%; Score 413.8; DB 13; Length 573;
Best Local Similarity 82.5%; Pred. No. 1.5e-95;
Matches 472; Conservative 1; Mismatches 99; Indels 0; Gaps 0;

QY	1135	ATTCCATATATGAATATATATGATCCACCCGAGAGAGAGTATGCTTCCACAC	1194
Db	1	ATTCCATACAGCGAATATATGATGATCCCGAGAGAGAAATATGCTTCCACAT	60
QY	1195	CCAGGCCAAAGAACCAAGTCGCTGAGATATATGAATCTCATATGGAATGAGTAGT	1254
Db	61	CCAGGCCAAAGAGACCAAAATACATAGATATATGAGTCACACATCGGAATGAGCAGT	120
QY	1255	CCGAGGCCAAATTAACATACATGCTGAATTTAGAGATGAAGTCTTCCTCGCATAAA	1314
Db	121	CCGAGGCCAAATTAACATATGCTGAATTTAGAGATGAAGTCTTCCTCGCATAAA	180
QY	1315	ACCTTGGGTACATCGCGTGCAGATATGCTGATTCAGAGCATCTTATTATGCTAGT	1374
Db	181	AGGCTTGGCTATAATGCTGCCAGATTATGGCTATCCAGAACATCTTATTATGCCAGC	240
QY	1375	TTTGGTTATCATGTCACAAATTTTTCGACCAAGCAGCCGTTTTCGACGCCGACGAC	1434
Db	241	TTTGGTTATCATGTCACAAATTTTTCGACCAAGCAGCCGTTTTCGACGCCGACGAC	300
QY	1435	CTTAAGTCTTTGATTGATAAAGCTCATGAGCTAGGATTTGTTGCTTCATGACATGTT	1494
Db	301	CTTAAGTCTTCATAGACAGACCCCATGAACTGGGTCCTGCTTCTGATGATATTGTA	360
QY	1495	CACAGCCATGATCAAAATATCTTTAGATGACCTGAACATGTTTTCGACGCCAGATAGT	1554
Db	361	CACAGCCATGATCAAAATATCTTTAGATGACCTGAACATGTTTTCGACGCCAGATAGT	420
QY	1555	TGTTACTTCTATCTCGGAGCTCGTGTATCATGATGTTGGGATTCGCGCTCTTTTAA	1614
Db	421	CATTACTTCTATCTCGGAGCTCGTGTATCATGATGTTGGGATTCGCGCTCTTTTAA	480
QY	1615	TATGAAACTGGAGGTACTTAGGTATCTTCTCAATGCGAGATGTTGGTGGATGAG	1674
Db	481	TATGAACTGGAGGTACTTAGGTATCTTCTCAATGCGAGATGTTGGTGGATGAG	1706
QY	1675	TGCAAAATTTGTTGATTTAGATTTGATGGTGT	1706
Db	541	TACNAGTTTGAATTTGATTTGATGGTGT	572

RESULT 13

BU005876

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BU005876 717 bp mRNA linear EST 22-AUG-2002
QGG9F08.yg.abl QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGG9F08, mRNA sequence.

BU005876
BU005876.1 GI:22440271

Lactuca sativa

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
Lactuca.

1 (bases 1 to 717)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L., and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)

Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig6851, see http://cgdb.ucdavis.edu/
for details.

Plate: QGG9 row: F column: 08.

Location/Qualifiers
1..717

/organism="Lactuca sativa"
/cultivar="L.serriola"
/db_xref="taxon:4236"

/clone="QG9F08"

/lab_host="E.coli"

/note="Vector: pRCNDSFIAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_LIB-QG_EFGHJ lettuce serriola
TAG_TISSUE=germinating seeds

TAG_SEQ=TCGTGCGGG

BASE COUNT 233 a 122 c 155 g 206 t 1 others

ORIGIN

Query Match 13.0%; Score 411.8; DB 14; Length 717;
Best Local Similarity 75.1%; Pred. No. 5.4e-95;
Matches 526; Conservative 0; Mismatches 173; Indels 1; Gaps 1;

QY 645 TTCTGAGAGACAATTTATGATGAAATAGACCCCTTTTGACAACTATCGTCAACCT 704

Db 19 TTCTTTATTTGATATTGATAAAGAAAGTGAAGAATTAGAAATATTCGATTCCTCC 78

QY 705 TGGACTTGTGACAGATTTATGAATAGACCCCTTTTGACAACTATCGTCAACCT 764

Db 79 TGGAAAGGGGAGAAATATATGAATTTGATCCACTTTTAAGCAATCATCGTGAACAT 138

QY 755 TGATTACAGGTATTCACAGTACAAAGAAATGAGGAGCAATTCACAGTATGAGGGTGG 824

Db 139 TCAGTATAGATTTACATTTACAGAGATCGTGAAGCAATTTGACAAATATGAGGTGG 198

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